

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1253:

5 TTAGTAGTCA TCGGTATTGG TGGTTCCTTAC TTAGGTGCAC GTGCAGCAAT CGAmATGTTA 60  
 ACGTCATCAT TTAGAAACAG CAATGAATAC CCTGAmATTG TATTTGTTGG TAATCACTTA 120  
 TCATCAACAT ATACGAAAGA GTTAGTTGAT TATTTAGCAG ACAAAGATTT CTCTGTAAAC 180  
 10 GTTATTTCTA AATCTGGTAC AACTACAGAA CCAGCAGTTG CATTAGATT GTTCAAACAA 240  
 TTAGTTGAAG AAAGATACGG TAAAGAAGAA GCACAAAAAC GTATATTGTC AACACGGAT 300  
 AAAGAAAAAG GngCTTTTAAA ACAGTTGGCT ACAAACGAAG GTTATGAAAC GTTTATCGTA 360  
 15 CCTGATGATG TAGGTGGAAG ATATTCTGTT TTAACAGCAG TAGGATTATT ACCAATTGCA 420  
 ACAGCTGGAA TTAACATCGA AGCTATGATG ATTGGTGTCTG CA 462

## (2) INFORMATION FOR SEQ ID NO: 1254:

- 20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 25 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1254:

30 ACTCATAAGT GAATGGTTGA TTACCACTAG TTAAAACTTC ATATACTATA GTTCTTTTTT 60  
 TTATTTTGCA ATTAGTTATT TTCATTATAA ACTTCCTTTC AAACACTGCT GAAATAGACG 120  
 TCTTTTTTCAA ATAAGCATGA TTAATACTTC AATTCTTTAA TCCACATATA TTTAAAAGTG 180  
 35 AGGTAGTAGG TAATAAATAT AAGACTTAAA GTTAAGATTG CTTTTTTCAT GTTTCATAAT 240  
 TAAACCTCT GTAAATTTAA GGTAGTATT ATGAAATAAT GGATTGGTTT ATTCTTTAGT 300  
 ACTAACTTCG TAGTAAATTA TATAGTTCGC TAAATTGTAT TTATCTACTA TATTTTGGGA 360  
 40 ATAAACAATT TCCTTTTCTT TCTTCAGTAA ATTATAAAAA 400

## (2) INFORMATION FOR SEQ ID NO: 1255:

- 45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 137 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 50 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1255:

nAATCTATGT ATGGGGGCAT CCAAAGATTT CATAGACTAC TTATTTGTTG ATGAAGCCGG 120  
ACAAGCAATC CTCAAGC 137

(2) INFORMATION FOR SEQ ID NO: 1256:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 139 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1256:

TGAAATGTAG AAATTGAATT AGAAATGAAG ATTAAAAATC nACACGTATC GTTCAAGTGG 60  
TGCAGGTGGT CAGCCGTAAA CACAACTGAC TCTGCGTACG TATTACCATT TCCACTGGTG 120  
TCATTGCAAC ATCTTCTGA 139

(2) INFORMATION FOR SEQ ID NO: 1257:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 177 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1257:

TTACCAntTA TTtTAACACC ATGTTTtagAC CAATTTGATC TGACTAAATT AATCGCTGTT 60  
TGTACCTCCA AATTGTTACA ACGTACACCT TTAGTTTTTC TAAATTAATG TATATTCATC 120  
ACATCTTCTT CAGTTAAGGG TCAAAGTATA ATTGTGCGAA ATTGTGAAGT CGTTGTA 177

(2) INFORMATION FOR SEQ ID NO: 1258:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 250 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1258:

AAGACCAACC GAAATGAATA TCGACATGGA TTAAGCCTAT ATTCAGATGT AAACGGCGAT 60  
TATATTAAAA AGCCAATTAC AGAATGTAGT GGTTAATGAA ATATGCCCAA GAATGGGCTG 120  
TATCACTTAG GTGTATCAAA CTGACCAAAA ATTGGAAGGA CTTTAGGCCA AAAACCATGC 180



TTAATTTTTC

250

## (2) INFORMATION FOR SEQ ID NO: 1259:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 170 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1259:

ACATTTCACGG GACATTTTCAT TACATCACCC TGCTTTATTT TGGATTATGG CCTAATTTAT 60  
 ACTGATAAAT CTAGGAGGTG GAAAAAGAA TGCCCTGCAA TTTAATTnCA TTTAACCAAA 120  
 TAATGAAACA ATAAAAACA TTATATCGTT ACTTATTAAG TAATTTGGCA 170

## (2) INFORMATION FOR SEQ ID NO: 1260:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 313 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1260:

TTTGTACTION GATACGTTGT ATTGAGGTG ATGACACTAG GAATTTGTAA TGATCAATTT 60  
 CTCTAATTCT TTACAATTGA TAGAATTCTT CGATTTGTGG ATAGACATTC ATATCATTGT 120  
 CTAATGATTT TTGGTGATTC ATAAATGTG ACTAAGCTT GGATGCTTTA GGATTGTAGC 180  
 TGAGACACAT GTTGCCTGAC TGNnGATTTA TCAnATAATC TCAATCACGT GATCCnATCA 240  
 CATTATCAG CTCATAAAT CAAGATGATC GTCGTTTATG GGCGATTAAT GGCGTACCGC 300  
 CAGTGTCGGC ACG 313

## (2) INFORMATION FOR SEQ ID NO: 1261:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 206 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1261:

TAGCGATCAT TTAATCAAGG TTAGATTATT TAATGTCAGC ATTACGTTTG ACAATGAACT 60

GTTTGAGGTT ATCACAATGC CATTTAACAC TATGCGCACA TGGCTGAACT AATnAGCGAC 180  
 GAGATGACTT CAAACCTTGA TTAGGT 206

(2) INFORMATION FOR SEQ ID NO: 1262:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 144 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1262:

AAGTGTGTAC ACGATAGCTA AACTCAAATA TCACAGAACA ACAAATGTCT TAGTACTTTG 60  
 TGCCGGTGGT GGTACAAGTG GATTATTAGC CAATGCACTA ATAAAGCAGC TGAAGAATAT 120  
 CATnTGCCAG TGAAAGCGGC ACTG 144

(2) INFORMATION FOR SEQ ID NO: 1263:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 132 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1263:

ATAACGACAC CTAATGCAAT TTGAATAAAG CAGTAGAATT TGTGGGAATC GATTATTGAT 60  
 AACCGAAGTA ATAATCACAG CAAAAATAAA ATTAAAAATG CTCTAATAGT GCCTACATnC 120  
 TCCTCAAATT TT 132

(2) INFORMATION FOR SEQ ID NO: 1264:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 159 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1264:

TATGTCAATT TCGTAGAATT GGTTTTAnGC GCTATTTAGA ATAGCCATCA GATAAAAATCA 60  
 TTATTTAAAC GTATAATAGG TCAAAATATA GAGAGTTACT ATACAAATTT CTAACTTTCA 120  
 CTTAAATAAA AATATATATA ATTAAAGTGG AGGAGAAGG 159

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1265:

ATAGCTCAAG CAATCATTAT GTTTATAATG ATTGTATGGT TCTTTATAGA TGCTTTATTG 60  
 ATTAATTAAT AAAAAGCTTA TTGCAAAATA TGTTTTTCGG TAACTGTAAT TTAGTGATT 120  
 TATCATTAAAC AG 132

## (2) INFORMATION FOR SEQ ID NO: 1266:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1266:

CATGGATTTA TCTTAGCGAT TGGTCTAATT TTACCTTTAG GTGCACAAAA TGTATTTATT 60  
 TTAAACCAAG GAGCTAATCA ACCAAAATAT AGATATGTAT TGCCTGCAAT AATTACAGCC 120  
 GGGTTGTCAG ACAGCTTACT TATTATTATT GCAGTGGTAG GAGTWTCTAT CATTATTATG 180  
 TCTTTACCTG TACTTCAWGC AWTATTTTAT ATAGTTGGTT TAATTTTCTT GATGTATATG 240  
 GCTTGGACCA TTTGGCATGA TAAACCCTCA ACAGATGGAG AAACFCAAAT TATGTCTCCA 300  
 ATGAAACAAG TAAGTTTTGC TTTATCAGTT tCATTACTCA ATCCACATGC TATTTtAGAT 360  
 ACAATTGGAt TAATTGGtAG TAGTGCTGCA TTATATAGTG GcNcGC 405

## (2) INFORMATION FOR SEQ ID NO: 1267:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1267:

TCTTTATATT GCAGTACAAA ATTGCGTGG AGGTTTAAAC CAAGTAGACC GCACAAGATT 60  
 TAGCGTCTGA AGGTATTACT GTGTAATGCA TTCGCACCTG GtTATCGTTC AAACACCAAT 120

## (2) INFORMATION FOR SEQ ID NO: 1268:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1268:

TTTGCCCAAG TGACGTAAAG TACCCAATGT CCATTGTAC TTGTATCGCC ATCAACAGTA 60  
 ATCATATTAA ATGTATGGTC AGTCGAAGAT TTTAATAATT GATGAAGTGT ATTCGATTCA 120  
 ATCGATGCAT CGTGTATATAA AAGCAAGCAT GTAGCCAATT GGGAATCAAC CCGAnCTTGG 180  
 CACACATGTA CGTTACACAT TAGAACnCAA GTGACCGACG GTAATCCTAC CCGCTCAACA 240  
 CAAGCGC 247

## (2) INFORMATION FOR SEQ ID NO: 1269:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1269:

TCATTGTATA TGACGAGATT GGCTAGGCGG TGGCTGGACT GACGGAATCG ACACCCGGCT 60  
 GGGGTTGGGA AAAGTACAAG ACGCAACATG CTATGATTTT CCTATGTGGT TATCGTCCGA 120  
 TTTAAAGTGA GCAGCGCAGG GTCAGTCATC TCTCACAGnA CCTAAAAAGA ACAGTAAGCn 180  
 CAACCTAAAG CAGTGGAAC TAAATCATC AAGGT 215

## (2) INFORMATION FOR SEQ ID NO: 1270:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1270:

ACAATAAAGA CTATTAAAAG AGATATAGGT TAGATATTAC ACTTTTAGAG CAAGACGGTA 60  
 TAAATGCAAG TAAATTCGTG TATTTATCAA TACAGCAGGT nGAGTGAAAG GCCCAGCAG 119

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1271:

CGTGGCACGT TAAGCGTTTA ACCATAGCAT TAAGATGATT GTCTAGCAGA GGCGATTTCG 60  
 GGGCTCACTA CAGTGCATGA TGAACCTAAT GCTTCAAATG TAACATTAAÀ AATAAAAGCA 120  
 ACGATGTCAC TTCTTACTTC TACATCTGCC ATnTTCGTGA TTTCGTATCT ATCCCGCATC 180  
 TCATCTTGAA CGTACGAGCC TAATCGCCCh GCGCGATCCT GCC 223

## (2) INFORMATION FOR SEQ ID NO: 1272:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1272:

TAGTTACAAT ATCTGTCAAT TTCTGGAGAA CCACTAAAGC TATGCATAAT CCCGCCTACC 60  
 TCTTCAGCAT GCTCCTCCAA TAAGATATCG GTACAGTCTT GAGnTGCTTC ACGGTTATGA 120

## (2) INFORMATION FOR SEQ ID NO: 1273:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1273:

TTGCGCGGCA GTAAATTCA AACTATTGGC GTCATTTTGC CTAGCTTAAAC AAATCCGnTT 60  
 TTCTCAGCAC TGATGCAAAG TATTCATGAC CATAAACCAT CTGATGTTGA TTTATGCTGG 120  
 TTAACA 126

## (2) INFORMATION FOR SEQ ID NO: 1274:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1274:

GATTCTGAAG GATCAATACn ACATGTACAA TTTTGGCGTA GGTGCAAAGG CATCAGGTTT 60  
 5 GCTTGCTAAT CTACATCGAA GCGGCTACCT AAATTAATGA GAAATCACAC TCAGTTAATG 120  
 CATGTACTAG C 131

## (2) INFORMATION FOR SEQ ID NO: 1275:

10

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 159 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1275:

20 TGGAGTATTA CCTCAAGTGA ATACAACATA CCTGTTGGAA GATTTTTCAA AACTTTAATT 60  
 GGACCAAGTG ATGCCATTGA TGAGTTAAAT CCTAATAGAT TCAGGTTACC TCGGATGATT 120  
 GATACTAATT TGGCCTGGCG CACGCTTTAG TAnTAGTGG 159

25

## (2) INFORMATION FOR SEQ ID NO: 1276:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 577 base pairs  
 (B) TYPE: nucleic acid  
 30 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1276:

35

GAAGTAAATA ATATATAGAA TATAACAGGA AATAAAATAG ATAATATTAA TGTTGTTTTT 60  
 TTACGCATTA TAACTTTAAA TTCGATTTTC AAGTAACTTA GTATCATAAT TAGATCCCCCT 120  
 40 TTGCTTTTTA TTGnTGAAGT ATGAATCAAC AATGAGACT tTTTGtATTT CAATATCATC 180  
 CAAATTAATA TGAAGTTGTT GAAGATATAA AATCGTATCA TTTACATTTG AAGTAATAAT 240  
 TTTsATAGTG CCATTATGAT TTTyycTGAA TAACTAAATC ATCTTTATCT AGTTTTAACT 300  
 45 TTCTTATATA TTCATCGGAT AACGTAATCT GAGATTGCTG ATTGGTTCTA ATATGTGACG 360  
 TTGAATCATT AAGTATTATT TCTCCATTTT CAATGAGAAT AATTTTGTCT GACATACGTT 420  
 CGACTTCTTC AATATAGTGC GATGTATAGA GTATCGTTTC ATTATCTTCT TTTAAATTTT 480  
 50 CAATAATTGA CCAAAAATAT TCTCTAATTT CTATATCCAT AGTCGATGTT GGTTCATCTA 540

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## (2) INFORMATION FOR SEQ ID NO: 1277:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1277:

CTAAANTAG GTAATAGTTA CCAAGTACCA TATCTGTGG ATGGTGTACT ACAGGTTTAC 60  
 CATCTTTAGG TTCAAGATGT TTTGATGACT GCTAACATCA ACATTCTTGC TTCAGCTTGT 120  
 GCCTCTTTTG A 131

## (2) INFORMATION FOR SEQ ID NO: 1278:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1278:

GTTTGCAGATA TTTTAGGCAG ACAACCTAAC TTTACAGAAA CAGGTATCTT TTCTGTTATG 60  
 TGGAGTGAAC ATTGCTCTTA TAAACATTCT AAACCGTTTT TAAAGAATTT CCTACGCAGG 120  
 TGCCATGGTT TGGGCTGGAG TCAGGTGCGT TGTGTATAGC TGATna 166

## (2) INFORMATION FOR SEQ ID NO: 1279:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 418 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1279:

CATAATTATG AAAATGATAT GATTTTTATT AGACCATTTA AAAAAGCATA ATTTAAATCG 60  
 AAGGCAGGAC ATTGAAATAT GAAATTTTCA ACTTTAAGTG AAGAAGAATT TACCAACTAC 120  
 ACCAAAAAGC ACTTCAAACA TTATACGCAG TCTATAGAAT TATATAATTA TAGAAATAAA 180  
 ATAAATCATG AAGCACATAT TGTGGGAGTG AAGAATGATA AAAATGAAGT TATAGCTGCA 240  
 TGTTTATTAA CAGAGGCACG AATTTTTTAAA TTCTACAAAT ATTTCTACTC TCATAGAGGT 300

ATTCATTAT AAAAATAGAG GAGTATTTAT TCTTGTGAT CCATATnTAA TAGAGAAT

418

(2) INFORMATION FOR SEQ ID NO: 1280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 449 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1280:

GACATATCAT AAATTACATG GTGATAAAAT TnTCGGCTAC GATACTAACG GATTCCCGAT 60  
 TACCTGGTTT TATCCATTAG GTGAAAAGAA AGTTGAACGT AAGGCACCAA AATTAGAAAA 120  
 ATAATTAAAT AAAACAGCTT AATGATGTAA TGAAATTAGT GAGTTAATCA CTGACTTCTA 180  
 CGTCAITGAG CTGTTTTTTT GTGCTTTGTT ACAAAGCATT ATTGAATTTA TTTTACGTGT 240  
 TCATATTTTG AAACATCAAA GCCGTCTTGT TTAGCTTTGT TGATAATGTC TTTGATTGAA 300  
 TGTAGTCCTT TATCGGCGAA GTATGATCTT AAGTTGTCTT TTGTAGCTTG GTCAGCATTC 360  
 TTATCTAATA ACACATCAAT ATAACCTAAT TCATGTTCTA AGAAGTTTGC ATCATCATGT 420  
 AGTACGAGTC CATTTTGAGA ATAACTTT 449

(2) INFORMATION FOR SEQ ID NO: 1281:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1281:

TATTTATATG TACTGATGAT GAAGTTTATT ATCTATCAAG TGGATCAAAT CCGAAATATA 60  
 ATCAGTATAT GGGTGCATAT CATCTACAAT GGCATATGAT AAAATATGCA AAATCACATA 120  
 ATATTAATAG GTATAATTTT TATGGAATAA CAGGCGTCTT TAGTAATGAG GCGGATGATT 180  
 TTGGTGTTC ACAAATTTAA AAGGGTTTTA ATGCACATGT TGAAGAATTA ATTGGTGATT 240  
 TCATCCAACC AGTAAAACCC ATTCCAATAT TAATnTGCCA AACCTnAAT 289

(2) INFORMATION FOR SEQ ID NO: 1282:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1282:

5    ATTGAGGTCG AGGTGGCCCG GCTCCATGCA CCGCGACGCA ACGGGGGAGG CAGACAAGGT    60  
      ATAGGGCGGC GCCTACAATC CATGCCAACC CGTTCCATGT GCTCGCCGAG GCGGCATAAA    120  
      TCGCCGTGAC GATCAGCGGT CCAATGATCG AAGTTAGGCT GGTAAGAGCC GCGAGCGATC    180  
 10    CTTGAAGCTG TCCCTGATGG TCGTCATCTA CCTGCCTGGA CAGCATGGCC TGCAACGCGG    240  
      GCATCCCGAT GCCGCCGGA GCGAGAAGAA CTAATTGATA CAACACTTTC TCAACCTGAT    300  
      CTTCTTTACC TTCTACATAG CGCGTGAGCA GAACCATCTT GATGgCACAG CTAAATAATG    360  
 15    CaATgGGAAT GATGTATGAC ATTCGGGGTG CATAATTTCT CT    402

## (2) INFORMATION FOR SEQ ID NO: 1283:

## (i) SEQUENCE CHARACTERISTICS:

20    (A) LENGTH: 224 base pairs  
      (B) TYPE: nucleic acid  
      (C) STRANDEDNESS: double  
      (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1283:

25    TATTGACAAC CAGAGTACAA ACAGCAGCTA TATTATAGAC TTAGGTCTGA AGTGGTAGTG    60  
      GCGGTGGACT ATTGTTGCGA CTGGACACCC GAGATATTGC TCAGCAAGC ATCATATACA    120  
 30    GGAAGTATTA AAAGAGACTT GnCGAGTAAC AAATACTGAA GTAATAAGAT TAAAAGAGTG    180  
      AGGTGTATAA TTATCCTCGT TCTTTTATAT TAGTATGATA GAGA    224

## (2) INFORMATION FOR SEQ ID NO: 1284:

## (i) SEQUENCE CHARACTERISTICS:

35    (A) LENGTH: 146 base pairs  
      (B) TYPE: nucleic acid  
      (C) STRANDEDNESS: double  
 40    (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1284:

45    CGTGGGAGAT TGTGCATATT GATTATGCAA GGAAGnACGC CATAAAAGTG GATGGCCAGA    60  
      CATCATTAAT ATTATTGATA CCACATCAGA AGGTATTCAA AGTGAATCGG TGATAAGTGA    120  
      ATCAATTAAG TCTGCCAAAG AAAAGA    146

## (2) INFORMATION FOR SEQ ID NO: 1285:

- (A) LENGTH: 137 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1285:

10 ATTTGCGGTG ACTGGACTTG GATCCGCAAC TTGGTAATTT AAGGAATTCT TGTCAATTATA 60  
 AGCCCTCCAT TTCATGATTT GATTGCCCAC TCGGTAACCA TTGGGGTTAC AGCTTCACTA 120  
 GGGGAnATAC GAACCTC 137

15

(2) INFORMATION FOR SEQ ID NO: 1286:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 594 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1286:

25

GCTATTGATT ATGGTTAGCm TGTTGTTWC TTTACTCAIT GTTCCTTGGt TAAGCTCrAA 60  
 AAAAGCACGT ACTTTAAAGA AACATGCAGC TAATGAACAG GCCCGATTTT TAAATCATT 120  
 30 TTATGATTAT AAAGCTGGTA TGGATGAACT ACGTCGATTT AATCAAATTA ATCATTATCG 180  
 AGATAATTTG ATGGCTAAAT TAAATCATT TGATAAATTA CAACTTAAAG AGCAACGCTT 240  
 TTTAACGATT TATGATTTTA TATTAAATAT TATTGCTATG CTTTCGATTT TTGGTAGTTT 300  
 35 AGTTCTAGGA TTAATTCAA TTAATGCAGG CCAACTAAAT ATTATTTATA TGACGAGTAT 360  
 AGTTTTAATG GTCTTAACTT TATTTGAACA AGCTGTACCA ATGACAAATG TCGCGTATTA 420  
 TAAAGCGGAT ACTGACCAAG CATTGCACGA TATTAATGAA GTGATATCTG TACCTTCTAC 480  
 40 TAATGGAAAA AAACGTCTTA ATGATAAGTA TGATGCAACG AACATTTATG AAGTTAAGGA 540  
 TGCTAGTTTT AAGTATTGGA ATCAGCAAAC GTATGTrTTG TCGGATATTr ATTT 594

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(2) INFORMATION FOR SEQ ID NO: 1287:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1287:

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TGAAGTAGTA ATAAACCCGG AACCCCTAAAA CTGGATGGAG GATGAAACCA AAAAGGAACC 120  
 AGCCAAGCCA AATTGGGGAA ACCAGGACGG CCCAATGGAG GTCCAACCA TCCAAACCCC 180  
 ATTCCGCTAA TgNCTATGGG TCCCAATTAG GAATCCAATG GATGGATGGA TTh 233

## (2) INFORMATION FOR SEQ ID NO: 1288:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 132 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1288:

AATCCCTGTA CGTTCGTAAA GCTAGCTGGn TAATAAAAAA GAGTCTGGAA AGTAGGCAAC 60  
 AATCAATGAC AATGAGCAGA TCCAATCGCA GTATGCTTAC TCGTGTAAGA AACGCAAACA 120  
 TGGTGCCTCA CG 132

## (2) INFORMATION FOR SEQ ID NO: 1289:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 154 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1289:

TATCTGATAA TTCTGTACCC AGGCGTTTTA ATATGTTTAT CTGGTGTCAT GATACATAAA 60  
 CATTGTACCT TTAGGTCATA CGATGTCGCA AATAACTGCT CTTGCCGTTA CAACACCATT 120  
 ACGGTTATAC ACTTnTAGCC AATCATTATC TGGG 154

## (2) INFORMATION FOR SEQ ID NO: 1290:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 145 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1290:

AAAAGTGGCA CATGCGGCTG TAAAGTCCTC TGTtTCTGAT AAATCATAAC CTATATACAT 60  
 GTCTACCTTC CAACTCATCT AAGAAATAAG TCATATTTTT TTGAATGTTG GATAATCAAT 120

## (2) INFORMATION FOR SEQ ID NO: 1291:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1291:

CTTAATGCTA TATATTCTTT GTTTTTGATA CCATTCATC GTCTTCTCTT GATTTCTAAA 60  
 CAATTAGAA AATAAAGAA TATACGCTTC AGACTTATTA AAACCCGCTA TATCATCTTG 120  
 ATATTGTATT AACAATTGAG TAAAGCTGTG TATTAAGTCA TCTTTCTTCG ATGCAATGGT 180  
 AGTTAATGAT TTTACACGAT AAGCATATTT ATCTGTAAAT AACTTAGCAA CTACCCACCC 240  
 TAAATCATGT CCTAGAATAT GTGCCTCATG AATATTTAAC TTCTCCATTA GAATTTTAA 300  
 ATCCTCAACG TGATCGTTTA AATCGTATGA TTCACTTTTA GAAGACTTGC CATGACCTCT 360

## (2) INFORMATION FOR SEQ ID NO: 1292:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1292:

TGTGTTAGTT GTTTATGTTG TTGATATATA CTGCTCGTGC ACATGGTACC CAGACGATTC 60  
 AACGnTGAGT ACACAAAATA CAAAATCTAC GGCACATGGT ACCGTTTATA AAAGATGTGG 120  
 AACCTTACTA GCATTTGTTG AGAACGCTAC ACGTTTAAAT CAAG 164

## (2) INFORMATION FOR SEQ ID NO: 1293:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1293:

TTAATTTTCT ATATATTTCT TAGGTTATAT TGGTATCTAT GCCAGTAAGT GACATGACGT 60  
 TAGATCATTG AATCCAAGAT CGAnACATTG GGACATATTT ATTAACGACA TGGCTTCAAC 120

## (2) INFORMATION FOR SEQ ID NO: 1294:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1294:

GTCATGCnTA ACAGGTGAAT ACCTAGTAAT TCAGATATTA TCATTTATAT ACCCTCTTAT 60  
 ATTTTAGTGC ATTATCTCGA AATCGAGATA CTTAATGTAA ATTTTtagTG CAGCCTACAC 120  
 TTCGTGATTG GGCANTAGTT CTTAAACGCT GTGTAAGAT GTTAATTCAT CCTTGGTTAA 180  
 CACACAAACG CTTGGTTAAT GCTCAGCAGC TAG 213

## (2) INFORMATION FOR SEQ ID NO: 1295:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1295:

AAGAAGTTTG AAGTCTATGA AAACAATCAA AAATTGCCAG TGAGACTTGT ATCATATAGT 60  
 CCTGTACCAG AAGACCATGC CTATATTCGA TTCCCAGTTT CAGATGGCAC ACAGATGAAA 120  
 TGTTTCTCGn CCAATGAGAG GGAGAACATA GTATCAATAG ATG 163

## (2) INFORMATION FOR SEQ ID NO: 1296:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1296:

TAGCTTTAAT ACATTCTGAT TTTTAAACGC TTCGAAATGT TTTcAGTAAC TAATTTTGCC 60  
 ATAATCCCCA AACTCCTTG ATTATTAACT GCnTTTTGAT TGGCTACATT AAGGCTTTAT 120  
 ACACATCAGC TCACCATGCC CATATCTACT AATGGTTATA TCCCTAGAGT CCCAGCGATA 180  
 TAACATCAAC GCTTACnGGA GTTTCAG 207

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1297:

ATGGCATCGG TTGGTTATGA AAAGnCAAGC CATGGGGAGG CCATATTTGG GGTGGAATCA 60  
 TACCTGGAAC CTTTGGTGCC TACCACCAAT TGGTAACGGT TTTACCATCG GATTTTTTAGT 120  
 GATACAGCGA TATGTTTTGT ACAGG 145

## (2) INFORMATION FOR SEQ ID NO: 1298:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1298:

TCCAAAAGTT AAAGGTCAAT TGAAACAGAn AAAGCTTATT ATGTCTGGAA AAGTATTAAA 60  
 AGTAATGGTA TCAAATGACA TTGAACGTAA TCATTTTGAT AAGGCATGTA ATGAAGTCTT 120  
 TCAAGCGTTG AATTGTGGT 139

## (2) INFORMATION FOR SEQ ID NO: 1299:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1299:

GATATTGGCA ACCTTCAGCC GATGACCTCA TGGCAAATGA TTGGGAAGTT ATAAACCCAA 60  
 CTAGAGACCA GGAATTATTG AAGCAATTAT AGAAATGCTA TCAATGATAC TTTTAAATT 120  
 GTTTTAAAC TCATTTTCAA AGTAAACAAC AGTCTTGTCT GAAATTGTTA CATGATAAAT 180  
 AGTGTTACTA GCATACACGC CGTTTAGGAA CCCAGAGTTT TTAAGTTTAT TTAAATCGTA 240  
 TTTTACATCT TCGAAATGTA GTTTTGTAAA ATACTTTGTA TGTATATCTT TAGCACTTCC 300  
 AAAATTTATT GGCAGGTAA TTTAATCGAA CCTAACTTTA CACATTCTAA ATAATCTTTG 360

## (2) INFORMATION FOR SEQ ID NO: 1300:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 693 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1300:

CTACAGTGCA ATTTAACCAT GAAGTTGTTG ATTTTGAACA ATTATCAAAT GGTCAATGGG 60  
 AAGTTACTGT TAAAAATCGC CTAAGTGGTG AGAAATTCAA ACAAGTAACT GACTACGTAT 120  
 TCATCGGTGC TGGCGGTGGA GCAATTCCAT TATTACAAA AACAGGTATC CCTGAAAGTA 180  
 AACATTTGGG TGGATTCCCT ATCAGTGGTC AATTCTTAGC TTGTACAAAC CCAAGTTA 240  
 TTGAACAACA CGATGCCAAA GTTTATGGTA AAGAGCCACC TGGTACACCA CCAATGACTG 300  
 TACCTCATTT AGATACGCGT TACATTGATG GTCAAAGAAC ATTATTATTT GGACCATTG 360  
 CTAATGTTGG ACCTAAATTC TTGAAAAATG GTTCTAACTT AGATTTATTC AAGTCTGTTA 420  
 AAACATACAA CATTACAACCT TTATTAGCAG CAGCAGTnAA AAACCTACCT TTAATTAAAT 480  
 ACTCATTTGA CCAAGTAATT ATGACAAAAG AAGTTGTAT GAACCACTTA CGTACTTTCT 540  
 ATCCAGAAGC ACGTAATGAA GATTGGCAAT TATACACTGC TGGTAAACGT GTACAAGTTA 600  
 TCAAAGATAC ACCTGAACAC GGTAAAGGAT TCATCCAATT CCGTACAGAA GTGGTTAACT 660  
 CACAAGACCA CACTGnAATT GCATTATTAG GTG 693

## (2) INFORMATION FOR SEQ ID NO: 1301:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1301:

CATACTTGGG TAATGCTGCC CATGGnACGC TGGnACAAGG TAAAGTTGCA CGTTTAATTT 60  
 GTGnATGTAT ATAAACAGA TGGGAACACC ATTTGAAGGG GATCCTCGTG CAAACTTAA 120  
 ACGTGTATTA AAAGAAATGG AAGATTTAGG cTTCACAGAC TTTAACCTAG GACCTGAACC 180  
 AGAATTCTTC TTGTTTAAGT TGGATGAAAA AGGGGAACCA ACTTTAGAAC TTAATGATGA 240  
 TGGTGGATAT TTCGATTTAG CACCTACAGA TTTAGGTGAA AACTGTCGTC GTGATATTGT 300

TCAACATGAA AtTGACTTaa ATATGCAGAT GCTGTTACAG CATGTGATAA TATCCAAACA 420

TTTAAATTGG TTGTTAAAAC AATCGCACGT AAACATAATT TACACGCAAC A 471

5

(2) INFORMATION FOR SEQ ID NO: 1302:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

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(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1302:

CATGTGATTA AGAACGTTCA CTGATGAATT TTTGATGATC GTTCGGTTTT TGTTTGGATT 60

TTAATGATTA TTTATACAAA AACAGCCGTA TTTCAAGCCG TACATTTTAA ATTTAACTAA 120

20

ATTTGCATCT AGTTAATAAT TGCAATTATC AAATTTGTCT TATTGATCCA ATCTAATTTG 180

TACTCACAAA CTAGTTTTAA ATTCTAACTT TATCTCTCAG TTCGTTATCA ATCATCAGAC 240

ATAAACCAAT GAAGCAATCA GAAACACTC TAATTTTCTa TTAGAAATTT GnTTTAATAT 300

25

AAAAAAACAG GCTTACTTCA TATAATTTAT GAAATAAACC CGTCAATTTT TGTTTAATAT 360

GCTTGGTGAT CThTTATTCT GCGTAATAAT GCTAAACCTG 400

30

(2) INFORMATION FOR SEQ ID NO: 1303:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 128 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

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(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1303:

40

AAAAGCTTAG TTGAACTTTC AACGTATCTT AGCTACTGAA GGTGCAGAAG TTTTAGAAGC 60

AAAAGACTGG GGTAAACTnC GCCTAGCTTA TGAAATCAAT GGATTTCAA GATGGGCTCT 120

ACAACATC 128

45

(2) INFORMATION FOR SEQ ID NO: 1304:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 141 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

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(D) TOPOLOGY: linear

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TCCTTCGGAT TCTAAATGGC ATTGGACAGT GTTTACAAGC TCGCATTCTT CCACTTTTTTG 60  
 CAATTTCTTT TACAATTTCT AAAGCTTCAT CAAAGTTTCC TTCAATAGnA AACGATTTCT 120  
 GCACCATACA TTACTGACTT G 141

## (2) INFORMATION FOR SEQ ID NO: 1305:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1305:

GACTGGTAAA CACTAAGTGA ATTAGCTGGA CAATGAAAAA TATCCACAAT CATTAAATTAA 60  
 CGTACGCGTA ACAGATAATA TCGGTTGAAG AAATGTTGAC GTTAAGAGTT ATGACTAAAT 120  
 AGAGTAGAAT GATGGTGAGG TCGATTTTAG TAGACTCTGG AC 162

## (2) INFORMATION FOR SEQ ID NO: 1306:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1306:

TTCTTAGTTG CTCGAATAA TAATTTGCTT AATAATGATs TAGCTGTTAT TGTGTCATAT 60  
 TCTAAAGGTG CCATAAATTT AAAAATAATA GTAGTTGTTT TAAATTTAGT TGTGGTGAA 120  
 ACTTTGATAT GTATATTTGG TTGAGATTGT CTAATCAAAT ATATAGCCTC CTCTATATCT 180  
 TCTTACATCT ATATTTTCT AGTGATTTTA AATTGAACIA AGCTATTTT CATATAATTT 240  
 AATGAATACA AAATAGGTTT ATCTGATTCA TTATAGTGCG TA 282

## (2) INFORMATION FOR SEQ ID NO: 1307:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1307:

AAGGAAAAAA CCCTTGGCCT TTGGAAAAAA CCCAAAAGGA AAGGGGTTTA AAAAAA  
120  
AAGTTTAACC CGTTTGGCCC CAATTCCCGC CCGGGGAACC CAAAAGGANT TTTAAAAAAG 180  
5 GAAACCCAAT TCCCGGCCGG AAAAGGGTTT TTAAGCCCAA CCGGATTTTA AGGAAAACCA 240  
TTTTAAGATT ACCTGGGAAA AAAAACCGTT TAGGAA 276

## (2) INFORMATION FOR SEQ ID NO: 1308:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 692 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1308:

20 TGTATTTAAT GCTCGTACAC ACAATTACAA AACTGCAAGA GAAAAGCAT TGAGTAATAA 60  
TCATATTCCA GAAAATGTAT ATGACAATCT AGTAAAACT GTACATAAAT ATTTACCATT 120  
GCTACATAGA TATACTGAAT TCGCAAAGA ATTGCTAGGT TTAGATGACT TGAAAATGTA 180  
25 TGATTATAT ACACCATTAA TTAAAGATAT TAAGTTTGAA ATGCCTTATG AAGAAGCTAA 240  
AGAGTGGATG TTAAAAGCAT TAGAACCAAT GGGTGAAGAA TATTTAAATG TAGTTAAAGA 300  
AGGCTTAAAC AATCGTTGGG TCGATGTCTA TGAGAAATAA GGTAAACGTT CAGGTGGCTA 360  
30 TTCATCAGGT GCACATTAA CTAATCCATT TATTCTACTT AACTGGTCTA ATACTATTTT 420  
AGACTTATAC ACATTAGTTC ATGAATTTGG GCATTCAAGCA CATAGTTACT TCAGTAGAA 480  
ATTCCAACCG TCAATTCTA GTGACTACAC TATTTTTGTC GcTGAAGTTG CaTCAACTTG 540  
35 TAACGAAGCA CTTTTAAGTG ATTATATGGA TAAACATCTT GATGATGAAA AACGCTTATT 600  
ATTATTAAAC CAAGAATTAG AaCGTTTCAG AGCTACATTA TTCCGACAAA CAATGTTCCG 660  
40 AGAATTTGAG CATAAaATTc ATGCAATTGA AG 692

## (2) INFORMATION FOR SEQ ID NO: 1309:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1309:

GGACTATTCG ATGATAGCTT TTTTGACTGG ATTTACTAAA ATGAAAGCAA GTACTATATA 60

atCGAGTAAT ATCTATATAT GACATTTTAA A

151

(2) INFORMATION FOR SEQ ID NO: 1310:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 115 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1310:

TGTGCATTTG ATAATATTCA CTATGATTCTG TGGTCATTCA CATCGTCTAC GCTCACCGGT 60  
 CTAAACGTAC CTAACCCAAC ATGTAATGAA CAAATGCGAT ATTAnCACCT TTATT 115

(2) INFORMATION FOR SEQ ID NO: 1311:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 164 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1311:

CACCCAACTG ACCTCAATGG TATAATGCAT TTGTGAATAC CGAATATCAT TGGAAATATCT 60  
 CCTATCATAG GAATATAATA TGTATATATC TTCGTAATCn TGTTCAATTTT TAAGAAAATC 120  
 AATAGAAGTG TATCGATTAA AACTACATTT GAACCATTAC TTTG 164

(2) INFORMATION FOR SEQ ID NO: 1312:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 141 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1312:

GAGGAAAATC GAAGTGAAAT TATTAAAATA TGGCGATGGT GGAATACGAA TAGATGGTGG 60  
 TTTAATAGGC GGCTTTATTC GGGTGTATT GTATGTAAAG TGAAAAATTT AAnCCCATTT 120  
 CAAATTGGTG ATATCGTTGC G 141

(2) INFORMATION FOR SEQ ID NO: 1313:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 133 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1313:

AATTGGTATT ATGCATAGTG CAATGGATGC TGGTATTAAA nTCCAGAGGA TTACAATTAT 60  
TAGTTTCAAT AATCACGATT AGTTGAGATG GTTAGCCACA ACTTTCTAGT GTATCACCAT 120  
TATATGTATC GGT 133

(2) INFORMATION FOR SEQ ID NO: 1314:

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(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 629 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1314:

TTGCAATTAG AATGCTGTTT CACCCCTTTA AACCATACTA TATATTTAAA TTTAGAGTCC 60  
CATTTACACC AGGTTTAATA CCGAAAAGAC GCGAAGAAAT TGCAACTAAA ATTGGCCAAG 120  
TGATTGAAGA GCATTGCTT ACAGAACTT TAATTAATGA AAAATTGAAA AGCGAGCAAT 180  
CACAGCAAGC AATAGAATCT ATGATTCAAC AGCAGTTACA AAAGTTGACG AAAGATCAAT 240  
TGTCAATAAA ACAAACTACT TCTCAAATCG tATTGATTTA GAACAAGTAT TACaAACTAA 300  
TGGAAATCAA TATATTGAAT CACAATTgAA TAATTATTAT aCAAAGCaTC AAAACCAAAC 360  
AATAGCATCT TTATTGCCAA ATCAACTTGT AACATTTTTTA AATCAGCATG TAGATAACGC 420  
AACAGACTTA TTATGTGATC GTGCAAGGAA TTATTTATCA TCTGCAAAAG GCACACAAGA 480  
TATTAATGAT ATGTTGGATA CTTTTTTCAA TGAGAAAGGT AAGTTAATTG GTATGTTGCA 540  
AATGTTTATG ACAAAAGAGA GTATTGCAGA TCGCATTCAA CAAGAACTTA TACGTTTAAC 600  
ATCTCATCCT AAAGCAAGAA CAATTGTGA 629

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(2) INFORMATION FOR SEQ ID NO: 1315:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 399 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1315:

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ATACAGGTAC GTTCGTTATC AATGGTGCAG AACGTGTAAT CGTATCTCAA TTAGTTCGTT 120  
 CACCATCCGT TTATTTCAAT GAAAAAATCG AAAAAAATGG TCGTGAAAAC TATGATGCAA 180  
 5 CAATTATTCC AAACCGTGGT GCATGGTTAG AATATGAAAC AGATGCTAAA GATGTTGTAT 240  
 ACGTACGTAT TGATAGAACA CGTAAACTAC CATTAAACAGT ATTGTTACGT GCATTAGGGT 300  
 TCTCAAGCGA CCCAAGAAAT TGTGTACCTT TAAGGGGACC AATGGAATAT nTACCGTAAT 360  
 10 ACCTTTAGGA GGAAAGACCG GCACCTGAAA CCACTGGAA 399

(2) INFORMATION FOR SEQ ID NO: 1316:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 778 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1316:

ATAAACATTT TAATATGTAA TTAGAAATT TTTTGTAGTAC AAAATCTTTC TTAATAATGA 60  
 25 TTAAGGAGGT CAGTAATGAT TGAAATTAAA ACATTAACGA ATAATGATT TAATGAGTAT 120  
 AAGAGACTTG TTTCGACAGT CAATGAAGAA TTCACTCAAG ATTACATTA TAGTCAAACA 180  
 ATGACTGACA CCTTAATACA TGACATTTTA AATCAAGGTT CACCGAAATG TATTGTATTT 240  
 30 GGCTGTTATG AAAACGAAAC ACTTATCGCA ACAGCTGCCT TAGAACAAAT TCGATACGTT 300  
 GGAAAGAAC ATAAATCATT AATTAAATAC AACTTTGTTA CTAATAACGA TAAATCGATT 360  
 AATAGCGAGC TCATTAATTT CATTATTAAT TATGCACGGC AGAACAATTA CGAATCTTTA 420  
 35 CTTACATCAA TTGTGTCAAA CAACATAGnn GCTAAAGTTT TCTATAGTGC ACTAGGATTC 480  
 GACATTCTTG GTTTTGAGAA AAATGCAATT AAAATCGGAA ATACCTATTT CGATGAACAT 540  
 40 TGGCTTTTTT ATGATTTGAT TAATAAGTAA TACAGTTTTA TATATTCTAC rTTTCTCATA 600  
 AATTCAAATC ATATAGGTTT TATTTTTTCAT ACACTACTC TACTATTGAG TAGTTGTTTT 660  
 TTATTTGATA TGATAACAAT AAGTTTTTTT CAGAATATTC TATGTTTTAG GGGTGTCAA 720  
 45 ACTTAATGGG TAACCGCAAT TATTCATGGA nTTATCnTAA GCGATTGGGT CCTAAnTT 778

(2) INFORMATION FOR SEQ ID NO: 1317:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 465 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1317:

5 TGCACAAGGT GGTGCAGCAA TTGCAGCGTT CTTTATTATT AAACAAAATA AGAAGTTAAA 60  
 AGGTGTGGCA TCTGCCGCAG TATTTTCAGC ATTACTTGGT ATTACAGAAC CGGCTATGTT 120  
 TGGTGTACT TAAACTAAG ATATCCATTT ATTGGCGCTA TCGTTGGATC AGGTATTGGT 180  
 10 TCAGCATATA TTGCTTTCTT CAAGGTTAAA GCAATCGCAT TAGGAACTGC TGGATTGCCA 240  
 GgATTtATTT CAATCAATCC AGTACATGCA GgATGgTTAC ACTaCTTTGT TGGTATGACA 300  
 ATATCATTcA TCATTGcTAT AACAGTTACT TTAAtTTTAT CtAAaAGAAa AGCAAATAAA 360  
 15 GAAGTTGTAG AATAAAAAA GAGGTATGAC AGTAATCAAA GTATCASTCA TTGCAATGC 420  
 AATAGGATGA AACTTTAAGC TGTACATCCT TTAATTAG TTATA 465

## (2) INFORMATION FOR SEQ ID NO: 1318:

20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 150 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 25 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1318:

30 GACTTAATAT AACTGATCTT TTGCTATTAT TGAAACATAT TTATAAGAA AATAGCATTG 60  
 CATAATACCC AAGCAATAAA TACTATAATA TTTTGAAGT AACTAATCAA ACATCTAAGA 120  
 CATGATTGAT AnCACCACAG AAAAATAAGA 150

## (2) INFORMATION FOR SEQ ID NO: 1319:

35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 131 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 40 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1319:

45 CCACCTTTTA ACGTACGTAT CCATGAATCA TATGATTAAT TTAATATCAT TATTACTTAT 60  
 TTCTTATCTT TATTnTCTTT TTTTCTTCTG AAAAGTAGTA ATGAACCTAT TGATGCTAAT 120  
 AATCCCCAAA T 131

## (2) INFORMATION FOR SEQ ID NO: 1320:

50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 140 base pairs

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(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1320:

10

TAGTGTCCAA ATGAAAGTGT GGCTACCTAT AGCTGGTCCA TGAAGCTTTA TTTTAACTG 60  
GTTTGTACAA TATTTAAATA TCAAAATCTT CTCGCGnTTT GGACAGTTTT TTTGGTATTA 120  
ACCATTAATA AACGGAAAGA 140

(2) INFORMATION FOR SEQ ID NO: 1321:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 140 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1321:

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CTTATTATAT AATTCTAATC CTAGTACATT ATACATTTTA TCAAATAGTC AACTGGATAA 60  
CTTTGAAAGT GAATGATnCT TTTAAATAA AGAAGATAAT ATAAAGTGCT TGATAATGGA 120  
TTTGTAGTTG ATGATTAAA 140

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(2) INFORMATION FOR SEQ ID NO: 1322:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 185 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1322:

40

TCGTTGCAAC ACAGGCACTA TTTTACCTTT ATATGTTGTA ATAGTTTGAT TGCTGCCATT 60  
TAAACAACCA CCTTCTTAC TCCACAAATT TACCATGAAT AGCGCGCGCG CCATAGCGGG 120  
ATACTAAAGT GTTCTGCACC TTGCCTGTCT CCTTCAAnTT TCGATTACTG TAGAGCACAA 180  
GTACG 185

45

(2) INFORMATION FOR SEQ ID NO: 1323:

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 148 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

55

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1323:

ACCTGCAATT TTCGTTATTC AAAACAATAA CTATGCAATT TCAACACCAC GGAGCAAGCA 60  
 AACTGCTGCT GAAACATTAG CTCAAAAAGC AATTGCTGTA GGTATTCCTG GGTATCCCAA 120  
 GTTGGTGGTA TGGTGCGGTA nTTGGTTT 148

## (2) INFORMATION FOR SEQ ID NO: 1324:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1324:

GAAAGCATTG ATGGACAAAG ATGAACCACC AAATGAATGG CGATTAGATT CCAATTGATA 60  
 TGGCTCACGG AAAATTTATG CTACAATTGC GTCCAGTAAA CAGTGGCACT AATAGTCCAC 120  
 TTAnGCTCCC TAGTGGATGA A 141

## (2) INFORMATION FOR SEQ ID NO: 1325:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1325:

TTATACTATC GTGAAGGGTT TATTACTCAA TTAATGCCTA AAAAGGATAA AAGTTATTTA 60  
 GTTATTGATA ATTTTAATCG TATAGATACA GACATTTTCC AAACGTATAT TAATGTGTTA 120  
 GAAGGCTATG AAGTAACATT ACCACGTTAT AATAAAGACG GTAATATGAT TAAATGGTCA 180  
 CGACAAAAAG ATTCTTTCTA TTAT 204

## (2) INFORMATION FOR SEQ ID NO: 1326:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1326:



TTTGTTAAAA GTCTTCATTT CGGATGAAGC TTTATCTATT GAACGCTCCA AATTATTTAA 120

AGCAGCTTTT TCTTTATTAA CAGCTGT 147

(2) INFORMATION FOR SEQ ID NO: 1327:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 530 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1327:

CATTnAATGA AGAAACTGAA CCCnGAACTA TACGACGCAG AAGGCAATTT AATTAATAAT 60

AGTAAACAT CCAGCTTAAT CCATTGATGT GTTATAAAAG TGAAAAGCTC CAATCAAAGT 120

TGACGCTCAA ATAGTTTAAC TTTGATCGGA GCTTTTTTAT AATGTATACC GAAAGGTTCA 180

AATATTATAT AATGGTAGAA TTGAAAGAGA ATATAAAAAA GTGAGGATAT AAAATGAAAG 240

TTAATCCTAA TAATATAGAA TTAATCATTG GTGCAGTAAA AGAAGAACAA TATCCAGAAA 300

CAGAATTGTC TGAAGTGCAC TGACCGGTCTG ATCTAATGTA GGTAAGTCTA CATTTATCCA 360

ATAGTATGAT TGGCAGAAAA AATATGGCAC GTACATCACA GCAACCCGGC AAAACGCAAA 420

CGTTAAATTT TTATAATATA GATGAACAAC TTATTTTTGT GGATGTTCCA GGGTATGGAT 480

ATGCTAAAGT AAGTAAACA CAACGTGAAA AATTGGGAA AATGATTGAG 530

(2) INFORMATION FOR SEQ ID NO: 1328:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 153 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1328:

AAGAAAGTTT GATCTAGGCC AACCTTTCTA ACAACGATAC GACAGTTTAA TAATGTCTCA 60

TATCTTGACT TCCCATGATG ATATGGTCGT TAATCACATC AATGACTTAA ATCTGGATnA 120

ATAGATGCGA ATGGATCTTG AAAAATCATT GTA 153

(2) INFORMATION FOR SEQ ID NO: 1329:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 115 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1329:

5 TGTAGTTCGT TTGTGCTCTA ATTAAACGGT CGAAACCATG GATTAGACCT GCGATTACAA 60  
CTGCAATGAT ACCTGAAGCA TGAACCTCTT CTGnTAAAAA GTATACGACA AAAGG 115

(2) INFORMATION FOR SEQ ID NO: 1330:

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1330:

20 AACAAAGTTAT CTACATCTGC TGATAGGCAT ACTATTACTA ATAAATAATG CATCTTTTTG 60  
CCAGATGTTT TCTTAATCAA TTGCACCAAC GAATGGCACT CTCATCTGTA Gn 112

(2) INFORMATION FOR SEQ ID NO: 1331:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 203 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1331:

35 TTCATTGCAG ACAnTTGGTG AACCATGTGG ACGAACTAGT CCTAGATTAA GATAAGAGAT 60  
TAGTGAnCAT TGCCACCACT GCAATTAAAC ATTCTTGGAA AAATTAACCTT AAGTTAGAAT 120  
CTTAATGCAT ACAGATACGG CGAAGATGAT GCCAAAGAAC GTCACGACTT TATGATGATG 180  
ACTGAACCCA GTTTTTACGG AAG 203

40 (2) INFORMATION FOR SEQ ID NO: 1332:

45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1332:

55 ATGATGTACT AATATCTAAT AAGCTTGCTA AGTCTTGAGA CCTCATTTTA ATCACCTTTT 60

GACTATCTAT TTCTGTTAGT ACGTTTGACA TATTAATCAC TCCaCyTTAA CGCAaTAWAw 180  
 TTTAwTAGCG TTGGCTATTG TTGTTTAACG CGATGGnATT TACAACTTGT AACGTAAGAG 240  
 5 AATGAAAAAT AAGCTGnATA TGTTGTTTG 269

## (2) INFORMATION FOR SEQ ID NO: 1333:

10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 142 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1333:

TAGCTTTTGC CCAATATGGT GAATCATGCG CCGTTCTGTA ATAATCTTCA CTTGGCATTC 60  
 20 TTGGAATTTG AACACATCC TGTTCATTTT TATAGAnTGC TTAAATGGTA CAGCTGAAAA 120  
 ATCAAAGTAA TGTCTTTTTC TG 142

## (2) INFORMATION FOR SEQ ID NO: 1334:

25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 211 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 30 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1334:

35 ACTGATGCCC AATATGCATC TTGnCAATTG CAGGTGTGCA TGAATAACA CATGACAAAT 60  
 CTGCCTGACT TTTTGCTGAC CCATAAATAA TTGGnCTAAC TTTTGCATC TTGATCTTGC 120  
 ATCCTTGCCT TCCTATTTAA AATGCTACAA ATAAATTTGC CGGCGAGTGA ATTTAATGT 180  
 40 TTTACAACGC TGTTCAATAC CTGGAATAA G 211

## (2) INFORMATION FOR SEQ ID NO: 1335:

45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 129 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1335:

CTTGAATCTC TTGTGCCTCT GTGATGTATC ATCAAATTAT TTGCACTGCT TCTTCTTTTA 60  
 55

TCCGCTCGC

129

## (2) INFORMATION FOR SEQ ID NO: 1336:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 633 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1336:

15	CATGATGGCn TCTTACCAA GGCGATTTTA AGAGCAATGA TACCAAGATA TTTTAAATAC	60
	TGATCAAAGT TCAGGTGGTA GCACAATTAC ACAACAACCT GTTAAAAATC AAGTTCTTAC	120
	CAACGAAAAA ACATATAGTA GAAAAGCAAA TGAATnCGCC TAGCAATTAG ATTAGAACAC	180
20	CTACTCTCAA AAGATGAAAT TATATATACA TATTTAAATA TAGTTCctTC GGTAGAGATT	240
	ATAATGGCGC TAATATTTCC GGAATTGCAT CCGCTTCATA TAGTCTATTT GSTATTCCAC	300
	CAAAAGATTT ATCAATTGCA CAATCTGCAT ACCTTATCGG TTTGTTGCAA AGCCCATATG	360
25	GCTATACACC CTACGAAAAA GATGGAACGT TAAATCGGA TAAAGATTG AAATATAGTA	420
	TTCAAAGACA ACATTATGTA TTAAAGCGTA TGTTAATCGA AGATCAAATC ACTGaaaaAG	480
	AATACAACGA CGCATTAAAA TATGATATTA AATCACATTT GTTAAATCGA AAAAAGCGTT	540
30	AATTGATGCT CACTTTTTAA AGTAACCACA ACAATGAATC CAAATATTAA AAACAGCACT	600
	AAGATTATTT TCAATTAGAA AATTCTCAC TGC	633

## (2) INFORMATION FOR SEQ ID NO: 1337:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1337:

45	ATCAATATTT AGCAGTTATC ATTATGCTTG AACGGTGGT AAAGGCGGAG AAGTCATCCA	60
	CTTTTTCCTA TACTACAAGG ACCTTTACTT TAAACAACG AATTACAAA ATAAAAGGCA	120
50	TAATTTCTTT TCTGTCACAT CGCTCATTCT AACTACTAGA CTTTTAAAT CGTTCCTGTA	180
	ATTTAACTC AATCAACTnt CAATTAATGA TGCATAATAT GATTATAAGT ATAGTAGTTA	240
	ACTTCAAATA TCTTAGAAAT GTCCTGTACT ATATCTCTTT TATTCTCAA AGTCATAGGT	300

## (2) INFORMATION FOR SEQ ID NO: 1338:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1338:

TACGGCATAT ACCTCGTTCA TCAATGTTTCG TAAACATTAT TTAAAACATC TCTTACATCT 60  
 TCGGTTGGAA GTTCTTCATA GTCGAATTTC ATTGTnTTAT CAAAGTTTTTC CATTGCGAC 120  
 ACTCC 125

## (2) INFORMATION FOR SEQ ID NO: 1339:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1339:

GAGCTTCGTT CCATTGTTAT CAAACGATTG CCATTCTGAA ATGCTGTAAA TAGCATGCTT 60  
 CAAATCATCT TGTGCCTGCA GCAGTTTCTT TGAATATGC TTCATATCAT T 111

## (2) INFORMATION FOR SEQ ID NO: 1340:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1340:

TCACACGTTT AGTTTTCTAT GAATACCAAT ATTTTAACAC CATGTTTAGC CAATTTGTCT 60  
 GCTAAATTAA TCGTGTGTTGT CCTCCAAATT GACACGCACC TTTAGTTTTT CTAAATAATG 120  
 ATATCATCAC ATCTCTCAGT TAAAGGTCAA AATATTTG 158

## (2) INFORMATION FOR SEQ ID NO: 1341:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1341:

5 GCTTCAGGTC AATTAAAACG TTCAAGAGCT TTCACATCTC ACTTATTCGC AAACAAGAGC 60  
 ACTAAACAAA AACGTCAATT ACGTAAAGCT AGATTAGTGT CTAAGAGCGA TATGAAACGT 120  
 GTAAAACAAT TATTAGCATA CAAAAAATAA GAACAAATAC AGAAATCGGT AGGAATTACC 180  
 10 TAAGGAGGAA TTTTATATGC CACGAGTTAA AGGTGGAACA GTAACAAGAG CGCGTCGTAA 240  
 AAAAACGATT AAATTAGCTA AAGGTTACTT CGGTTCAAAA CATACATTAT ACAAAGTAGC 300  
 TAAGCAACAA GTAATGAAAT CAGGTCAATA TGCTTTCCGT GACCGTCGTC AACGTAAACG 360  
 15 TGACTTCCGT AAATTATGGA TTACACGTAT CAACGCAGCA 400

## (2) INFORMATION FOR SEQ ID NO: 1342:

## (i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1342:

25 GTTGAACAAG GGCAACAAA ATTCGAGCG AAACAGATTT TTGAATGGTT ATATCAAAAA 60  
 30 AGAGTAGATT CGATTGATGA AATGACGAAC TTATCGAAAG ACTTACGACA GCTTTTAAAA 120  
 GATAACTTTA CTGTTACAAC TTAAACAAC GTAGTAAAC AAGAAAGTAA AGACGGTACA 180  
 ATTAATTCT TATTGAATT ACAAGATGGC TATACAATTG AACTGTTTT AATGAGACAT 240  
 35 GATTATGGAA ATTCAGTATG TGTAACGACA CAAGTAGGTT GTCGCATCGG ATGTACGTTT 300  
 TGTGCTTCTA CACTTGGCGG CTTAAAAAGA AACCTGAAG CTGGCGAAAT TGTTCACAA 360  
 40 GTTTTAACAG TTCAAAAAGC CCTTGATGCT ACAGAAGAGC 400

## (2) INFORMATION FOR SEQ ID NO: 1343:

## (i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 399 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1343:

50 GAAAATTTCA TCAGGTGTTG GCgTGAACG TACATTCCCA TTACACACAC CAAAATTGA 60

55

TTTACGTGGT AAAGCTGCTA GAATCCAAGA AATTCGTTAA TCAGCATTTA AACAAAGCTA 180  
 TGATGAGTC AAATTCGACT CAAACAATAA AGCCATCTAG GTCACITTTA TGGAGTGATA 240  
 5 TAGATGGCTT TTTTGTCTGT TTAGTTAATG TAAAGTTGAT AATGTAATTG TTTATTCCTT 300  
 CTCTATTTCAT AACGTGTTTG CTCAAAATGG TTATATAAAC AAAAATCTAC TAAGTGCCAT 360  
 TGAAAAGGAC TTAGTAGATT TATTAAATAT ATGCGTANA 399

(2) INFORMATION FOR SEQ ID NO: 1344:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1344:

AAC TTACAAC ACCAGGTAAT AACAGCAATA AAGGCACCAG TTAGTGCGGT AATGCCANTA 60  
 TCTAGGCCCTT TAGGTTGCCA TAGTACGAGA TGTAGAGGTA CTAGAGGAAT GAGTGTGCGT 120  
 25 AAAGTTGTCG TCGT 134

(2) INFORMATION FOR SEQ ID NO: 1345:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1345:

TCATAATAAA CAAGTTCACA TGAATCACAA CATCTGAAGA CAATGTTCAA AATGAGGCTG 60  
 40 GCACAATAGA TGATCGCAAG TCGnATCATC ACACAGTACT GAAGCAAGA 109

(2) INFORMATION FOR SEQ ID NO: 1346:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1346:

CCATATCTGG nACGACCGAC ACCTTTACCA CCAACGATTG GTGCCATTTG TTTGCATAAG 60

## (2) INFORMATION FOR SEQ ID NO: 1347:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1347:

CAATTGAAAG GTGAATTTTA TAGGTCCATG ACAAATAAG GCTTGTTAAA GCTTATTAAC 60  
 ACAGTTTCAT CAAATAGTTA AATTAGTTTT TGTTTTGCAA TAAATTGGGT ATAGATTACA 120  
 AntG 124

## (2) INFORMATION FOR SEQ ID NO: 1348:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1348:

CATCAGTGGC CTGATCACCC CAACATTTGA CATCAATGCA TACCAGTTGA TTTGAACAAT 60  
 GATTGCATTG AGCTATCATC AAGTTTGTCT TTAAGCTACT AAACCCACGA ACCATGTTAA 120  
 CCCCCTGGTC ACCATCACCA ATTGCTCGAT CTAATTCAGT TAATTCAGAT TCATGTTTTT 180  
 TAAACGTTTC TTCTAAATTT AATAAACGTG CTTTCATATC ATcAtTTTCAT TGTGCaCtaT 240  
 AAaTgTATAT TaTTCATATT CACTTCTnAT TTAAAGTATG ACTTGTGTGTT GGTGCTAAAA 300  
 ATGChTCCAA ATATTCTGGT TTATnAGGCA CGATAGT 337

## (2) INFORMATION FOR SEQ ID NO: 1349:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1349:

CAGCACGTAA ATACAACAAA GCGATCCCCA GCTTGTGGCA CATCATTAAT ACCTGTAATT 60  
 TCAACAGGCG TTGATGGACC AGCCGTTTTG ATTCTTTGAC CTAAGTCATT ACATGCCGAA 120



## (2) INFORMATION FOR SEQ ID NO: 1350:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1350:

CAATTTTACT TTGAATTTCT TTTTATCTT TTCTAGTTTT ATCGTCCCAC TCTTCAATCC 60  
 ATTTTTTAGC TTTATCTTCA TTATTAGTCA ACTTGCCTAT TTCTTTTAAT ATTCTTTATG 120  
 ATTGTATTTA TTGTATGTAT ATGGGATTGT TGGCGCTATT TTTTGGTATT TTTTATATT 180  
 TTTATCCATA GcATCTACAA CAATTAAATC TGTTTTGcT TTAGCAACTC TTTCAACATC 240  
 ATTTTCTCCA ATATAATCAA CCCCTTTTAA ATAAGGTTTT AAAATTGAAG AATCTTTAGT 300  
 TATATCTGAA ACAGCAATTG GTTTGATTCC TAACTTTATA AAATCACCAA CATAAAATCC 360  
 AGTTAATACA GCAACTCTTT TAAGGTTCTC nGGGACTTT 399

## (2) INFORMATION FOR SEQ ID NO: 1351:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1351:

TAAAACTTAG GCGGTTTTGC ATGATTATAG CGCTCAACAC GTTTGAAATT ATAGGTCATC 60  
 TCTGGTATTC TTGTACGATT CTTTTTCCAA TCTAAATCAA AGTTTTC AAT TTCTTCTTTT 120  
 GAGTTTAGAC TTAATCGATC ACGTTCATGT TCTTTAAAAG ATGGAATAAC TTGTTTAAGT 180  
 GACCCTTCCA TTCTTAATTG ACCATGTGAA AACCAAGCTA TGTAGTTACT CACTTGTGaa 240  
 ATTTTATCAA TATCATCACC AATTGACACA ATCGTTAAAT TATTTTCAAT ATAATCATTT 300  
 GTTAATTCAA TCGCACGTTT CATAAATTGT GGTGTTAAAT AGTCAATAAC ATGATTTAAA 360  
 ATAATAATAT TTGATTTTGA TGAGCGTGCA ATACTTAATA 400

## (2) INFORMATION FOR SEQ ID NO: 1352:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1352:

5 AAGGGAACAA AAGCTGGAGC TCCACCGCGG TGcGgCcGCT CTAGAACTAG TGGATCCCCC 60  
GGGCTGCAGG AATTCGGCAC GAGCATATCT AGTATTTTAg GACGGAGGnA GTACATT 117

## (2) INFORMATION FOR SEQ ID NO: 1353:

10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 153 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1353:

20 AGTTCAGGAG AGTTATAAAT ATTAGGGTGG TACATGCCCC AAATCATTGG AATTGTTAAA 60  
GTAGATTTTA CAGTTTAGAG ATAACAGACA TGTCTATATG AAGGGCTGTC TACCCTCGTA 120  
AGGTTATATC CTACAGnTGA ACGTATCAAG CTT 153

## (2) INFORMATION FOR SEQ ID NO: 1354:

25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 159 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
30 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1354:

35 TGTGTGAACA GCTCTCTATG TTTACGTTGG AAGTATGGTT TATTTTTTCAT CTTACATTT 60  
AGTTCCTTAT TTAAAAGTGA TAGAGCAATT GCACTCGTAG GTCAAGAAGC GGGATGCCAA 120  
CACAAAGTTC ACAAGAnAAT ACACTTTTGA AAATATTGG 159

## (2) INFORMATION FOR SEQ ID NO: 1355:

45 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 118 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1355:

50 CGnCTTCCTT CAACCATTGT AGAAGTTGTC TCATATACTT ACTACGGCTT GCTAATACTC 60

55

## (2) INFORMATION FOR SEQ ID NO: 1356:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1356:

GGATTCATTG GTGCTTATTT ATTTACATTC AATAATGAGA nCTTTACACA ACCAATTGGT 60  
 CAAATTATAG ATGTCAACAT GTTTCTTCGA CACCTACAAA AGATGCACAA 110

## (2) INFORMATION FOR SEQ ID NO: 1357:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1357:

TAATGGTGGG GTATATTTAT ATTAGTACCG AATTTTAGGn GCCTCACTAT CATTTATCAA 60  
 ATTATTTAAA GTGGGATCCT ATCGCAATCA ATTGGCAGGG GCAGAATAAT GGCATTAGTC 120  
 GTTGAAGATA TCG 133

## (2) INFORMATION FOR SEQ ID NO: 1358:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1358:

GTGTCGGTAA GTCCACTTTC TTAAATCATT ATCGTCCAGA ACTTAATCTT GAGACAAATG 60  
 ATATATCAAA ATCATTAAAT CGAGGAAAGC ATACTACAAG ACATGTCGAA CTATTCGAAC 120  
 GTCAAAACGG TTATATTGCA GACACACCTG GATTCAGTGC TTTAGATTTT GATCATATAG 180  
 ATAAAGATGA AATAAAAGAT TATTTTCTTG AATTAAATCG ATATGGTGAA CATGTAAGTT 240  
 TAGGAATTGT AATCATATCA AAGAACCTAA TTGTAATGTT AAGCATCAAT TAGAGATAGG 300  
 GAATATTGCG CAATTTAGAT ACGACCATTA TTTACAATA TTTAATGAAA TTTCCAAATA 360

## (2) INFORMATION FOR SEQ ID NO: 1359:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1359:

CTGTTTTAGT CTTATTGATT GCCTGACCAT TAACTAAGTA ATTTGTGTTT GAAGCGGTTA 60  
 ATTGAGCAAT GATTGGAATG TCGTATTTCT TTCTCGTTTCG TGAAATGACA TTTGTTAAC 120  
 CTTCTAGGTC GTAATACGTT TCGAAAAGTA GCGCGTCAAC GCCTTCTTCA ATTAAGGTGT 180  
 CTATTTGAAT TCAGTATGAT AAAGAATAGT TTGTAAGCTG ATATCCCCCT GTTTGGATAC 240  
 CTCTAAACCC CACCAACTGG GGCCCAATAT ATACGTAAnc TnTAATTGGC nGGCTTTTTT 300  
 GCGATGCGAC GGGGGGCTGG AGGATGCTTA ACCTTAACCT CCAGACCGAA CCGTTTAACC 360  
 TTTCCAAAAT TGCACCATAG GAATGGGTGG AT 392

## (2) INFORMATION FOR SEQ ID NO: 1360:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1360:

CCATGGTTAT TTCTTCACA TTTCATGTAT ATATATTTGT TTATTATCTG TCTCTACTAG 60  
 ACTGTAACT CCAACATATC TGTTTTATAA ACCAGAGAGC AGTCATTCAA TAAATAAACA 120  
 GATCTGAGGG CCAACTGGCA TGTTGTCAAC TTATGATATT 160

## (2) INFORMATION FOR SEQ ID NO: 1361:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1361:

GTATCCTAAA GATTCAGTTA ATCGGAGCGT TGTATTGCAT GAAGGTACAT TCGGGAATGC 60

ATATTTATTC ACGATnTTAT TTAGCGAC

148

(2) INFORMATION FOR SEQ ID NO: 1362:

- 5 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 147 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1362:

15 AAAATTACTA TGAAGATTGC ATTAGGATGC GACCATATTG TTACAGATAC AAAAATGCGT 60  
 GTATCTGAAT TTTTAAATC AAAAGGACAT GAAGTCATTG ACTGACACTT CACTCATnAG 120  
 TGGCGACAGT GTACGTATCA GACTTAG 147

20 (2) INFORMATION FOR SEQ ID NO: 1363:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 108 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1363:

30 CTGGCAAAGA AGACAACAAC AAGCTGGTAA AGAAGCAACA ACAAGCCTGG TAAAGAGACA 60  
 ACAACAAnCT GGCAAAGAAG ACGGCAACAA GCTGGTAAAG AAGCAACA 108

35 (2) INFORMATION FOR SEQ ID NO: 1364:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 153 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1364:

45 GACAATGTTG CTGTAATGGG GAAGGnAATG GGTGGTACC GCGAATTGAA TAATTTAAAA 60  
 CCGTAATATA TAATCGTAAT TGTTAAGCCC TCATTTTAT AAATTTTGA CCTCTTGAAA 120  
 AAGTTACGTT TTCAAGAGGT TTTATTTATC CTA 153

50

(2) INFORMATION FOR SEQ ID NO: 1365:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 184 base pairs

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(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1365:

TAAGAGAATT ATATGCATT CAAACGAAAC AACAGAAAA ACGGACCAAA CTAAGTGTCA 60  
CAAGTACAAT CGCTGTACTA CTGCAAAACA CGCAAAACGA AACTTTACGT ACACACAAAA 120  
AGACCACCAT TCACGTCGGG ATTATTAAAA AGGTAGTCTC GTACATTTAT TAACTACTT 180  
ACGT 184

15

(2) INFORMATION FOR SEQ ID NO: 1366:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 452 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1366:

25

ACATTAGATG GGTCAATCAT GTTATACACG GTGATTTAGG GGAGTCAATC AAATATAAAA 60  
GGCCGGTAAT TGATGTTATT GAGGAAAGAA TTCAAATAC AATATTACTC GGTGCTATGT 120  
CATTAATTAT TACTTATATT ATCTCATTG CTTTAGGAAT AACGTCAGGT AGATATTCTT 180  
ACAGTTTGAC GGATTATACT GTGCAAATAT TTAATTATTT GATGTTAGCC ATTCCATCTT 240  
TTATTGCGGG AGTATTTGCA ATTATATTT TTTCTTTTGA ATTACAATGG TTCCCGTTTC 300  
AAGGTTCTGT TGATATTAAC CTAAAGAAG GTACTTTTGA ATATcATATG AGTAAAATAT 360  
ATCACACATT TTTACCTGCA TTCACCTTAG GTTATTATC TACTGCTGGT TATAWTCAAT 420  
ATTIACGTAA TGaTATTATT GAAAATTCTA AA 452

40

(2) INFORMATION FOR SEQ ID NO: 1367:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 141 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1367:

50

TTGTGAGTAA TTGGACAATA TAAGTGTGG TCTTGGATGG CATATCCTTG GTACGACCTG 60  
GGCAACTTGC TTCATAGCGC AGTTAGGAAC TGATCAATCA TTGGCGTTTT GATACCTAGC 120

55

## (2) INFORMATION FOR SEQ ID NO: 1368:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1368:

TGGTGCAAAT TAAAACGGTT GCATATGCAC GTACGACGTA TTGCTAAATA CAATCAATTA 60  
 TTACGTATCG AAGATGAATT ATTGAAACG CTAAATATGA CGGTATCAAA TCATTCTATh 120  
 ACTTAG 126

## (2) INFORMATION FOR SEQ ID NO: 1369:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1369:

TGhAAAGTTC ATCAGGGAGC CATTTTTACA ACACAGGGCA CATACGGGTT GTGTTTAGGT 60  
 GCAATTGCCC CAAGCGGACA AAGCATTATT TAAAGTTTCA AGTTCTTCAA CGATTTATTA 120  
 GTGCACAGGA TCCTGTTAAG AGGTATTTTG AAGACTTCCG 160

## (2) INFORMATION FOR SEQ ID NO: 1370:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1370:

AGTAATTCTG CAAATGCCGC AGATAGCnGT ACTTTGAATT ATGAGGTTTA CAAATACAAT 60  
 ACCAATGACA CGTCAATTGC TAATGACTAT TTTAATAAAc CGGCAAAGTA CATTAAAGAAA 120  
 AATGGTAAAT TGTATGTTCA AATAACTGTC AACCACAGTC ATTGGATTAC TGGAATGAGT 180  
 ATCGAAGGAC ATAAAGAAAA TATTATTAGT AAAAACACTG CCAAAGATGA ACGCACTTCT 240  
 GAATTTGAAG TAAGTAAGTT GAACGGTAAA ATAGATGGAA AAATTGACGT TTATATCGAT 300

AATGGACCA CTGATGTAGC AGGTGCTAAT GCACCAGGTA

400

(2) INFORMATION FOR SEQ ID NO: 1371:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 345 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1371:

CATCAAGAAC ATGTGAGACC ACAATTTGAA TCACTTGAAA AAATAAATAA AGACATTGTT 60  
 GGATGGATAA AATTATCAGG AACATCATT AATTATCCAG TACTACAAGG TAAGACAAAT 120  
 CACGATTATT TAAATTTAGA TTTTGAGCGA GAACATCGAC GTAAAGGTAG TATTTTtATG 180  
 GATTTTAGAA ATGAATTGAA GAATTTtAAT CATAATACTA TTTTATACGG GCACCATGTC 240  
 GGTGATAATA CGATGTTTGA TGTGTTAGAA GATTATTTAA AGCAATCGTT TTATGAAAAA 300  
 CACAAGATAA TTGAntTTTG CAATAAATAT GGTAATCTCC ATTGC 345

(2) INFORMATION FOR SEQ ID NO: 1372:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 154 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1372:

TTGAAAAGCA GTTTGGATTT ATGCTCAAAC CATGGACGAC GGTTAGGTTT ATGAATGTTA 60  
 TTCCAAATAG GTTCATCTAT AAAAAGTAGT GGAAAGTGA AAAAATnAGT GGACCTTCGA 120  
 TAATACGATG TATTTATCGT TAGAAGCAGT AATA 154

(2) INFORMATION FOR SEQ ID NO: 1373:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 136 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1373:

GAGCCTAATT ATTCAAGCCA AATCGCATAT GAAATTGATA AAGAAGTTCA ACGAATCGTT 60



CTATACnAGA ACTATC

136

(2) INFORMATION FOR SEQ ID NO: 1374:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 358 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1374:

15	ATCTTTAACA ATTAAAACCA TACTATCTTG AATCATCATC AAATTTAACG CATGTGCGTC	60
	AAGTTGTTTC ACTTTAAAGA CTTCAATTATT AAGACCGACC TTAGACTGCT TTTTAAAAAT	120
	AGGTACATTC GTAATCATAC CTATACTTTG ATTGTCTAAG TGTAATTTGT TTTGGTGATA	180
20	TCGATTATAA TCTTGTGCAG TAAAAGCTGT AATCATTACT GATTGTCTTG AAAATATCGC	240
	GCCTTCATTA CCAATGAAGT CTATTGGAAT aTCATCACTA GCCTGTTTTA ACTTGTAATA	300
	AGCACGATTC TnTTCTAAAG AAGCTCTAAA TAATGTCGTT TCATATACTT TGAAGTCT	358

(2) INFORMATION FOR SEQ ID NO: 1375:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 122 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1375:

35	ATATTGTGTG CTAAATTGTC TTAAGTATGT TTTTGTGTTG nAAGTAAGCA TATGTTATTG	60
	TCTTTTAAAT TGTTGTAAAA GTGCTGTTTT CATAGAATTA ATATCAGACA TCTTTATTAG	120
40	TA	122

(2) INFORMATION FOR SEQ ID NO: 1376:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 467 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1376:

50	CATTTTCTTC GGTTTCTGTC TTTTATGCG TAGATTATT TTCTTGTCT TGTTATTAC	60
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CGATAATTAC GATGGTAATA AGAAGTTTTT TCAAATATAA CGCCTCCATG TTAATGAAAA 180  
 GTAGTTGATA CGTGAAGCTA AATAATTnAT TTCAATATTG CCATAATCAT TTTAAAAAAT 240  
 5 AAATATTAGA AAAGTAGGCG ATATTAAATAT TTTCAATTGTt TTTTGTGTAC TTCAATTAGT 300  
 ATAACAAAAC TGTTATGTAT TTATAAATAT AATCATTAGT ATTTTATATGG CTGAAAAAGT 360  
 TATAATAAAA GTGTAAGGAA TAAAATATTT GTATGGAAAA GAGAGATAAT TATGAATAAA 420  
 10 ACCAGTAAAG TTTGTGTAGC AGCAACATTA GCATTGGGCA CACTGAT 467

## (2) INFORMATION FOR SEQ ID NO: 1377:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 128 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1377:

AGGTGTTAGA ATTTATTTTA AGTGTATAC GTGTCTTCCA GAAATTGTAA TGGCATTATA 60  
 25 TTTATnAAAG TGTGGCAGG TTATTTTCAG GTGTATTAGT TTAGGTATCA TTCGTAGTAT 120  
 GCTTGGGA 128

## (2) INFORMATION FOR SEQ ID NO: 1378:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1378:

GGACGCTAGA GGATCCCGGT CTGGAAAATA TCGTCCAGAA CTTAGAAATA TGAAATATT 60  
 CCCAAGACCA ATCGATAATA TATTGCCAAT ATGGCGTGCT GTTGGTGGTC CACCTGCAAG 120  
 TGCTATTAAA GCGGGAAAAC AAGGTGTGCC AATGATGATT ACAACCCCTG GTGGCCCAGC 180  
 45 AATGAACTTT AAAGTTCTA TAKATGCTTA TCGTCAAKCG GCAACTGAaG CAGGTTTCGA 240  
 TGCTTCGCCT AAGTCTTTAC CAGTAAGTAC AGCGAGTCTG TTTTATACAG CTGAAACAAC 300  
 TCAGGATGCT ATGAGAGAAT TTTATCCACA TTTGAATACA GGGATGTCAT TTATTCGTGG 360  
 50 TnGTTGGTTA TCCGAAACAG CAATnGCTAA TTCGTCAGTT 400

## (2) INFORMATION FOR SEQ ID NO: 1379:

- (A) LENGTH: 108 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1379:

10 AACTACAACA ATTAAACGAC CAACCTTAAA AaAATACGCT CTTATGCATT GGATTAGTCC 60  
 TGATTATACA ATTAACTGA ACAAATACCC ATCATTTAAA AGACTTAG 108

(2) INFORMATION FOR SEQ ID NO: 1380:

15

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 118 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1380:

25 AAGTGGGGGG AATCAGTATG TTACATTTAC ATATATTAAG TATTAGCGAT TATTTTATTT 60  
 ATCGCTACAT ACTTAACCAT TTCAAAAATT CAAGGCGGnT CACCATTTTC CAACCCGT 118

(2) INFORMATION FOR SEQ ID NO: 1381:

30

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 114 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1381:

TCATGAAAAC ATTTATTTTA AAATTTGATA TTTGTTCAAT AATATTCGAA ATTAACCTnT 60  
 40 GTGTATAGAT TTTCTTTATA TCCTGAGAGA CATGTACTAT AATGTTTGTG AATA 114

(2) INFORMATION FOR SEQ ID NO: 1382:

45

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 165 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1382:

CGGTATTGAT CATATAAATA GTGTTTAGAT GCTATAGTCG GntGACTTAA GTAATTTAAA 60

55

GTTTTCTTCT GCCTTGCTTA AAGATATATG ACAGGGTGCT GGCAT

165

(2) INFORMATION FOR SEQ ID NO: 1383:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 111 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1383:

TTTGGTGTGA TGGAGTATAT TTAGGTGTGG AAATCAAGAG GGAATTCCAT TTTCAAACAT 60  
 CCAATTAGAG TCGnAATAAG AACTCGCTAT CGGTCCAATT AACTGATTCA G 111

(2) INFORMATION FOR SEQ ID NO: 1384:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 144 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1384:

CATTTAAATA ACGTTGTGAC CATGTGCTTT ATGCTATGTG CTAGAAAATC CATGTTTTTA 60  
 TCTAATTTCT TAATAAATTG ACATTAGTT GGATTCTTGT CnCTTCACG TTTCGACATT 120  
 GGATGACTGA ACGCATGAAA TCAG 144

(2) INFORMATION FOR SEQ ID NO: 1385:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 103 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1385:

TCGTTGTGCA GCAACTGCAT TACGCTGTCT CATTAAATGTA AGCGCAATGG CCATTGGTT 60  
 TTTCnATAGT GGAATACTTG TCAAAATTGA ACATTGTATC TTC 103

(2) INFORMATION FOR SEQ ID NO: 1386:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 533 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1386:

5 CCAGnACAAA TACAACGTTA TATTCAACAA TTAGAAGACT TAGnATAGAT ATAAATTGAG 60  
 GGAGGACATC GATATGGCAT TTGAAGGGTT ATCAGAAACC TTGCAAGCGA CGATGCAAAA 120  
 AATGCGTGGT AAGGGTAAAC TTAAGTGAAGC TGATATAAAG ATAATGATGC GTGAAGTAAG 180  
 10 ATTAGCGTTA CTTGAGGCTG nACGTAAACT TTAAAGTGGT AAAAGAATTT ATTAAAACAG 240  
 TATCAGAACG CGCATTAGGT TCCGATGTAA TGCAATCATT AACACCAGGG CAACAAGTTA 300  
 TTAAATAGT TCAAGATGAA TTAACGCACT TGATGGGTGG AGAAAATACG TCGATTAAAn 360  
 15 TGTCAAATAA ACCACCTACT GTTGTtATGA TGGTTGGTTT ACAAGGTGCT GGTAAAACAA 420  
 CAACTGCAGG TAAATTAGCA TTATTGATGC GTAAAAATA CAACAAnAAA CCTATGTnAG 480  
 TTGCAGCAGA TATTTATCGT CCAGCAGCGA TAAATCAATT ACAAACAGTA GGG 533

## (2) INFORMATION FOR SEQ ID NO: 1387:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1387:

30 TTATTTACAA GCCATTAATA TATTTTAGGT TTGTTCTGCA TCGATTCATT GGTGCTATTT 60  
 TATTTACATT CAATAATGAG ACTTTTACAn CAAACCAATT GGTCAAATAT AG 112

## (2) INFORMATION FOR SEQ ID NO: 1388:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1388:

45 ACACCTACAG TTAATAGTAT CAGTGCACAC TAAAGTCCTA ATACTTTCAA CCATGACTAA 60  
 TGATGTATCh TCTTGCCCAA CGAACGCGTT GTGCCAAATT GAATTAGACT GGACGGAC 118

## (2) INFORMATION FOR SEQ ID NO: 1389:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1389:

CGACGACACA ACTTTATAAT AAAATCTTAG ACAATAACGA AGGGTATTAA CAGAACTTGG 60  
10 TGCTGTTAAT GCAAGTACTG GAAAATATAC TGGTCGTCGC TAAAGCAAAT TTTTGCTCTG 120  
ACCTnCAATG GTACTTGTTG GGAATA 147

(2) INFORMATION FOR SEQ ID NO: 1390:

15

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 161 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1390:

TTTTTGATCA TGATTTTTGG GCATGGATCA ATCACTTGCT TGGCCAATGG TCTTTCAACA 60  
25 ATTTGGATAT CTGACCTTAT TCGCTTTATC TAGCACTTTT GnCAATTGT TGGCATTGGA 120  
AAACATGTGT TTAGATTTTT GTATGCCTCT CGCAGGCTTT T 161

30

(2) INFORMATION FOR SEQ ID NO: 1391:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 102 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1391:

40

GCCGCACGCG CGCGATTCTC GGCCTAATAA GAAAACAAAT AATTCCAATT CATATATGnA 60  
CATTTTTGCC TCCTTATTTT TGAAAATGT GGAATTGGAA TT 102

45

(2) INFORMATION FOR SEQ ID NO: 1392:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 412 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1392:

55

AAAATGCTAT TAACAACGTA TTAAATAATC AAGATTACCA TGGTATTAAA GATAAACCAT 120  
 TCGCATTATT CGTAACTGGA TTTTTCGACA ATGTAACAGA TAATACTGTT GGTATTAACT 180  
 5 TTAAGACAAA AGACGGTTCA ATAGCAGTAT TTATGCGTCC AGATATTGGA GAAACATTTA 240  
 GCGAGTTTAG AACATTCTTA GCCGTCTTGT TAATGTTGTT ATTATTTATC TCGATTTCAT 300  
 TAGTTATCGC ATCAnCCTAT TCAATCATTG GTCCAGTAAA AAAGTTAAAG CTAGCGACCG 360  
 10 AACGCTTAAT TGATGGTGAT TTTGAAACAC CTATCAAACA AAcnCGCAAA GA 412

## (2) INFORMATION FOR SEQ ID NO: 1393:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1393:

AGCAAnTGGA TTGCAATGAG TTTCTTATAT TTACAAGGTG GTAGATTGAT TGATGTTTTA 60  
 25 ACTGCGATAT TAGCAGTAGT CTAGATACCT AGTCACTGAG ATTTTAGATC GAGTTACACG 120  
 CACATTATCC GATCTGTCTA TATGGATATC CGTATGACTA CCTATCCCAC GGACTGCACA 180  
 TACTGG 186

## (2) INFORMATION FOR SEQ ID NO: 1394:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1394:

TCTTTAAAAG AATCAGGAGC TTGGAAGAAG TATATCAGGA TCATTAAAGTC AACAAATTAC 60  
 45 GCGATATGAA AATTTGAATA ACAATTTGnA AAAGCATGCT TCCGATAATC AGCAAGCC 118

## (2) INFORMATION FOR SEQ ID NO: 1395:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

GGTTACCTCG GATGGATGAT TACTATTTTG GGCTGGGCGC CGGCTTTnGT TATTAGTGGT 60  
 GGCAATAGTG GCAAAGTGTC ACAAAAAAAT CCAATAGCTG GAAACCCGGG TATATTTGGG 120  
 5 TATTAACGCC GGTGGCCGGG ATTTGGCCAA TCGCATTAAT TTAATGGCCA TTGGG 175

## (2) INFORMATION FOR SEQ ID NO: 1396:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1396:

AGAAACTTAG ACGATTAGTA TCATATATTA GAACACnGCA CCGAACTTGA AATCATGGCT 60  
 20 GATATCGCAC CTTGAAGAAG CAAAAATGCC GCACGACTTG GCTTTGATAT ATTGGCACGA 120  
 CTTACATGGC AT 132

## (2) INFORMATION FOR SEQ ID NO: 1397:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1397:

AGAGGTCCGG CTATCTATCA AATAAAGTGG TCATTTAAAG CGTACACTTC GGGTGCGTTG 60  
 35 ATTTCTTACT TTAGGTGTAG GACAATTGTA TCGCATCTAT CTTTACnCTA CCTGCATTGT 120  
 T 121

## (2) INFORMATION FOR SEQ ID NO: 1398:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1398:

CGTTCGTATA ATCTCACTTG CATCnTGAAT TGAACAACAT CCTGTCATTT TAAGACTGCT 60  
 50 AAAnGTACAG CTGAAAACCA AGTAAGTCCG TTTCGTCTGG CTGTGAAATG GATCAAGGAG 120



AAACACCTCA TCCAAAGTTC AG

202

## (2) INFORMATION FOR SEQ ID NO: 1399:

5

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 165 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1399:

15

CGTTGGATCA CTGATGCATT CATAAATGGG TGAACnTAAT GTAATGTTAA ATCTATCACA 60  
 GCGCGATAAC AGCAAGAATA TAGTGAACAC CATAAATTGA GCATATCAAT GCCATATTCA 120  
 TGGATACACA TAGTTCACCT GGTGGTCGGT GAAAGCCTGT AGATG 165

20

## (2) INFORMATION FOR SEQ ID NO: 1400:

25

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 107 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1400:

30

ACACCTTTGT TTTTGCAAAG CTGTACCACA AAGTACTGGG TAGAATTCTA CGTTATATGA 60  
 GnCTTGCGCT ATAGCTTCTT TTAATTCATA AACTGTAAAT TTCTTCG 107

35

## (2) INFORMATION FOR SEQ ID NO: 1401:

40

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 106 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1401:

45

TTTTGTCTAG AACATCTGC TTCTAATAAT GATCGATCAG CAGCCATTGT GCTTAATCTT 60  
 TCATCCCACA TCACAATCTC AATAGAAGGA TAAGCTTCTA ATAATT 106

## (2) INFORMATION FOR SEQ ID NO: 1402:

50

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 102 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

55

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1402:

CAATGTTAAA CCTACACCGT TAACAGCACA CATGATACTA AATTGTTGGG GTGTCATATT 60  
 5 ATACAATGTT GAGTAA TAAA TGGCGATGCA GATGAATAAC TA 102

## (2) INFORMATION FOR SEQ ID NO: 1403:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 169 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1403:

TTTATTATTT GTGCTACAAC TACTTAAAAA AATCAGTAGA TATAGCATTAA AACATATTTT 60  
 20 CATCCCCyTG AATTTTAAAA ACTTTTTC AAAGCAACACC TCTAAAAATA AATaCAATAT 120  
 ATTATAGCAA ATAGAAATTA TTATTTTGTT AAATTATGTT GTnCATGTT 169

## (2) INFORMATION FOR SEQ ID NO: 1404:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 106 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1404:

TTAGTTGATA AGTAAATCCG AGTGACATTG GGATTACCCC CAACCGACTC TATTCCAGTC 60  
 35 TGAAATACGT GAACCCATAA nATCCTATGT CCAGATTAT ATTTCT 106

## (2) INFORMATION FOR SEQ ID NO: 1405:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 309 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1405:

TATTTTTGCA GCAGAGATGT TCGCGACAAG GTTTACGCCA AATTGTCACT GCTACTGCGA 60  
 50 TGTGTATTGC ATGCAAGTGC AGGnAATATA TTGAACATTT AAACGATCAG TTTAATTGCA 120

CTTTAATAAG CAATTTGTAC TGACTGTCGA CATTGCGTCA TGGTCTGTTT TTGTTTAACT 240  
 ATACTATnGG TGCGAAGTAG GCCTATGTTT AGAGGTCTAA CATGCCGTAG GTCTAATGGA 300  
 5 TCAGGAACC 309

(2) INFORMATION FOR SEQ ID NO: 1406:

(i) SEQUENCE CHARACTERISTICS:  
 10 (A) LENGTH: 144 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1406:

GTGGACCTGC AGTTAATTCA ACGATTTCAA GATGGGCGCC AAGAACGAAA CGTGGCCGAT 60  
 20 ACTTAGGATT CTGGAATCAT CACATAATCG TGTGCATGAG GTGTTTCACT TTGGGGTCTA 120  
 ATGATTCTTC ATGGAAnGTA TAGG 144

(2) INFORMATION FOR SEQ ID NO: 1407:

25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 115 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1407:

ACCTTTGCGT CCAGAATTAG CTACATGGTA AAGCTTCGTG TTACTATTTT AGGGATATCT 60  
 35 TCAACnCGTT TCACTTGTAT AATTTGTTTT TGTAATTGGT GAAGTCATAG TATAG 115

(2) INFORMATION FOR SEQ ID NO: 1408:

40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 115 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1408:

ATTGGTATTG GCGCTGTAGT ATAGCTTCAT TATCTGATGC CATTAGTATA CGCACACTnT 60  
 50 TTATTTATGG GCGTGGTATT CATCCTTATC GGGATCAATT ATTGGGTTAC ATTTT 115

(2) INFORMATION FOR SEQ ID NO: 1409:

55

(A) LENGTH: 123 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1409:

10 AACCAGATGa AAAGCAAATA TACATATATA ACTCTACATG GGGTCGTGGT TTGGATATTG 60  
 TTCATGATGC ATTCCGTATG CCAATGACAA AGCAATATAA AGATAAATTn CAAGAAGATA 120  
 AAA 123

15

(2) INFORMATION FOR SEQ ID NO: 1410:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 120 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1410:

CTnTTTATAT TGAGGATTTT GTATCATATA TGGATAATCA TTAAAGGTGT ATGCTCTTGT 60  
 TATCAGATCG CTACGGGTAA AATCGCTTCT ATAGGCATT TACATGCGGG CTTCTGCCGG 120

30

(2) INFORMATION FOR SEQ ID NO: 1411:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 455 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1411:

40

TCTCGTATTG CGTTTAGAGA ACATGCGCAC AAAGGACAAA TTCCAGGTGT TAAAAAATCA 60  
 AGTTGGTAAA ATCAAATTC GTACTTTAGC CCATTTACAA TATCAATAAA ACAATGTACA 120  
 GTATATACGA ATGCTATAAA CTGAATGTTT TCTCATATTA ATAAGGAAAC ATTCGGTTTT 180  
 45 TAATTTGCGT TAAAAATAA TTAGTTTTTA AAGGGGCTAT TTAAAGTGAA AATATTTGAT 240  
 TACGAAGATA TTCAATTAAT ACCTAATAAA TGCATAGTTG AAAGTAGGTC TGAATGTGAT 300  
 50 ACAACTATCC AATTTGGTCC GAAAAAATTC AAGCTACCTG TAGTTCCTGC GnATATGCAA 360  
 ACAGTTATGA ATGAGAAATT AGCGAAATGG TTTGCTGAAA ATGATTACTT TTATAATCAT 420  
 GCATCGTTTT GATGAAGAAG CAAGAATACC TnTTA 455

55

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 118 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1412:

ACAAATGTCAA ATCACAATAG CTGTTGTAGG CATTGTGATTA CAATGAACTA AAGGCAAAAT 60  
 TGGAGCAGTT ATCCATGAAT GATTAATAAC AACAAAAAGT ATGGGGTCAA GTTTAGGG 118

(2) INFORMATION FOR SEQ ID NO: 1413:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 245 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1413:

TGTTGACGAT ATAGGAATTA GCAAGAAATA GGCTAAGATA GTTTCGCACA ACTTGGGGCC 60  
 CAAACCACTTG CTGTTTGTGA GAATTAGGGG TCCATTTCTC GTGTTGGGGC CCGAACTAAT 120  
 AGTATGAATA TATATATCTA ATATTA AAC GGCAATATTT ATATGGTATA CATTTTTATA 180  
 TTTAGTATTT GTATAGACAT GCTAATTAGC ACTTTCTAAA AAGGGTTGAA ATGATATACT 240  
 GATGA 245

(2) INFORMATION FOR SEQ ID NO: 1414:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 252 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1414:

TTTTTGTTAT TCAAAATTTA GAGTGTGTTA TATGATAACG GTTTTTTCAT AGCGACTTGA 60  
 TCATTTTTTCG AAATGATGAA AGATATGCAA GTTCAATCAA TCGGAACAAA AATACTATAT 120  
 TATGGTAAGA AATTCCCGAA GACTAGCGCA CTCACACACA AGTGCATCCT CGCGAACAAT 180  
 GCGCACTTTT CACAAGCACA CAAACACAAG GCACAAGTGC ACGCANTATT AGACAATGGT 240  
 CTACCTACCA GA 252

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1415:

ATCTGCTGGA AGAGAAAAA GACGCTCTTA AACTGGCTT TAGAAGGTCA AGATATAGAA 60  
GnTATTAAAT CTAAAAAGA AGGAAGTTGA AAAAGTGATT CCAGGAATTT TC 112

## (2) INFORMATION FOR SEQ ID NO: 1416:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1416:

CTCAATTACA TTCAAGAAAA TGGGTGGAAT TACACAACGT TGGACTGAGA AGTATAGTTA 60  
ATAGCGCAAA TGChATAAGC CTTATATAAA AATGGGCACA ATTATTTTCAT GTACCAACAA 120  
GAAC 124

## (2) INFORMATION FOR SEQ ID NO: 1417:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1417:

TTCAAGAGCA CATACTGTAA CTCGTACGAG AATTTTTTTCA AAATGACGCG TCAATCTCAA 60  
TATCATCATA TGGTATTCCG AGTAATACCC CTCGnCACCT TTTTtaggTA GCGTCAATAT 120  
T 121

## (2) INFORMATION FOR SEQ ID NO: 1418:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1418:

CTACGCCATC AAGAGGGTGT TAGTGCTATT AACTATTGCG GCGAGAGCAA TTAGTCGAAT 60  
 5 GCAAATTAGG ACAAGTTGAT GAGTAACTAC nGCCAATATC GGTAAGTTTC ATGGCGGTTTC 120  
 AGC 123

(2) INFORMATION FOR SEQ ID NO: 1419:

10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 109 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1419:

20 CTTATAATCC TTACnGCAAT TTCACCTTGT ACGGAATTAA ACAACGGAGG CATTACTTA 60  
 CCCCCTTTAC TTAATACGTA CCAAACTTG GTCGTATTCA ACCATTGGG 109

(2) INFORMATION FOR SEQ ID NO: 1420:

25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 121 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1420:

35 GCTGTnGTGC TGCCAAGATG CTGATTGAAA AGTATATATG ATTGCATCAG TAGAAGAGCG 60  
 AGCAGAAAGA AGATATAAAG ATAATCAGTT AAGAGGTGTC GAATCAAATT TTGAAGATT 120  
 A 121

40 (2) INFORMATION FOR SEQ ID NO: 1421:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 128 base pairs  
 (B) TYPE: nucleic acid  
 45 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1421:

TGTTTTTACA GTCACATACA CTAGGCATCC TAGCATTATC TAAATTTAAT ACCATCGCAA 60  
 CTTGCGCTTT AATCTTCAAG GCCAATTAAA CCTCCTTCAT CTTTCTAACT GCTTAnATAT 120

55

## (2) INFORMATION FOR SEQ ID NO: 1422:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1422:

GCCAATCATT GTCAATGTTT AGGCATCANA TTTATCGAAT GATTTTCATT TGCCATGATC 60  
 AGTCAAGGCG GGGATTTATT CAAAAATTAT GACGCCTAGT AAAAAATTTT 110

## (2) INFORMATION FOR SEQ ID NO: 1423:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1423:

ATTACCTTGC ATGAATTTCC ATCTGTCAAA TGTGCGCCTT CACGAATTTG TTCGATAAAG 60  
 ATACGTTGGT CACCGTGAAT AATTTACCA GCTGCATTTT TCCATGGACC A 111

## (2) INFORMATION FOR SEQ ID NO: 1424:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1424:

TGTTGTGTGA TTGCGTATTC TCAGGTGAAT TCTTACATAT ATAGTACTTT TTGTTTCCGC 60  
 TTGATTTGAC CTTGCATATC TTTACATTC TTCGAAAATT GATCAAAGCh CTATTGAAAA 120  
 ACCGTATCAT ATACAnACCT CTAATTTTTT TGACTAACAA AAAGAATTCT TTGACGTATC 180  
 AACTATATCA TCATGACTTC 200

## (2) INFORMATION FOR SEQ ID NO: 1425:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1425:

5 TTTCTATAAT TTTAGACTAT TTCTACCATG TTGCTGAACA ATTTACTTAG ATAAAAATTA 60  
 TAAAAATTTG GTCAATTAAC AAAGTTAGTT TGTAAAAACG TATACTTTAA TTATTCCGG 119

## (2) INFORMATION FOR SEQ ID NO: 1426:

10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 116 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1426:

20 AAAATGGCGT TGCAATTTTAC TCTAATAACG CTCAAGGCGA CGGCAAAGAT AACTAAAGG 60  
 CACCTATTAT CGAACATAGT ACTCCTAaCG GACCTGGAAT TTAAATCAGA GCGGCC 116

## (2) INFORMATION FOR SEQ ID NO: 1427:

25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 212 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1427:

35 TTTTATTTAC GTATAAGTGG GCGTTAGGTG TCACAGCGGT TGTCGATCAA AATATCATCA 60  
 TCAATCTTGT ATATGGGTTT GCGGATTCTT ATTTTATGAT TTTACAGAAC TATCCTAGGC 120  
 TTATTCTTTA TTAAGAGATG CAACnAGTTA TATAAAAAGA CGAATCTATC AACGCGAGCT 180  
 GCTCACAAGG CATCTCnTAT AGCGTCCACA TC 212

## (2) INFORMATION FOR SEQ ID NO: 1428:

45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 265 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1428:

50 GAAAAATTGG TTCTGAATAT AATGGTGCCG TATACTTTAC GCCTCAAATC AAAGATTTTA 60

55

ATTTTAATGA AAAACATCGG TCGAATATAA CATAAAAAAA CGTCTATATC AAAAGCATCA 180  
 TGAATAAACA GAGGAGCACA AAAATGAnTA AAAATATAAT CATCAAAAGT ATTGCGGCAT 240  
 5 TGACGnTTTT AACATCAATA ACTGG 265

## (2) INFORMATION FOR SEQ ID NO: 1429:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1429:

CGTACGAAGG ATTTGCAAAC TTCTTCATTC AACAAAGCTAA AGAAGAACGT TTCCATGGAC 60  
 20 AAAAGATTTA TAACTATATT AACGACAGAG GTGCACATGC AGAATTCAGA GCAGTTTCAG 120  
 CACCAAAAAT TGACTTTTCA AGCAT 145

## (2) INFORMATION FOR SEQ ID NO: 1430:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1430:

ACACCGCTAA GCGTATTAAG ACAGGATCTG AAAATGGACA CATCGCAATC GAATTATTGC 60  
 35 AATGCCAAGT CATATCGGGG GTGAACCGCA ATTTAGGnA TTAAGTGGAT AGGTA 115

## (2) INFORMATION FOR SEQ ID NO: 1431:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1431:

nATGTATTnG TGAAAAGGTC CTGAGTGGAC AAAAGACCTA AATATTTAAT GGTGATTAT 60  
 50 CGCACGTCCA TAGTTGGTGA ACAGGAACCTT ACACGTACAT CTAATCGCAG ACTATGCGTA 120  
 AACTTTGGAA ACTGCTAGTC ATTGAAGCGT GGTATGTGTA TGCACGTAAA TATGCATTAG 180

## (2) INFORMATION FOR SEQ ID NO: 1432:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1432:

GGAATGATTG ATAAATTGGA CTA CTAAAG ATTTCGGTAT CGTGCATTT GGCTCAGTCC 60  
 ATGTTTAATC ACCTATGnTG ACATGGTATG ATATTAGTGA CTACCAGAGA TATGGATGAT 120  
 TTGGAACGTG GAGGACTTGA TCGTT 145

## (2) INFORMATION FOR SEQ ID NO: 1433:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1433:

TTTATTGCAT TTACATAATA ATATCCTTTT GTTGTTTTGG TATTTCTATT CATATACAAG 60  
 ACCATACCTT TAACTTTTCAG AGCTTCCCCC TTATTTTGAG TTGCCATTTC AGAACCAATA 120  
 ATCCATGTAC CTTTATCATT TTTATCAAAT TCGTCATCAC GATAACCTn 169

## (2) INFORMATION FOR SEQ ID NO: 1434:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1434:

GATCTATAGT TCTGTAATCT GACGTGCTTT GCCATGTGCA CCACTCGTCn TAAAAATCAC 60  
 TTACACTTAA CCCTTTTCCA CCTTTATCGT ATCCACCTTC AA 102

## (2) INFORMATION FOR SEQ ID NO: 1435:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1435:

5 TTCTTATTAT ACAAATAGAA GCCATGTGTG CTTATATCGC AGCATCATGA CTCCTTTTTC 60  
 ATTTGAATAT ATAAATAATA CAGnCGCTTT CGAATAAATT TAGGCTAATT CTACCA 116

## (2) INFORMATION FOR SEQ ID NO: 1436:

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 144 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1436:

15 GGGGGTTTAT GTACTGGTGG ATCTGCAAAC TACTTGGCGT AAAGAATATA CAGATATGGT 60  
 20 AAnGAAAAGT TTAGATTCAC ACGCCATCAC AATGGATTAG AAAAACCGAA TTTCTTCAGC 120  
 AATTCTACAA TTTCTAGTAT ACGC 144

## (2) INFORMATION FOR SEQ ID NO: 1437:

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 101 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1437:

30 GTTGCTGGGn AACCTATGGT CGAACATGTA TTGGTAAAGT GTGAAAGGCT CTGGTGGCGA 60  
 TCAAGTTGGT AACCATCGTA GTACATGGTG CTGTAAATGT A 101

## (2) INFORMATION FOR SEQ ID NO: 1438:

## (i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 321 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1438:

45 AAAGATGGTG ACATTTTATA TAATCCGAAT GTGCCAAGTT ATTcAGCAAA GTATCAATTA 60  
 50 AGTAATGATG ACTACAATGT GAAGCAACTT AGAAAGAGGT ATGATATACC AACTAnGAAA 120

AATTTAGAGT TTACATTAT AGAAAATAAA GAAGAAAACA TCTATTTTAC GGATAGTATT 240  
 AATTTCAAAC CTAAGAATA GGGTTAATAG AAGTTTGAAA TGAAAATTC nTAAAGTGTG 300  
 CAAAATAATT TGTCGCTTTA G 321

## (2) INFORMATION FOR SEQ ID NO: 1439:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1439:

CAGTTGTAAT GGGACCTGGG CCAATCGGAT TACTTGTAGC ACAAGTGTTA AAAAGTAAAG 60  
 GCGCAACTGT TGTGGGTACT GGGTTGGGAC AATTGACCAA GTCAGATTAG ATTAAAGCCA 120  
 GAAnGCCATT GCCAC 135

## (2) INFORMATION FOR SEQ ID NO: 1440:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1440:

AAATTATTTT GAACACTTTA TGAAATTTT ATTTCAACT TCTATTAACC CTATTCAGTA 60  
 GGTTTGAAAT TAATACTATC AGAAAAATAC ACATTnCTT CTTTATTCTT 110

## (2) INFORMATION FOR SEQ ID NO: 1441:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 436 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1441:

TCTCTTTTGG ATTCATTAAG ATTGCnGCAT CGATACCAAC GTTmAACGGT GATTGTGTAA 60  
 TGAATTTTGG CCACCAAGCT TTTTAAACAT TATTCTTTAA TTCAACACCT AAAGGACCAT 120  
 AATCCCATGT GTTTGATAAA CCACCGTAAA TATCACTACC AGGGAACACA AAACCTCTGT 180

GAAAACGCCC CATGGAAAAT AACAGCATAG TAAATATGCT TTACTTCCAT GGGACGAGTT 300  
 AATATTTTAA ATTGTATATA ATACAAAANA AGTnACGTAT TTAACCCGCG GTTCCACCCA 360  
 AATTAGTGTA GTCAC TCGCT TTTATTTTAA AATGATTTCGT TCGGCCAATC TTATTGTTAA 420  
 GCTTACACTA TCCTTA 436

(2) INFORMATION FOR SEQ ID NO: 1442:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 461 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1442:

ATTTTGTAGAA GCATACTGCG AACGTCATCA CATCGATTTA CATATCAAAA AGTTAGATTT 60  
 GTCGCATAGT CTCGACCGAA ATAACAGCAT TCAGAATGAA GCTCGAATTA AACGTTACGA 120  
 ATGGTTTGAT GAAATGATGA ATGTATTAGA AGCGGATGTA TTGCTAACGG CGCATCATTT 180  
 GGACGATCAA TTAGAAACTA TTATGTATCG TATTTTTTANT GGGAAATCAA CACGTAATAA 240  
 ACTAGGATTT GATGAGTTAT CGAAGCGAAA AGGTTATCAG ATTTATCGAC CACTTTTAGC 300  
 TGTCTCTAAA AAAGAAATAr AACAAATCCA AGAGAGATAT CATATTCCAT ATTTGAAGA 360  
 TGAATChAAT AAAGATAACA AATATGTTAG AAATGATATT CGTAAnAGAA TTATTCCAGC 420  
 TATTGATGAA AATAATCAAC TTAAAGTATC GCATTTATTA A 461

(2) INFORMATION FOR SEQ ID NO: 1443:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1443:

AAAGGTGATA AAAAACAAG GCATTGTAAA TTAATTGAAA ACCAAGTGAG TTATTACAG 60  
 ATTCTAATTG GGATAATGCG CGATATTTTA TTCCACACTT GTTACATTAT TGCTTTACGT 120  
 GGGGGTTAGC GTGGAnTCAT CAC 143

(2) INFORMATION FOR SEQ ID NO: 1444:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs

1743

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1444:

TGGTGTGGT TCATCAGTTG TAAACGCGAT TGTCACAAGA CTTAGAAGTA TATGTACACA 60  
GAAATGAGAC TATATATCAT CAAGCATATA 90

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(2) INFORMATION FOR SEQ ID NO: 1445:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 218 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1445:

ATTGAACAGT GACAACAAAT GACAACAATG AATGACCAAC TGAGTTGCAG AATTGACCGA 60  
CCTGACTTGC TGTnAGATGT GCATTGCCTG TGACCAGTTA ACTGCTGTTT GTACATTATG 120  
ATTGTGCACG TGAAGTCTTT GCAAATGACT TTAAACATTA TGCTGCTAGA GCCATCTTTT 180  
AAAGATGTTT GGACTAACGT nCATGATGTG AATATCTG 218

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(2) INFORMATION FOR SEQ ID NO: 1446:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 105 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1446:

TTTGACTTGA CATTATAGAA CACAAATTCA TTTGAAACTA TGTTTTCAAA TTTATTTATT 60  
GTTACTGGGA ATTTACATT ATTAGATTTA TTTATTTTCT TTGA 105

40

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(2) INFORMATION FOR SEQ ID NO: 1447:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 104 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1447:

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AGACTGAAAA CTGCATATGC AGAGGCGATG AACCAAAATG CCAT

104

(2) INFORMATION FOR SEQ ID NO: 1448:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 104 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1448:

TTGAATTAAC TGAAGAAATA GCACTGCAAG CAGGATTGTT GATATGACAA CATTCGAGTC 60  
 AGAATGGCAA CAACAACGTG ATTCGTGCAC TCCAAGCAGG TGCA 104

(2) INFORMATION FOR SEQ ID NO: 1449:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 349 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1449:

TATTAATTTT TTTAATATG GAATATTCAT TGCATCGCTT TCCTATTCTT CAAGCCCACT 60  
 TTTTATCTTC ATATACATTA ATTAACCACC kTCAAACATT GTCGTTAGAT TCGCCAAATT 120  
 GAATCTATTT TTAGCACAGC AAAAAACCGA ACTGCTGAAA TAATGCATCT CCAACAGTCC 180  
 GGTCTATTAA ACTATTTACT TATCTTTATT AAACAATTGA CATGATTTAT TAGAATAACC 240  
 CAATTGGCAT GACCATGCAT CAGTAACATC CATGTTTAAT GGCTGCTGGT TTTTtaggTA 300  
 AACCAGGCCA GAGTCATGGn TGGCACCTGn GCAACGCnAC GATAAAGCC 349

(2) INFORMATION FOR SEQ ID NO: 1450:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1450:

GATTTTATAT AAATATAGCT TTTCACAAA ACAATGATT GAATTTCTAG GAATTGAGTC 60  
 ATTAAAAAAA CACTTGAAAA ATTCAGGTGG GATTGCGCTA TTGCCGGAAT TTATTGTTGC 120



AGAAACAACA TTGaTAATTA ATCCTGAATC GAATAAGCAm GTACTTGAAT CTTTTGTAAA 240  
 AGATGTTTTT TTATAATTAT TGGTGAAAC GTGTAGTTAT GGTGAAACTC AAAGATAATA 300  
 5 ATTTAAATGA GATGTTAATG AAAAAGTAAT TCAATATAnA ACAGGTGATT TAnATCTTAA 360  
 TAAGGnTAAT TCCAGGTTGA ATTCCAATTG CGGGCATCAT 400

## (2) INFORMATION FOR SEQ ID NO: 1451:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 124 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1451:

20 TCGGTTATAG TTGCTATTCT CAATTATGTT CGCGATAATT TTAAGTAAAA GTAAGCACAG 60  
 ATATTGAATT TGATAGGAGT TAATTGATAT ATACATACGA ACTTTCATGG ATCACTTAAA 120  
 TTTg 124

## (2) INFORMATION FOR SEQ ID NO: 1452:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 126 base pairs  
 (B) TYPE: nucleic acid  
 30 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1452:

35 TGTATTAAAA ACCTTCCACC TTTAAAAGCA ACAATGCGGT GTCCTTTAAA TTCAAACATA 60  
 ACCATATACG AATTACTCGA TAATTCTGTG TGTTTAATTG ACAGATGTCG TGTGAATTGA 120  
 40 TnATTT 126

## (2) INFORMATION FOR SEQ ID NO: 1453:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 280 base pairs  
 45 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1453:

50 ACTTTGGCAA CATCTGGAAT ATCATATAAA TCAAGTAACT TACCTAACCG ATGATTAATA 60

CTAACAGTTG TTTCCATGCC TACACCTCAC GATATTATCA CTATTCATAT TAACATTATA 180  
 TGTAAGAAAT TAAAATCTTT TGAAGCATTa AGATTACTTA TCATTThTAA ATTTCAATTT 240  
 5 AAACTAACAG TAATTTATGT AGCTTTTGna ATTCTCATAA 280

## (2) INFORMATION FOR SEQ ID NO: 1454:

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 242 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1454:

ATATTCTTTA AATTAACTG ATCACTTGAA TAATTAACAT TACTTAATTC TATGGCATTG 60  
 20 ATGATGATTG CTCCTCATAA ATGAACGTTA AAATATCCTG CAGTTCCTCA AGTGACATTT 120  
 CGATGGCTTG CGCTTCATTA ACCAATTCTT TAACCAAATT TTCAATGGTA AAAAAATTGTT 180  
 TCTCTTTTAA AATAGGAACT ATTCTThGCT CCTTAACAAA GGrCCCTTTT CCTCTAATTG 240  
 25 TT 242

## (2) INFORMATION FOR SEQ ID NO: 1455:

## (i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 110 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1455:

ATAAAATTGC AGACTTAGAT TACTCTTGTT CAGCATTTTT AATGTATATC GGTATAGATA 60  
 40 TTGATGTGAC AGATCAAGTG AGACTTGCAT AntGGTATTT TATTCAGATG 110

## (2) INFORMATION FOR SEQ ID NO: 1456:

## (i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 551 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1456:

50 ACCAGTGGTT GCCTTTTTAA GTCCCGCGTG GGACAAAAAT TAACCTCTTT ACACTTGCAA 60

AAAGCGCTTG CAATATATTT TCGATTGTt ATTCAACmAA ACGTTTTATT tTATTCGCTG 180  
 TAGTCAAATG TATACCCTTA TACTGACTCG aTAATCATTT GCTTATnATT TGAGAcTAGG 240  
 5 ACATAAAATca ATGCTCTAGA ATCCAAAAAG TCACATTAGT AGTAGTTAAC CGAACGAAAA 300  
 TGCACCTTGTA ACAAGCTTTT TTCAATTAAA GTCAGGGGCC CCAACATAGA GAATTTGAA 360  
 ATGAAATTCT ACAGGCAATG CGAGTTGGGG TGGGACGACG AAATAAATTT TGCARAAATA 420  
 10 TCATTTCTGT CCCACCTCAC TCAAAATAAA TTTCACTATC CGTAAATAA ACAACTAACT 480  
 ATTTAAGTAT CATCTCTCCC CTAATTAACA ATTATAAAAA TAAGAACCAA TATTCGAGAC 540  
 15 AACCTAATTA A 551

## (2) INFORMATION FOR SEQ ID NO: 1457:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 109 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1457:

ATCnGGGGCT GCATAAGCGA TATCAAGTGT GAGCATTGAA CGATTCAGGA CTGACCAGCA 60  
 30 CGCCGTTTGC CTGCTTTGAA AGATCCACCG ACAAATCCGC CAACATCGT 109

## (2) INFORMATION FOR SEQ ID NO: 1458:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 112 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1458:

ACCAGAGCCT CTTTGACTTC CTAAGTCGAA TAGCATCGTT GATATAGTTA AAGATGACGC 60  
 45 TAGATTTAGn AATCCAAACT CATAACACCT CCACCATTC ATCACATCTG GA 112

## (2) INFORMATION FOR SEQ ID NO: 1459:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 224 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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CCCCAACCAA TTTTTTAAAA AAGGGGGCCT TTGGGGGGGC CAACCAAGGG GGAACCCCTT 60  
 AACCCCAATT TTGGCCAATT TTAAAGGGAA GGCCTTGGAA CCTTTTGGG AATGGGCCGG 120  
 5 TTTTAAACCC TTGGTTTCCG GAAGGGGAAA ATTTTAAAA AAACCGGAAT TGTTGGCCC 180  
 CCTTTAAATT AAAAAGTTCC CThAAAAANA AATTCCCCCA AGGG 224

(2) INFORMATION FOR SEQ ID NO: 1460:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1460:

20 TTTCGACAAT CAATTCGACG TCACTGCCAC TCCATCTATA GTAAAGCGTT GATACTTTCA 60  
 ATAATAACTG GATCACTGTC TAATTATAAA TGGATTCTTA CATCCCACCA TAATAATTn 120  
 CATATGTTCA TCACC 135

(2) INFORMATION FOR SEQ ID NO: 1461:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1461:

35 TTATAGAACC TCGTACTCCT nTCGACACTT GAATTTAAAT CAGAGCCGCC AGTGGAGAAG 60  
 CATGAATTGA CTGGTACCAC TCGCAGAAAG TAATGATTCT AAGCCACTTG ATTA 114

(2) INFORMATION FOR SEQ ID NO: 1462:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1462:

50 GTTGAATTGT TGGTGATGTG GTTACACGAA TTTCAATAA TTGTTCTTTA CGTCAAAACG 60  
 TATCGTTCCA AAGTAATCCC CnGGTAATAG TTACCAACAA GTTCA 105

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1463:

TTGTATGACT CTTCCGACTT TGGTAAATTT GTGAACGCTG GntGAATGAT TTTTGTTTGA 60  
 CAATTGGCCT TATCATCATT AATCGTATTT TTAAGCTGCT CGGATATAAG TTCTCAGCGA 120  
 GTTCTTTTTG ATGTATCATT AGTGTAGAAA ATAGCTGTTT GT 162

## (2) INFORMATION FOR SEQ ID NO: 1464:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1464:

TAAATTGGAA AGTCACATTC AAnATGCGAA AATGTTTTAA AATGTCCTGT AGGTGCTTAA 60  
 TAGTTTTGCA TTTGCAAATT TTA CTGAACC GGTTTAAACG AAT 103

## (2) INFORMATION FOR SEQ ID NO: 1465:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1465:

AAATTGTATA ACTACCAAGC TTATATGAAA TGGTAAACAA AATATTATCA CTTGTTTGAT 60  
 AAGTAGCGTG GAAAATATTG TATCTTTCTA AATGTACACG TTAGAantCA TGCTTATGTA 120  
 TTACACGCGG GGCAC TGGA CCTAAGGGCC TAT 153

## (2) INFORMATION FOR SEQ ID NO: 1466:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1466:

TTTCAGTAAC ATATGAAAAC TTAATTAACG ATGTTTCAGTA GGTTCATACA TTTTACTTTA 60  
 5 TGATGCTTAA TTGAATTACA nTTAAGATAT GACCAGCTAA AAAGAGTTAA TGTGATATTT 120  
 AACC 124

## (2) INFORMATION FOR SEQ ID NO: 1467:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1467:

AAGGAATTAA GTTTGCGACA CCAGCAAATA GTACTAATAA AGGAATATAT GGTAAGTCAA 60  
 TAATTGAATA ACCGATATAT AAGAATATAC CTAAAATAAC ACTGACAGTT ACTTGACCTT 120  
 GAATGTAAGA TTTTAATGTA AAGTTTAAAT CAGTTAATAA ATCTACGAAA AATACTTTAC 180  
 25 GTTCACCTTT GAnAAATTTA GCAACAGCTG GGATAAATTT TTCATGGTCT TTTAACATAT 240  
 AAATTAAGAA GAATGGAACC ATAATCAATA AGAAGATGGT TGAAATTAAT GATGTAATGT 300  
 ACTGTAATGA ATTAGATAAn ATATTAGnAA CGCCATCACC CATTGATTTA ACCA 354  
 30

## (2) INFORMATION FOR SEQ ID NO: 1468:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1468:

TGCAAACTAG GAACAATAAT GTTAATATAA CTATGATGnA AGTTAAAAAA TAAAAAGGAA 60  
 45 CACTCTATAA TATGAATTAG GGGTTACAGT TTTTGTAGTA TTTTACAGTA TCAAAGTTTA 120

## (2) INFORMATION FOR SEQ ID NO: 1469:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

TCTAAATGCT GACTAAAAC AGCAACACGA GACTCATTAT TATTAGACAC GATTGTAATA 60  
 GTGATTCCTT TTTCATTAGC TTCCTTAAAC CATGCTTTAA CACGTTCTGT AGGTTCTTTA 120  
 5 ACATCCCAAC CTACTAGCGT ATTATCTAAA TCTGTAATAA TACCTTTAAC GCCTTTGTCC 180  
 ACTAACTTGT CTAAATCAAT TTGAAATATT GATTGAACAT ATGAATTCGG CATAAAAAAC 240  
 TTGCGAACTA AACCCATTTA ACTCACCTTT ACCTTTTAT AATTGAGACA CTAATGCTTC 300  
 10 AACAGTTTGA CTTGATGATA CAGCTGCTTT TTCTAAAAAT GCTTCGAAGC TCATTTCCGC 360  
 TTCTCCATTT GCTAAGTCTG AACTGCACG AACTACAACA AATGGTACAT TAAATTGATA 420  
 15 ACATGTTTGT GCAATTGCAG TTGCTTCCAT TTCAACCGCC ATCGCATTTG GAAATG 476

## (2) INFORMATION FOR SEQ ID NO: 1470:

## (i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 156 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1470:

CACCATACAT GGGTAAGGAT ACTACTCAA TCACTTGAA ACCAATAATn CATGACCATA 60  
 TGTGTGCCAA TGAATTCAAT TGGAAAGACA ATGATGAGAT ACTATTAAAA CGATTATATT 120  
 30 TATTGTCACT TGTTCAAACG CACTCCTTTT CCAAAT 156

## (2) INFORMATION FOR SEQ ID NO: 1471:

## (i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1471:

AACAAAAGTT TGAAAAGCC GGGTGCCAGC GAAAACCTAA AAAGCACTTT ATCAGAAAAA 60  
 45 GCTAAGAAAA AAGATTAATA TTCATTCAAT AAATATAAAT CCAATTTAAT TTGTTGTTTA 120  
 AGGTCTACAA GTGTATGTTT AATATACAAT TCATCGTTTG ACGGTAAATC AGATACTTTG 180  
 AAATCTTGTC GCTCAACCTC TAGTAAATCG AAATCGCTAC CAGCTGAATT ATAGGTTTTA 240  
 50 AGTTCACCCT CTTCAATGAT TCTGTTTTCA AAGTCTTTAA TAACTATAAA TACTGGTTTA 300  
 CCGTTGTTAT TAAACAACCT GTCTCTTTTG TCTAATAAGC TTATACAATC CAAATTCATA 360

## (2) INFORMATION FOR SEQ ID NO: 1472:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1472:

CTAGGATTnC ATCTATTTGG GATGAAAATA AGCGTTTCCT GAATCCACAA GAATATCCAG 60

TCGATTTAAG CCAGGCATGT TGGGGTAATA ACATAACGTT TTTTGA 106

## (2) INFORMATION FOR SEQ ID NO: 1473:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1473:

TATCTTACCT ACATTGTTAT CTGATGGCTG TAATCATTAA ATCTATAACA CCGAGTTCTT 60

CCATTAAATTT TCAGCTTCAT TCGACTGCCT TTTTATnTTT CGTACTATTA CGAATTT 117

## (2) INFORMATION FOR SEQ ID NO: 1474:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1474:

ATGCATGGCA CTGGAAnCAG CTGGGAGATA TAGGTAGTAT CCTAAAGAAG TTCAGTTAAT 60

CGGAGCGATT GTATTGCATG AAGGTAACAT TCGGAGTGC CAACAGGCGA AGTAAAACTT 120

AACGGCAACC ATGCCCTTATA TTAAATGCCC TTCCGGGAAA GGAC 164

## (2) INFORMATION FOR SEQ ID NO: 1475:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1475:

ACAGCAAGAC GTGACAAATC AGATACTATT AGTCATCAGC GTTAACATGT GGATAnGTGT 60  
 5 GAGGTACGAA TanCCGAAAG GAAATACGAC CTTTAACATT CGCGCACAAA ATGAGCTCAG 120  
 GCGCCTGCCT TGCCCATTTT TTAAATTATT TCCCTGGAAA TGATTGCTG TGTGCTGTTC 180  
 10 TGTCCACAAC AACACGATTA ATGCCATGAC 210

## (2) INFORMATION FOR SEQ ID NO: 1476:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1476:

AGGGTGATTT CACGGTTCGT CTGCCCATTT AATTGCGCAT TTTGCACACC ATCTACCGTT 60  
 TGCAATTTTG GTATTAATTG TTGCATGCAG TACTGTCCGT TGACTTTGnt GCAAGTGCAT 120  
 25 GCTCTTTC 128

## (2) INFORMATION FOR SEQ ID NO: 1477:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 641 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1477:

AAAATCTGGT AAAGTAACTA GAGTTTAATA AATATATTGC ACATAAAAAA TGTGACCTTA 60  
 40 TGTGGAGGAC ACATTTACTT AAGAACTAAG AGCTCAACCT CTTAGTTCTT TTTTGTTAC 120  
 CAAACAATAC ATAATGGTTC ATAGTGAAAT TCGAACTATC AATATAATTT GGTAAATACG 180  
 TTTAATAATG GTTCTCTGTC AAATTGGACT TATGGGTTCA ATATCGATTT TGGCACATAA 240  
 45 ATCAATGTAC TAGGACCTAC AATTTTCCTT TCAATAATAA ATCAGCCAT AATCTTCATT 300  
 AATTACAGCG TGATTCATCT ATTATTATGT TATAAATkCT ATCTATAAAC GTCACCTTAT 360  
 TAAATAACTC ATGCACTTTA TTAAAAATCC TCACAAATTT GAATATACTT AATTTAAATC 420  
 50 TGTACTTCTA ATTTGCAAAA TCAACCCATC ATGTACAGTT ACTTTGCTT GCAAAGACTC 480  
 AATTTCAATT GAAATAGTTA AAGTAGAACC TATATnAGC ATTTGTCTAG CTAAATTATA 540

GATAACTCTT ATCTTTTTCa ACTGTAGGTG ACCTTTAGGG C

641

## (2) INFORMATION FOR SEQ ID NO: 1478:

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- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 121 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1478:

15

TTAACCGTGA TGCAGAGTAG TAAGTGGATn CATGCTCTGT TATGGATGAC AAGACAAAGC 60  
 AGCGAATATT GCGTACTGCG ATTGATGAGC AGATGCATAT GATTGGATTG GTGCAGCTGT 120  
 C 121

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## (2) INFORMATION FOR SEQ ID NO: 1479:

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- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 133 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1479:

35

ACCATTGCTT AGATAAATAC CTCGCACTGA ACCGCATTAG TATAGCACTT CTAGCTGATC 60  
 GCATCAGTAA AGTATGCTAT TAATGTCTCA GTTTTATCTG TAATGCATGT TTAAGTTAGT 120  
 CATAGCATTa Ttn 133

## (2) INFORMATION FOR SEQ ID NO: 1480:

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- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 201 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1480:

50

TTTTGGGGnT TTAAATTTT AAATTCCCGn TGGGGGAAAT TCCCTTAAAA ATTCCCAACC 60  
 CTTTTAAGGG GTGGGGGTTT TTTTAGGGAA AAAGGGGCCC GGGGTTAATG GTTCCCAAAA 120  
 AATTGGGGAA AATGGCCCCC CAAATTTTAA ATTCCCGGTT TTAAATTTGG GGTGGGTAA 180  
 ATTGGAAAAA CCCCCAATT T 201

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- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 112 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1481:

CAGTATCAAG CATAGTAAAA AATGAGGGTA GGA CTGAAAA TACGGCGTTA TTGGTGGTGC 60  
 ATTCACGGTA AATATGTTGC ATGACCAGCA AGTTTTGGnC TTCTGATGCA CC 112

(2) INFORMATION FOR SEQ ID NO: 1482:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 127 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1482:

CAAAAAACAA GTTCTGATAT GCAGTAGCTG AATAATTTTG CTAGTTACAC CAAGTGATC 60  
 TTCTGGTGT TTACTTTTAA TAAATGTTTT CATATATTTT ATATGTATAA AAATGGGATT 120  
 TAGCGTA 127

(2) INFORMATION FOR SEQ ID NO: 1483:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 83 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1483:

AGTGGTGTAT TGGGTGAGTA ATGCTTAACT TCATACCTGG TGCATTGGCT GTTCAGTATC 60  
 ATTATATCTG CATGGGCGAT ACT 83

(2) INFORMATION FOR SEQ ID NO: 1484:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 201 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

TATTATTGAT GTTCTTTGGT TCATTCTTTG GTAATAATTT TGCACCTGAA AATTTACAAC 60  
 CGTTAGCTGG AACCTAGnCA AAGGGATGGG TTTAGTGGTC TATTGTGGGT TTATTGGTAT 120  
 5 TCCGTGGGCC ACCCCATGGG GCCATTATGG TTTGGGAATT TTGGGAATAA ATTAATTTnC 180  
 CCAACCAAAA ACCAGGCCAA G 201

## (2) INFORMATION FOR SEQ ID NO: 1485:

- 10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 210 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1485:

20 CTCACAGCAA CATCAAAGAG GCAGATATTA GTCAAGTTCA ACGTAATAAC ATCTACCTTC 60  
 ACAAGTCGAT AAAGGAGCAC CATCATTAAT AAGTAGATCA ACAAGTCAAC GAGAATTTTA 120  
 ATGTGCAGAA TAGAGAAGTA CACCACACAn ATAATCAAGC GATGTAATTA CTACTACATT 180  
 25 TTnCATGACA GAGTGAACCT CAACAGCGGT 210

## (2) INFORMATION FOR SEQ ID NO: 1486:

- 30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 158 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1486:

35 CAGGTTATGT TTGCATTAGA AGTTCTTGGA AAATCTTTAT GGAACGTGGT TTACACCCTG 60  
 40 ACTTTGAATT GCATCGATCT GATGAAGATA AATGAAATTG AATGGGATGG CChACATGGA 120  
 ATGCAACCTA TGAATTGGAT GGAATTAGAT GAAGCGGG 158

## (2) INFORMATION FOR SEQ ID NO: 1487:

- 45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 114 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 50 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1487:

TTGCAGCATA TAGAGGTAGA GGCATCGCGA CAAAGTTATT AACGTCATTA CTTG

114

(2) INFORMATION FOR SEQ ID NO: 1488:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 108 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1488:

TGCTAAGTGA TAAAAAGAAT GATAAGCCAG GTGTACCAAT GGGTCCTGGA TTAGACCATT 60

TGGGAGATAT CGTTGTACCA CATGTTGATC AACTAACGTT nCCACATG 108

(2) INFORMATION FOR SEQ ID NO: 1489:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 112 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1489:

CAAnACGTAA TTTCATGATG AAAGTGGTCG ATAATTTCTT GAAACATCGC TTTCAGTAAT 60

AACGCCTGCT TTAAGGTCAC GTTCCGCATA GGTGTACTGA GGATGTTGAT GT 112

(2) INFORMATION FOR SEQ ID NO: 1490:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 265 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1490:

CAGAACGTTT AAAACAAAGT TGGAAAAGTT TTCTAATCGT ATTAGCTGCA TGTTTAATAC 60

TTATTATTGC AAGTGAAACG CTTATTTTCC TTTAGTCATT TGACCGATGT TAAAGAGGTG 120

AGATGGTTAT TTAGAATCAT TGTATTGATT GTTTTTGCCG TAGTGATGTT CACAATTTAT 180

ATCTCTTATC ATCATTATAT GAATGACTTT TTAGTTACTA AGTTATTTAA TATTTCCGCA 240

GCGACGCCAT AGTTATTATG TCTAT 265

(2) INFORMATION FOR SEQ ID NO: 1491:

- (A) LENGTH: 113 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1491:

10 CAAAAATTGGC CAGGGGCTCA TCCAATATTA AAATAGGCGT ACGAGGGATT AATAGACCAC 60  
 CTAATGAAAC GCGTTGGTTG TTGGACCTCC AGATAAATCC TGGGGGTCGG TGG 113

(2) INFORMATION FOR SEQ ID NO: 1492:

15

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 276 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1492:

25 ACTAAGAAAA TCCGAAATCT TTTCCGCTTC TTTTAAATAC GTAATACTTC CTTTTTTTCG 60  
 CTCTAAATGT TTGGCATTCA ACTCATAACT ATTCATTAGT TTCGTTAAGC CTTCTGCATG 120  
 ACTCTCATTT TGAGAAAAAA TTTCCAAATG GTACGAAGAT GTTTCAGGGT TATTCACTGA 180  
 30 GCCACCTGCC AGAAAAGCTC CTCTCAAGTA ACTGCGTCTC ATTTGTCAT CTTGAATCAT 240  
 TGAAATGATC AATTTTCATGG CGnnAAAATG CCGTCT 276

(2) INFORMATION FOR SEQ ID NO: 1493:

35

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 110 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1493:

45 GATGACGAGC GCCAATTATG TCACTTTTAT GGCAAAAGCT GGAAGTAAAC AACCGAGCCT 60  
 GCCAGTAAAA TTGGCAATTG GGACGTTCTT AGCAGGTGCG TCATACATAC 110

(2) INFORMATION FOR SEQ ID NO: 1494:

50

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 200 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

55

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1494:

5 AAAAAAAGG TTTTACCC GGAATCCAA AnTTTAAATC CCTTAAAAA AATTCGGCC 60  
 AACCCCCAA CCCAAGGTTT TTTCTTAAC CTGGAAATA ACCAAGGTTT TTTTCCAAA 120  
 AAATTTTCCA AAAAAGGAAT TACCCAAACC CTAAAGGTT TAAAATTGG GGGGGGAAAA 180  
 10 AGGCCCTTTT AGGGGGGAA 200

## (2) INFORMATION FOR SEQ ID NO: 1495:

## (i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 253 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1495:

20 AAAAAATTG GTGCATTAT CATATGGAGT ATTAATCTGT AGAAGTAAAG GCGATATAAA 60  
 TGTTACTTTG GTAATAAAGA TTACAGCGAA CGTTATTATT GCTCAGGTCA GATCAAGAAA 120  
 25 TTGGTGTCCG GGTGACAAGA CTGGTGCG CGGTGTAGTT TGTCAGTTGT GTGGTCATCT 180  
 TAAATAACGC TATCGTACGG TGTGTATCAC ATGAAGGAC TCTTACTAAT TCTGCAAGTA 240  
 30 CACGTCACGC nnt 253

## (2) INFORMATION FOR SEQ ID NO: 1496:

## (i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 104 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1496:

40 ACGCTAGCTT CTGAAAAAAT AAGTGAAC TAAGATGCAAT GAnCCTATTC CTGAATGATA 60  
 45 TTAGACGTAG CGCACCTGGT GCAGAAGCC AATAAAAAGA CAAG 104

## (2) INFORMATION FOR SEQ ID NO: 1497:

## (i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 100 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

55

AGGGAGGCGC CCAAATGGCT CTATATTAAA AAAGGACTCT CAGAGCATTA ATGAAAAGTT 60  
 GAAGCTCAAA AGGAAnCGAA AGAAACAAGT ATCAAAACAT 100

(2) INFORMATION FOR SEQ ID NO: 1498:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 101 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1498:

TGGAACCTTG GGAAGTCAA ACGGTTGTAA TCCTTGAACA TAAAGTTAAA CACATTCTGG 60  
 ATCATGTCCA nCGCGTCCAT TTGATGGATA TAACGGGAAT A 101

(2) INFORMATION FOR SEQ ID NO: 1499:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 127 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1499:

AGTTCTGGTG CATCGTTTTT CATTGTATTT GTGACGATTA TCATTCCAGC ATTAGAATAT 60  
 TATGCATTAT ATTTAGGTGT GATAGGTGCA TTTATAGGTG GTTTAACTGT TTATACACTT 120  
 TCAGGTG 127

(2) INFORMATION FOR SEQ ID NO: 1500:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 560 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1500:

TCCCCGCTTT AATACCTTCC ACGATTTCTT TAATTGCTTG CGGTTGGTCA CCTTGAGGCT 60  
 CAAAATCAGA ATGTATTTTA AAAGGATAAT GTTCAACCAT TGTCACATAT GCCTCCTCTT 120  
 TCAACGTATT ATTTATATTT CCGCTCAACT CTTTGCTTTC TCATnACATA TnTTAGCAAA 180  
 GTAGTCACAC AAAAaGCAAA CGTTkGTTTCG TAAAAATGTC GAACAAaGAA AnACAAACAT 240



AAATACACAT TATATTAATC ATCATTTTGT TTCAACAAAT TTGTTTGAAA CATTATTTTA 360  
 AAGTTAATCT TAGCGATCTT CATCTTGATG TTTATGAAAT TCGAGTTGAT CTATAATTAA 420  
 5 ATAACCAGCT AATAATGACA CTACATCAAT AAAAATAATC CACTCGTTAT GGAAATACTC 480  
 TTTATAGATT GAGGCACCAA TTAAATTAA TGTCAGAATA GTACCGACCC ATTTACTTCT 540  
 10 TGTTATTACA CTAAATAATA 560

## (2) INFORMATION FOR SEQ ID NO: 1501:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1501:

ATTAAATCAT ACTnACAATT ACCGATGACA TTATTCCAAT TCAATCTAAT TCCGTGATGA 60  
 AAGAGCCACG TTTTGGTTAC TTCGTGGGCG TGAATTATTA TG 102

## (2) INFORMATION FOR SEQ ID NO: 1502:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1502:

TATGGTAGCT CCAAATGGTT GTATCGTCAC ACCATCATCT TCAAGTGCAA TGCGATGTAA 60  
 TCGATTGGCT GTTGTCTCTG TTACCCATAG TACTTTTCA TCTGTACTTA AAGCAATACC 120  
 40 ATTTGCTACG CTAATATTTT GAATGATAGG CGTCACTGTT CTAAAGTCCG GCGAAACATA 180  
 ATAAACGCCT CCTAGTGGAT TGGTAGAGTA TCCTCTAAAA TCTGTAAAAT AAAATCCACC 240  
 45 TTTAGAATCA AATACCATGT CATCAATACA ATATGCTGTT GAAAGATCTT CAATAATATC 300  
 TTGTAAGTTG TCACCATTTT CTGTAGCTGC AAAAATGCCT CcngGAGATT TAAAATCTCC 360  
 nAAAATAACC AACGnATAAA TCGGGCAnCT TATGGAATTG 400

## (2) INFORMATION FOR SEQ ID NO: 1503:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1503:

5 TACAGGTAGT TAACAGTTGA TGTAAATGG CGTACTGGAT TCTTTACGCA CGATTTTTTG 60  
 TTAATAAGTA TGGGATAGCA CATTACTATA TCCTACTTAC GACTTATTGG ATATGTCnTA 120  
 GCTATTCTTA AGCTCGAAAA GTTTCACAGG ATACATAAGG GACCAACT 168

## 10 (2) INFORMATION FOR SEQ ID NO: 1504:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 237 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1504:

20 CTACTGATTG TGTAATGTCG TTGGTAGGCT TGGGCTGTAC GCAGTATTAG GTGTAGGCAA 60  
 CTTGGCTTTT GGCATCTACC TTGTATGTGT CGTGTATCTA nGGCTGGGGC TTGCTCCTTC 120  
 25 AGTTGTTAGA CAGTAGGGGG TAATCTCAGG GGTGCAATGT ACTCCCTCCG TCCTAAAATA 180  
 CTnTATATGC TCGTGCCGAA TTCCTGCAGC CCGGGGGATC CACTAGTTCT AGAGCGG 237

## (2) INFORMATION FOR SEQ ID NO: 1505:

## 30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 209 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1505:

CGCATTTACC ACCATATGAT GGATCCAnCG ACGTTTTAAT AAAGATAAAA GTGACAGTAG 60  
 40 CGGGAAAACA GgncCATAAT TCACATCTCT TTTGAAAAAT ATGTTCAAGC TAGGATCATT 120  
 AGGAGACTCA TATTAATAAT AAAAATGTTG CAATCAATCG ACGTGCGTTG AATCTTAAAT 180  
 45 ACATAATAAA TGTTGTAGAA GATATGGGT 209

## (2) INFORMATION FOR SEQ ID NO: 1506:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 121 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 50 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1506:

AAAATGTGGC TATTGATTTT GACTTGAAC TTTTGAACA TTTCTCTCAA GGATTAAAT 60  
 5 GTAGGTAACA GGCAGGTAC TACGGTACTT nCCTATTTT TTATGCAAAT TTAAAAAAC 120  
 A 121

(2) INFORMATION FOR SEQ ID NO: 1507:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 144 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1507:

20 AATGACAAGG TCAGCATTAA AACCATTAA AAATAACGC GTTATGGTTA CTGGACGTAT 60  
 ACAACGTGTT TTGTTTAAAA ATTATTTAGA TAGACATAGC ACATTTAAGC CGAATGTAAG 120  
 25 GATATTATTA AAAGAnGTAT TTGT 144

(2) INFORMATION FOR SEQ ID NO: 1508:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 139 base pairs  
 30 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1508:

35 CCGATTGAAT CTGTGTACAC TTCACCAAAG ATATCTTCT TCGTTTCTTC AGATAAACTT 60  
 TCCATTGCTT TCTTATCAAC ACTTGTTTCT ACTAATAAGT GTGTTAATTT GTGCTTnTTA 120  
 40 ACAAACTCAA TAGCTTGTC 139

(2) INFORMATION FOR SEQ ID NO: 1509:

- (i) SEQUENCE CHARACTERISTICS:  
 45 (A) LENGTH: 155 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1509:

50 TCTGCCTGCC TCGCCTCCC AAAGTGCTGG CATTACAGGC ATGAGCCACC ATGCCTGGCT 60  
 55

CAAGTTAAAA TACAGATGTA AGACTTGACT TGATC

155

## (2) INFORMATION FOR SEQ ID NO: 1510:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1510:

ATCCCAATGC TAATGAATTT GCATATACGA TAAATAATGC TTTTATCAT CAATAAAGCT 60  
 ATGAATCTTT CAAGATCTTC ATTGAAC 87

## (2) INFORMATION FOR SEQ ID NO: 1511:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1511:

ATAGGCGTTT ACCAGTTATT TTCGAATCCA TATAATTATG TTTGTCCGTT TGGTTTAATC 60  
 CAATTAATTG ATTAAGTTTT TCCAATTCCT TTTTTTTTAA TTAAAATTCC AATCCTTAAA 120  
 AAAAAATTGGA AAAAAACCTT AAAAAAATT GGTTAATTTT CCCAAGGGAA TTAAAAATTT 180  
 TGGGGTTTTT TnAGGnCCCT TTTGGGAAAA ACCCAAC 217

## (2) INFORMATION FOR SEQ ID NO: 1512:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1512:

TGACATTGCA TCGGATTATG TTACATCAnG GACAACGGGC CTCAAAAAGC GGTGCACAAA 60  
 CGTTCCGTAA TCATATGCCA GTGCAATCGG ATGTAAAGAG A 101

## (2) INFORMATION FOR SEQ ID NO: 1513:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1513:

GATTTTATTG AAATGATTTT ACCTGTGATC AATTATTGTA ACAAATCTAC AATAAAATTG 60

10 TCTTACTGCA TGACCTAATA AATAGCAAC AGATATCATA CACACTTGTA ATTT 114

(2) INFORMATION FOR SEQ ID NO: 1514:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 77 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1514:

ACATATACAG GTACGTGTTT AGTCCGTCGT ATACTGCAAA ATTATGTCCG ATGAAATTAG 60

25 GGGAAAATTG TAGAACG 77

(2) INFORMATION FOR SEQ ID NO: 1515:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 102 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1515:

CCTTATAAAG TTAATGCAAG CAACATGGAC AAATTATTAT TTGAATAAAC TGCAAGAAAG 60

40 ACAACAATCA TTCTTCGGAA TGCTAGGAGA ATATATTTTA GA 102

(2) INFORMATION FOR SEQ ID NO: 1516:

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 89 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1516:

CAATTTTAAA TAGGATTTT AAGACCTTGG TTGGGTTTTG GTACAATTAA TGGGGACATG 60

55 ACTAGGTCTT GCCACGTTTA TATGCATCT 89

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1517:

GTAAGAGTGC ATAGTTTTTA AATGTTGCTT GTCTGGTnTC ATTTTGGCAC CATAcAGTTC 60  
 GTACCTGGAT TAGGGAAATG CCAATGTCC GCGTAGTGAT AT 102

## (2) INFORMATION FOR SEQ ID NO: 1518:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 448 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1518:

GAGAACTCCT TACCACAATC AAAAGTAATT GATTTAAATA TATGAGAAGA TAAAATGAAA 60  
 AGGTGCAAGC AGTATTAAGA ATTTAGGTAG CAAGAAAACA AGAAGTGGTA CATAcGATGC 120  
 TAACCTAAAA AGAATTGGAG ATTAAATGA TTATTAACTT TGAAACACAA CAAATACATT 180  
 TTGATTTAGA ACATGAAATT CCTATTTTC AAGCACCTGA GAAAATAGG ATACGCTTAG 240  
 ATATTGATGT TCTCAATAAA AAGCnAATTT CTAATATTAT TAATGTTATA TTTAATAACC 300  
 AATCAAAGAC GAAATGTACA TTTTGTCTG AATACTTATA TCCTGTTAAA TTTAGAGAAA 360  
 AAACAAGAAT TGGTCGTTTT TTTAATATTA CTAAGTGGTA CGAAGAAATC CATTCTACCG 420  
 ATGAGAAGTA TGnATTGCA ACTATTAA 448

## (2) INFORMATION FOR SEQ ID NO: 1519:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1519:

ATGGACGAAA GAAGATGTCA TTGCTTTTGA AAACCTAACA AATATTAAAG TAAATTTAAA 60  
 AGGTAGCGGT TTTGTGTCCC ACCAATCAAT TAGTAAGGGA CAAAACTTA CTGAAAAAGA 120

ATTCAAATTC AGATGGTnAA GAAGAAATCT GACAGTTAAA ACTGACAGGG ATAAGTCGGG 240  
 ACTnAACAGG AATGGGCTAC nTTTAAATTT AGGGATGGTA TTGGGCCACT ATTTGGTTTT 300  
 5 TGAC 304

(2) INFORMATION FOR SEQ ID NO: 1520:

(i) SEQUENCE CHARACTERISTICS:  
 10 (A) LENGTH: 322 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1520:

ATGACGTCGC ATGCACGCGT AcGTAAGCTT GGaTCCTCTA GAGCGGCCGC CCTTTTTTTTT 60  
 20 TTTTTTTTTT TTTCTGTTGG CCTTTGATAA TTTTATTGGA TCAGTAACAA CTTTTTGTGT 120  
 TTCAACTAAG ATAGCTAAAA TTCTAACTAT TATATGTAAA AATTACACTC CATTTTAGCA 180  
 CAAATGTTAA CAGAAATTAA CAGCACAGTG CCATGAAGAA ATGAnAAATA CACAGCTTTG 240  
 25 GTAGGGnAAT GGTCTGGAA ATAATGTAAT GCCAAGTnTC TGATCATTTA ACATATCACT 300  
 CACCTCCTTC TTCATCTGAT GT 322

(2) INFORMATION FOR SEQ ID NO: 1521:

30

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 105 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1521:

TAAATACAAA CCCTTTAAAC ATATTTACTA AGTCGTTCAA TTGTTGATTT GATAAnTGAT 60  
 GTGATGTGGT ATTTTGCATC GGTCTGCTT GATTCCAGAC ATGTC 105

(2) INFORMATION FOR SEQ ID NO: 1522:

45

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 118 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 50 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1522:

55

GATCGTATTT CCCAGATGTA AATTCnGTGG ACAATTGGCG TCAAATAGCT TCTAGTGG 118

(2) INFORMATION FOR SEQ ID NO: 1523:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 157 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1523:

CnGCATATAA TCCCGCGACA TGTCTTTTAC GGGTGCACTT GTAATATTAT TACCCCCCGT 60  
 ATAACCCATG TATATCTATA CTTTACCACA TAAATAATT CCGGGACTAT TTGGCACATG 120  
 TTTTGGGTGA ATTTCTTTAG TGGCACACCA CCCCTGG 157

(2) INFORMATION FOR SEQ ID NO: 1524:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 82 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1524:

ACTGAGGTAG GTTATGTAGG ACGAGATGTT GAAAGTATGG TTAGACATCT TGTTGATCCT 60  
 TGAGTAAGAT TAGTCAAGGC CG 82

(2) INFORMATION FOR SEQ ID NO: 1525:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1525:

GATACAAAAA AGAAGTTCAA TTTGAACTAT GAAGAAATTT ATATTTTAAA TCATATTTTA 60  
 AGAAGTGAST CTAACGnAAT CTCATCTAAA GAGATTGCTA AGTGCTCAGA GTTCAAACCT 120  
 TACTATTTAA CTAAAGCTTT ACAAAGCTA AAAGATTTAA AATTGTTATC AAAGAAAAGA 180  
 AGTTTACAAG ACGAAAGAAC AGTTATTGTT TATGTTACAG ATACACAAAA AGCAAATATT 240  
 CAAAAACTGA TTTCAGAATT AGAAGAATAC ATTAAAAATT AAATCAAGGT TAATTGCGTT 300



AAAATTAACT TAAAATTTAA ATATTGAAGA GCTTAATTAA

400

(2) INFORMATION FOR SEQ ID NO: 1526:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 125 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1526:

ACTGTCTAAT ATTCACCTCCC TTAAAGTGTT TTTCATATTT TTCTATTAAT GTTCATATTG 60  
 TAGGGTGTTG AATGCATCTA AGCATTnCAA GTTATTCTCC AAGTTCATCA ATTTCAAAAT 120  
 GGAAC 125

(2) INFORMATION FOR SEQ ID NO: 1527:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 112 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1527:

CATGTTTATT TATGTTTCGG CTTTAATGTT GAAGAGTTTT ACAAAGTTTA CCGATTGCAT 60  
 TTTATAATTT TAATGCATTA TTGGAGCATT GGCTATCATC TATTACTGCG nA 112

(2) INFORMATION FOR SEQ ID NO: 1528:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 115 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1528:

GCGAAGATGA GGATGAGATG ACTAAAGGAA AATATTGAAA AACAACCAAA AAAGTATGA 60  
 ACATTATTAA AAATTTACAA AATCAAATCG ACAACTTGAG CGCAAGAACH AACAG 115

(2) INFORMATION FOR SEQ ID NO: 1529:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1529:

5 ATGGATCTTC CGCTTCTCTT AATTGATCAA TTAAATCAGA CATTTCATGT TTTTGTAAT 60  
 AATGATTCGC TTTAATGGAT TTTTACATG ACATCATGAT TGCTACATCT TCACGTAATT 120  
 10 TTTTGATATC TACTTTTTTC TCTTCCAAA TTAGCTCAAT CATATCTTTA ATAATTTCTT 180  
 CTACTTCATC TTTAGGGAAC CAAACTGGAT AGCTACTTAC AATATAATCA TGACCACCAA 240  
 AATGTTCTAA CATGATACCT ACTTGTTGAA GCTCATTITT ATATTGATCA ATGACTAATT 300  
 15 GTTCATCTTT TGAAAAATGA AATGTTAACG GGATTAATAA ATCTTGTAAT TCATTGGTAA 360  
 CCTCACCTAT TTTATCTCGA AAATATTCAT ATTTATnCT 400

## (2) INFORMATION FOR SEQ ID NO: 1530:

20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 97 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1530:

TAACAGTCAA CCCACCCATT AATATATATT CAACGGCTGA CTGATACGAC GAACGTCAA 60  
 30 GAATATGAGA GGAATAGGGA CAAGATCATC ACACATA 97

## (2) INFORMATION FOR SEQ ID NO: 1531:

35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 150 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1531:

TCATAACGGT GCAACTTAGA GCTGACGTAT AGTTCATTCC AACTATATAC GATGTATCAA 60  
 45 CACCATGTTT CAGTTTTAGG TTAACGATAC TGTATACCGT ATTATGTCAG nGGCACCTTA 120  
 TCTTCACGTA CTTTACGGCG AGATGATGAC 150

## (2) INFORMATION FOR SEQ ID NO: 1532:

50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 138 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

55

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1532:

5     ATTCAATTCTG CTAACCAAGTA AGGCAACCCC GCCAGCCTAG CCGGGTCCTC AACGACAGGA     60  
       GCACGATCAT GCGCACCCGT GGCCAGGACC CAACGCTGCC CGCCTATCC TGAAGCCAAA     120  
       GGAAATGAGA TCGGAATT     138

## (2) INFORMATION FOR SEQ ID NO: 1533:

## (i) SEQUENCE CHARACTERISTICS:

15     (A) LENGTH: 460 base pairs  
       (B) TYPE: nucleic acid  
       (C) STRANDEDNESS: double  
       (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1533:

20     GGGGnCCnGG CAATGGAGGC GTGCTTGGAT GGTGCTTGA ATCATCCCTT TGGCCTCGAT     60  
       CATAAGCTTA AACTTTTGGT GCTGGnGCCA CTGGAGGGAA ATCTTCAATT CTGGCAAATG     120  
   25     GTAATTnCCT ATACCAACAT TTAAGGCATG TGGTAATGCT GGCTACTCCC GCTTCGTTAT     180  
       CAGCTACATG ACAAATACAG ATGCCATCAC CTTTGCCTCC ATTTTAATCG TTGATGCTTG     240  
       GAAATGTTTT TTGTAAATAT CAATGTTATC CTTGCTGTA TGTATCGCAT TTATATCTGG     300  
   30     TAGCAAAAAT GTTCCAACAG AAAGCCCTAT ACCTAGTTCG GCAGCTATTT TGGCAGATGT     360  
       TGCGCTACTA CTTAATAACC ACATTTCTGG AAAATGATCA TGTGTGGTGC ACTACGATCG     420  
       ACTTGCTTAT CTTTATTGTT AGATAATACG GAATACGnAA     460

## (2) INFORMATION FOR SEQ ID NO: 1534:

## (i) SEQUENCE CHARACTERISTICS:

40     (A) LENGTH: 145 base pairs  
       (B) TYPE: nucleic acid  
       (C) STRANDEDNESS: double  
       (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1534:

45     TAGCTAATA AATAGTTCAC TTTTCCATT TGTGTAGTCA GTCATTGTA TTCTTCAATT     60  
       TGCTCTTCAT TTAATGCCGC ATAAGCTTGA TCAATAATAT TTGGATTAAAG TTGTCCAATA     120  
   50     TACTCTAACT GGTCATGATA AACAn     145

## (2) INFORMATION FOR SEQ ID NO: 1535:

55

(A) LENGTH: 151 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1535:

10 ACGCGATTTA ATCGTTCGTT CCAACGATGT CCACTCCCCT ACTAATAATT AAAATCATT 60  
 CAAATTATTT CAAACTTTAC AATTnAACT AACAGTTTTTC TCAATAAAAT GCAAGCTTTT 120  
 CTCATTTGTT ATTTAGAATG ATTATGATTT A 151

15

(2) INFORMATION FOR SEQ ID NO: 1536:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 86 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1536:

25

ATAATAGAAT CATTACAAAT TATTTGAGAC TTTACAATTA AGACTAACAG TTTTCTCAAT 60  
 AAAATGCAAG CTTTTCTCAT TGTTAA 86

30

(2) INFORMATION FOR SEQ ID NO: 1537:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1537:

40

ACCAAAGTGT AAAGCCATAT ACTGAACATA TTGATAGCAT ACTCAATGAG ATCAAATTAC 60  
 ATCGTGAATT TATTATAGAA GTACCTTATA TGAATTCAAG GAAATTTGAG CTAAGTATTG 120  
 CTAACATTGA ACAACTTTCT GTCGAATGTC ATTTTAAGCG AACAGTCGA AAGTTATTTA 180  
 TAGAAAAGCT TAAAAGTGTT CAATATGATT TACAAAATAT ATTAGATGGC GTAACACnAG 240  
 AGGGTACTGA TGGTTAAAC AGTTTATGTA ACAGGTACA AATCATTCGA ATTAAACATT 300  
 TTTaAAGATG ACGCACCTGA AGTACATTAT TTAACAAT TTATAAAACA TAAAATTGAA 360  
 CAACTGTnGG ATGAAGGATT AGAATGGGnG TTAATACAAG 400

45

50

(2) INFORMATION FOR SEQ ID NO: 1538:

55

- (A) LENGTH: 136 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1538:

10 ATATCGTTAC TGCTGTATGT TTCAATATCT ATATTCATAA ATTTCAAATh CTGACACCTC 60  
AATTTCTTTA AAATAAGGGG CAGAACCCAC TATGACTATA GGATCTCTCA CAGGTCAATT 120  
CGCAAATCAC TCGTGC 136

15

(2) INFORMATION FOR SEQ ID NO: 1539:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 85 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1539:

25

TAAATATCTC GGCACAATGA TGCGGGATAT TTTTTTACAA TAGGCATAAA GGCTGGAAAA 60  
AACATATCTA GTGCTATGAT ACTTA 85

30

(2) INFORMATION FOR SEQ ID NO: 1540:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 73 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1540:

40

ACAATTTGTT TATTTCAACA AATTATCTTT ATTCCACGAT GTGCACAAGT GGTGAAATC 60  
AGCTGAAGAC ACG 73

45

(2) INFORMATION FOR SEQ ID NO: 1541:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 106 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1541:

55

TGCAGGAATT CGATATCAAG CTTATCGATA CCGTCGACCT CGAGGn

106

## (2) INFORMATION FOR SEQ ID NO: 1542:

- 5 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 87 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1542:

ACATCAACTC ACCCATAATA TATATTCACG GCTGACTGAT ACGACGAACG TCAAAGAATA 60  
 15 TGAGAGGAAT AGGGACAAGA TCATCAC 87

## (2) INFORMATION FOR SEQ ID NO: 1543:

- 20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1543:

GCTTATTCTG AAAAATATTT AAATTGAAGA AAAGAATATT CTAACCTACGG AAGTGGTATT 60  
 30 AACTAATAAC TAGTATCCTT TATAAATAAA CATAAAAATA TTCAAACGAA GGTCTACTAA 120  
 ATAACCTATCC ATAAAGTGAG TATAAGTTTG TTTGTAAAC TGAAGTAAAA AGCATAAGGA 180  
 ATTACACTTT AAATACATAT AGTACTTACG AATAGAAAAT AATCCCTTCA ACAGTAATTT 240  
 35 TTAAACAAAA ATAAGTGTTG TTTTATGTTG ACTCTACTAG AATAACTTGA TATTATATAA 300  
 AAGTCGTCAA ACGGCACTAA TATTTAnAA ACAAATGTTT TAAGTTGTTG GATTThAAAA 360  
 TATTGAATTA AAGTGTAAT TTGGACTATT GGAAATTGCG 400

40

## (2) INFORMATION FOR SEQ ID NO: 1544:

- 45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 103 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1544:

ATAACGCTAA TCAGCCACAT TCAGTATTGT TAAATGGACA CACAAGCAGT TGATGAAAAT 60

55

## (2) INFORMATION FOR SEQ ID NO: 1545:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1545:

GGCTGTTATT GTTGTGGAGT TAAAAATGAA GGAAAATTAT AACATGGTA AGCGTGTTC 60  
 TCGTATTACT TTA CT TAAAC AACCGGTATA ACCATACCTA ACTTAGTA 108

## (2) INFORMATION FOR SEQ ID NO: 1546:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 554 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1546:

AATATGTTT CATATATTAT GAATCTAGCC TTAATCATAT TGCATTCAAA ATAATTTTAA 60  
 AAAATGAAAA GAAAGGATTT AGCATGCAAA AATTCAAAGA CTTTTTTTAC GATGATTTAT 120  
 CGGTTACACG AGGAAATTAT TTTTAACTT TAATGGCAGC ATTTTTTATT ACTATCATTT 180  
 TATTTATCGG CATAGTTGTC AGTGAAGTAC ATTTACTTTA TAGCATGCTA ATTGTATTAG 240  
 TAGGTTTAAT TCTATTGAGG CTATTCAAAA TCAATTTATT CTCTTTTAAA AAATTAACAT 300  
 TGTCTCAAGT TATTTATATT ATAGGCGGTG CACTATTAAT TTATGGGTTA GATAATCTTT 360  
 ATTTATATTT TCATGACGTA CCGGCAATGA ACAACAATTA GAGCAAGCAA TACGGAAATA 420  
 CACCATTCTA TATTTCTATT TtCACTGTaC CATCATCCCC GCTATTGTGG aAGAAaTTGT 480  
 TTTtCGCGGT ATGATAATAA GGGkTATCTT CAGAAAACAC TTGTTTTTtag GGTTAATTGT 540  
 GTCTAGTTTA GTTT 554

## (2) INFORMATION FOR SEQ ID NO: 1547:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

TAAAGCAACA CTTTAAATCC CTTTGAACCT TAGTTTATCC GCTAAATCAT AAGCTTCTTT 60  
 TTTGCTACTT ACAAAAATCA ATCCTTGTA AATTTACCT GAATATCCAT AGTAATCTGT 120  
 5 CTTTGAATA ATATAATTAA CTCTTTCATC AGAAGTTAAA TATCTCAGTT TAGTTACATC 180  
 ATCTTCTTTA ATACCTTGAT GTACATAATC AGTCACACCA AAATAATGAA ATGGGACATA 240  
 10 AAATATCACT TTCTAATGCT GCTTGTAACC TTATTTTATA TGCAATATTA TAATCAAACA 300  
 GTTCAAATAT ACTTAATTCA TCTGGATCTT TCTGGTGGTA GGCAGGTCAT TCCCAGCAG 360  
 AACTTAGGGT TTGGAGGTAG GTTAAATAC TCGGTTGGAT 400

15 (2) INFORMATION FOR SEQ ID NO: 1548:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 73 base pairs  
 (B) TYPE: nucleic acid  
 20 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1548:

CGCTCTAGAA CTAGTGGATC CCCCAGGGCTG CAGGAATTCG GCACAGCATA TCTAGTATTT 60  
 TAGGACGGAG GGA 73

30 (2) INFORMATION FOR SEQ ID NO: 1549:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 73 base pairs  
 (B) TYPE: nucleic acid  
 35 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1549:

GTATCCAAGC AGCTTTTAAA CAATATGGCA TAAACATTAT TAACGGCTAT GGTTTAACTG 60  
 ATGGCACCTC TTG 73

45 (2) INFORMATION FOR SEQ ID NO: 1550:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 120 base pairs  
 (B) TYPE: nucleic acid  
 50 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1550:



GTAACATGTA TAGTGAAGTG ACTACTAAGA AGnCGTATTG TGATATTGAT AGCAGCTGAT 120

(2) INFORMATION FOR SEQ ID NO: 1551:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 192 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1551:

GGTATGTATT AATTAAAATG TGGTCATGAT TGAAACAGCA ATGTAAAAAT AGCACAACAT 60  
 AATTnATAAA GGAGAGAAAC GGCATGCATG AACAGATTT TAGAATTTTA GAGGGTCAAG 120  
 ATATTACTTT GCCAGAATTA GGTAGAGAAT TAGAnAATAT TACAGGACAT ACGATTGCTG 180  
 ATTCTACTGG CG 192

(2) INFORMATION FOR SEQ ID NO: 1552:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 76 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1552:

CTAAGTTAGA TGCTAGTATA CAAGATTTAC AACAAAAGGT ACTGGAATCG AATTGTGAAC 60  
 TAGACAAACT AAATC 76

(2) INFORMATION FOR SEQ ID NO: 1553:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 135 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1553:

TGTGTTGGGG CCCCGTATAT TGAAAATTTG TTATAGGTGT ATTTCTTTGG TTAACATTG 60  
 TTATATAACT TGTAGTTTTA GGATGTTGAT TTTGCTTACC TTGTCTGCTA TGTAATGTCA 120  
 CATCAACATG ATThA 135

(2) INFORMATION FOR SEQ ID NO: 1554:

(A) LENGTH: 104 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1554:

10 TTTGAnATCA AATTCACCTC GCAAACGTGT CCAAGCGTGA GCAAAGGGCT AGATGATTAA 60  
 TAGTTGCCCC ACTAACGGGA TCGCCCCAGT TATCCAACCTT ATCT 104

(2) INFORMATION FOR SEQ ID NO: 1555:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 100 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1555:

25 AATAAGAAAC AnGACACTAG CTCACCACGA CGCGCACGGC CTGCGTGTA AATGTTGGT 60  
 GGCGCGGGTT GGAGATCGTG TTCAACCAGA GCAGAAAATA 100

(2) INFORMATION FOR SEQ ID NO: 1556:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 86 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1556:

40 CAATGAAATT ATTTATTATT TTAAGTGCAT TAAACCCCGA TGATGGCTGT CCGGTACCAG 60  
 GTGCATTTTG GTGCCCATGG TTTACC 86

(2) INFORMATION FOR SEQ ID NO: 1557:

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 78 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1557:

55 GTCATGTTCC CATCAAACT AATTTGTACT TACTAAAGGC TCAGCAGCGC AACAAATTAGG 60

## (2) INFORMATION FOR SEQ ID NO: 1558:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1558:

AACTGGTTAC AGAAATACCA CGTTCCTGTT TCAACTTTCA TCCAGTCACT TGATCGCAAA 60  
TTTACCAGTC TTCTTCCCTT TA 82

## (2) INFORMATION FOR SEQ ID NO: 1559:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1559:

CCACAGCGGC ACTATAGCCA GCCCCTAATA TATACAGTAT TTGCATCTGA CTCATTGGTT 60  
CATAAGTATA TGCACTGA 78

## (2) INFORMATION FOR SEQ ID NO: 1560:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1560:

ACCATTGCT AACTTTTTAG CAGCGCAATG TTCTTATTAA CTGCTTACGC CATCTATAAA 60  
AATAAACGTT CAACAA 76

## (2) INFORMATION FOR SEQ ID NO: 1561:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

TTGGAACCCA AATTTTTTTTA ATTTTCCCAA AAATTGGGGG GGGACCCCCA ATTCCCTTAA 60  
 GGGTTTTCTT TGGGGGCCCG GGGTTAATTC CACCCGGGGT TAAAATTTTC CCAAAAATTA 120  
 5 ATTTTnGAAA AGTTTTAATT TAAGGAAACC CATtnGTCCG GAATTTTTAC CCCATCCTTA 180  
 TGGGGGGTCC CAAAGATTCC 200

(2) INFORMATION FOR SEQ ID NO: 1562:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1562:

20 AACACAGAGA ATAACCAAGA GAAGACGTTT TCATCTGAAG AAAGTAACAG TAMGCCATT 60  
 ATGGAAGAAA ATCAAAACGA TGAGATAGTT ATAAAAGAAG ATTCATATAA TCCATTCGTA 120  
 ACGAAAACAT CTGAAAGTTT AATAGCTGAT GATGAATCTT CTGGTTATAA TAATACACGT 180  
 25 GAAAAAGATG AAGACTACTT CAAAAACAA CAAGAAATT TACAAGAAAT GGATCAAACA 240  
 TTTGATTCAA ATGATGGTAC AACTGTGCAA AATTATGAGA ATAAAGCGTC TGATGATTAT 300  
 TATGATGTAA ACGATATTAA AGGAACAAAA AGTAAAGACC CTAAACGAGG AATTCCATAT 360  
 30 ATGGAATTGT TGGnCAGTCA TGGAACGTTA TTATTGCTCA 400

(2) INFORMATION FOR SEQ ID NO: 1563:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 454 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1563:

45 TCTTCATCAT CTTCTAATTT ACCAGCTGGA ATTTCTAGCA ATGGTTTTTC TACTGGTTTA 60  
 CGATACTGTT TCACTAATAC GACTTCTTTT TTAGGTGTCA CTGCACAAAC A<sub>r</sub>CAACTGCA 120  
 CCATTATGAT AAATAATTTC TCTTGTGAC GTTTCACCGT TTGGTAATGT CACTGTATGA 180  
 ATTTCTACAT CTACAATTTT GCCATTATAA ATAAGTGTTC GATCAATTGT TTTTTCATT 240  
 50 AAATCCATTA TAATCACGTT CCTTTAAATT CATATTATAT ATTGATACAC TATGCTTGTT 300  
 AGCTAAAGTG TATCGAAAGG AGAACAGACA TGCAAAAAA TATATTAAAA AGTGGTATTT 360

AAATTATAGG ATTGTGCTGT TGAAAATGGG TATC

454

## (2) INFORMATION FOR SEQ ID NO: 1564:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1564:

ACATCTCGCA TCGTCACGAC TTGCTTGAAC CACTAGCAGG TCAAACAAAG CTGTACAGGC 60

AACATCTGC 69

## (2) INFORMATION FOR SEQ ID NO: 1565:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1565:

TCCAGAACCA TTTTAAATCC CGGGAAATAT AATTACCTCC ACTAAGTAA TATATCCAAG 60

CCAAGACTAA TCCTCCTTAA GCCGGTTTAA GTAACCAGGT TGAGAAGGAT TTTTGG 117

## (2) INFORMATION FOR SEQ ID NO: 1566:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1566:

TATTGAGATT AACAGTCTGG GAAAAATGAA CAGCAATTGT nTAATGTGAC GATGCTGATT 60

ACITTTTAAAC AGTATCATTT AATAACTCAG AGATGCGCTT TAT 103

## (2) INFORMATION FOR SEQ ID NO: 1567:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1567:

5 AATGGATGGG ACAGCAATTA GTGCATAACG ACAATATATG CTCAATTTGT CGGCAACTGG 60  
TTAAGAATCG TATTGTCACA A 81

## (2) INFORMATION FOR SEQ ID NO: 1568:

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 80 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1568:

15 AATGGATTCA GTAGGTATTG GTGAAGCGCC AGACGCAGCT GATTTGAAAG ATGAAGGTTG 60  
20 ACATACTTTT AGCATACCTT 80

## (2) INFORMATION FOR SEQ ID NO: 1569:

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 95 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1569:

30 TTTTAAATA CGATTTTAAG GAGGCCATTA TAATGGCGAG TAAAAGTAGC GAATTAATGG 60  
35 TTTTGTTAG GAATTGGTCG TTTAGGCATT CAGGA 95

## (2) INFORMATION FOR SEQ ID NO: 1570:

## (i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 118 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1570:

45 CCCAATAAAA AAAGCCTGTT GTCACAATGG TCATAGACAC GTACATACTT TAAAGGTTTC 60  
50 TGTAATATAA ATATTTTATA TGCCACTTTA AAGTTGGnAC GTTCGTATGT TGTACTAA 118

## (2) INFORMATION FOR SEQ ID NO: 1571:

## (i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 104 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1571:

GACTTGATCA ATGAAGCATT GTGTGACAAT TGGTCTGTTT GCACACCGCA CGGATTGnGC 60

10

GTCATTTATT TGTACTAATT CAAAAACAT TGTTGTTTTTCTAG 104

(2) INFORMATION FOR SEQ ID NO: 1572:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 118 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1572:

CCGAAGTGTGTA ATGGTCCTAA TGTTTTACTC ATACCATATT GCGTAACCAT TGAGCGGCGA 60

25

TTGTGTTGCA CGTCGAGCAT TGAGACCGTT GTACTCGTAA NGTATATCTC TGTACACG 118

(2) INFORMATION FOR SEQ ID NO: 1573:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 74 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1573:

AGGGATCAAA GGTCCATCCC CCATGCATTG GATAGTGGGG GATGACTTTT GATCCTATGT 60

40

TCCAGTTGCT TATT 74

(2) INFORMATION FOR SEQ ID NO: 1574:

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 341 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1574:

AACCTTTTGA GTAAATTCAC CAATACTCAT CCCCTTATCA TTTAACAAAC TTTTATTAAT 60

55

GTTTTTGGTT ATATTATGAG TCTTTACTGC TTTTAGATTG TAAAAATTAT CGTCATAAAT 120

GTAATTAATG TAATAATAGA AAAGTGTATA TATCTCATAT CGCCACCTGC TATACAACTT 240  
 ATTAAATAAT TAATTCCAAG ACATATTAAT TATCTAATTA TAACCTTAGT TnACGTTATT 300  
 5 ACATAATATA AAAATATATA ATAACCTTATC CnCCGGCnCC T 341

## (2) INFORMATION FOR SEQ ID NO: 1575:

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 109 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1575:

ACGTGTACCA ACTTTTGGGC ACCATTGATA ATAnGTGTCA TAGGGTGA CT CAGCATAACG 60  
 20 GGCAAGCCTA TTAATGATAG CCAGATTAAG ACATACAGTA CATATGTTT 109

## (2) INFORMATION FOR SEQ ID NO: 1576:

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 79 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1576:

GCTAGATTGC GGAATTAAC AATCATCAGC GATTTAATAT TTGCACTGGA GACGTCATGG 60  
 35 TAATAAAAAA TTGATGAGA 79

## (2) INFORMATION FOR SEQ ID NO: 1577:

## (i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 69 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1577:

ATGATGGCTA TCATGAGATT GAGATGATAA TGACAACAGT TGATTGAAA TGATCGTGTA 60  
 ACTTTTCAT 69

## (2) INFORMATION FOR SEQ ID NO: 1578:

## (i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 104 base pairs



- (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1578:

AAATTGTCAC TnCAGGTCAT AACCAACCAG GTGGGACTGC ACGAGCGTTA CTAATGATCC 60

10 AACGGTCTTG CTTTGTGATG AGGCAACAAG TGCACTTGAT CCGC 104

(2) INFORMATION FOR SEQ ID NO: 1579:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 89 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1579:

GCTCAATAGA TACAACTATT AGGACAACGG ACTATCGTTT ACAATTTATT CCAGATAAGG 60

25 ATCGCGCAGG TCGTATGCGT AACTATGCA 89

(2) INFORMATION FOR SEQ ID NO: 1580:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 102 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1580:

TTGTCTCTAA TAATGGnTTT GGCTTTTCT AAAATTTCAG ATGTGGGTGC TGGTGAAGCA 60

40 CCGACTGGTT AATTTTCTTG TCGTCACGGC CACTTTTGT TT 102

(2) INFORMATION FOR SEQ ID NO: 1581:

(i) SEQUENCE CHARACTERISTICS:

45

- (A) LENGTH: 102 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1581:

AAGGTGCTGT TATTAGGATA ATGnATTTAA ACCCCATGGT ATGAAGGATA TCTGGAAGTT 60

55 AGATTGGATA TCCCTTAACC ATGGGGGGTT TTATTTTGG GG 102

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1582:

TTCAGGGGAG CTGAACATAT TGACGACTTT TGGGTCAATT CATTTTGCAT TTTACTTTTA 60  
 AATGCGTTGT TGCATGTAAT TGTATTAACG ACATACATGG TGGGGCTCTA AATnAATGCT 120  
 TGACTAATTT CTTGGATGGA GACCACGATT TACCAACTCA 160

## (2) INFORMATION FOR SEQ ID NO: 1583:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1583:

TAAAAGCAAG TACATTAGAG GTTAGATCAC AAGCTACTCA AGACTTGAGT GAATATTATA 60  
 ATAGACCGTT CTTTGAGTAT ACAAATCAGT CAGGATATAA AGAGGAAGGA AAAGTGACGT 120  
 TTACTCCTAA TTATCAACTT ATAGATGTAA CTTTAACTGG GAATGAAAAG CAAAATTTTG 180  
 GTGAAGATAT TTCTAATGTA GATATATTTG TTGTAAGAGA AAATTCTGAT AGATCTGGTA 240  
 ATACAGCTTC AATTGGTGGT ATTACTAAAA CAAACGGTTC AAATTATATT GATAAAGTAA 300  
 AAGATGTAAA TTTAATAATT ACTAAAAACA TCGATAGTGT TACATCAA 348

## (2) INFORMATION FOR SEQ ID NO: 1584:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1584:

AGCCAGCAGT AGATAGATAT ATTAATGAAT TCTTGGAGAA AGGTAGCTCA AATTGTCCAA 60  
 TTGAGATATT GAA 73

## (2) INFORMATION FOR SEQ ID NO: 1585:

(A) LENGTH: 255 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1585:

10 GTAAGGAATG GTCACGTATT CCACACTTCT ATATGAATTA TTATGTATAT CAATACGCAA 60  
 MTGGTTACAG TGCAGCTCAA AGCTTAAGTC ATCAAATTTT AHCAGAAGGT AAGCCAGCAG 120  
 TAGATnGATA TATTAATGAA TTCTTGAAAA AAGGTAGCTC AAATTATCCA ATTGAGATAT 180  
 15 TAAAAAATGC TGGTGTAGAT ATGACAACAC CTGAACCAAT TGAACAAGCT TGTGAAGTTT 240  
 TTGAACAAAA ATTGA 255

(2) INFORMATION FOR SEQ ID NO: 1586:

20

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1586:

30 TTATTAGGTG AntCCATTGG CAACATTGAT TGGTTTGTCA TTAGGACAAA TTTTATTATA 60  
 CATTGGCGTT ATTTTACTA TCTTATCTGG TATTGAATAC TTTTATAAAG GTAGAGATGT 120  
 TTTTAAACAA AAATAAATAT TTGTTTATAC TAGATTTTCAT TTTTCATATGG AATCTAGTTT 180  
 35 TTTTAATCCC AATTTTAGAA ATTAGCCACG CAATTGTTTA TAATGATATA TTGTAAAACA 240  
 ATATTTGTTT ATTTTTTTAG GGAAAATCTG TAGTAGCATC TGATACATTG AATCTAAAAT 300  
 40 TGATGTGAAT TTTTAAATGA AATACATGAA AAAATGAATT AAACGATACA AGGGGGATAT 360  
 AAATGTCAAT TGCCATTATT GCTGTAGGCT CAGAACTATT 400

(2) INFORMATION FOR SEQ ID NO: 1587:

45

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 561 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1587:

55 CAAAGCGTCT ATTATTGTTT GATTTTGATG AAACATATTT TAAACATAAT ACAAATGAAG 60

AAGTGATCAC TGCTGTATTG ACAGGAAGTA CATTTCAAAG TGTCATGGAT AaaATGGATC 180  
 AAGTTAATAT GACGTTTAAA CCATTACATA TCTTTTCTGA TTTGAGTTCT AAAATGTTCA 240  
 5 CTTGGAATAA TGGCGAATAT GTTGAATCAG AAACATATAA AAAGAAAGTC TTGAGCGAAC 300  
 CATTTTTATT TGAAGATATT GAAGATATAT TACGTCATAT TTCTGCGCAA TATAATGTCTG 360  
 10 AATTTATTCC ACAAAGAGCA TTTGAAGGTA ATGAAACACA TTATAATTTT TATTTTCATT 420  
 CAACAGGTAA TCACAACAAT GATAGTCGTA TCCTAGAAGC ACTnntCAGA TACGCAAATG 480  
 ACCAAACTA TACAGCGAGA TTTAGTCGAA GCAATCCATT AGCTGGTGAT CCTGAAAATG 540  
 15 CGTATGATAT TGACTTCACA C 561

## (2) INFORMATION FOR SEQ ID NO: 1588:

(i) SEQUENCE CHARACTERISTICS:  
 20 (A) LENGTH: 79 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1588:

CCAACAGTTT TATCATTATG GCAAGTTCTG TTAAACCTGC TGAGAGTTAT TTTGCACTGA 60  
 30 TTGCAAAACC AGAAATTGG 79

## (2) INFORMATION FOR SEQ ID NO: 1589:

(i) SEQUENCE CHARACTERISTICS:  
 35 (A) LENGTH: 73 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1589:

GCAGATATGC AGCAATTTAT AGAGGACTAG TAAACGCATA TATGACTTAC AGCTTTCAGA 60  
 45 CAAATAGCTT TGC 73

## (2) INFORMATION FOR SEQ ID NO: 1590:

(i) SEQUENCE CHARACTERISTICS:  
 50 (A) LENGTH: 71 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

55

TCATTTTATG GTTGATCATA GGCCTCGTCT TTTTCCTTGG GGATTTTATC TTTAAATACA 60  
CAGATTGGCG C 71

5 (2) INFORMATION FOR SEQ ID NO: 1591:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 78 base pairs  
 (B) TYPE: nucleic acid  
 10 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1591:

ATACAATACA ATTCACACCA TATATGGATA AAATGCAAGA TGCAATTACT GCAGTTGCAC 60  
AGTGCAAGTA GCAATACC 78

20 (2) INFORMATION FOR SEQ ID NO: 1592:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 168 base pairs  
 (B) TYPE: nucleic acid  
 25 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1592:

30 CCAATTAATT AAAAACC GGA AAACCAATTT TTTAAACCA TTAAGTTAAA AATTTTTTAA 60  
AATTGGGCCC CAAACCTTGG AAAAAGGTTT AATTTTCCTT TCCCAATTTT CCCAAAATTT 120  
35 TTAACCCAA AAATCCC GGT TTTGGGTTA AATTTCCCTn GGTTAAAT 168

(2) INFORMATION FOR SEQ ID NO: 1593:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 117 base pairs  
 40 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1593:

TGCTAGAAAG TATAGAACCT GGTTCAAACG CATGGTTTTA TGCCCTTTT TAAACnGATG 60  
50 TTTATTAAAA AAATATGGAA ATTGGCCACG TCCGCCAATT TCCTTAGAAA AGAACGT 117

(2) INFORMATION FOR SEQ ID NO: 1594:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 66 base pairs  
 55

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1594:

AGACGAAGCC AAAAAGTTAT TCGCCAAATC TGAAATATTT TCAAAGACCT TAAAGGCGTA 60  
AAATAC 66

10

(2) INFORMATION FOR SEQ ID NO: 1595:

15

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 100 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1595:

ATTTTATTTA GGCCAATAAC TGrCTACTTC TGAAATAAGT TGCTTTGCAT AGTCTGACGC 60  
GGGATGTTTG GATAATATCT TCTGTGTTAT TGCATTGCAA 100

25

(2) INFORMATION FOR SEQ ID NO: 1596:

30

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 73 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1596:

GACCAGACGG CCGTAAACCT GGATGAAACC GTCCATTAGA TTCTGAAGTT GGTATTTTAC 60  
CTAGAACGCA TGG 73

40

(2) INFORMATION FOR SEQ ID NO: 1597:

45

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 66 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1597:

CTTTATAAAA TTGTCTTTGA CTAACAGGAT TTTCAACGCT ATTCACAAAC CATGGTTTAA 60  
CATATT 66

55

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1598:

TATGGCACCC TCTTTGATnT TGTGACCGTT TTTGGTAATT CACCATTATT GTACGAACCA 60  
 TGGAAATTCGC TGCCTTCCTT TAGGCAATAA CATAATTATA TTTATCCCCT TCTTGTCAC 120  
 AGAGGTGCTG ACAACACCA 139

## (2) INFORMATION FOR SEQ ID NO: 1599:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1599:

CTCCTCTGCA TGCACATCTT GTTGTAGCAA GGTTCACATG TAATTTATTA AATCGAAACT 60  
 CTATCCAAC 101

## (2) INFORMATION FOR SEQ ID NO: 1600:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1600:

TTGTACCAAG GTTCACATGT AATTATTAA AGCGAAACGC GTATCCAAC 60  
 GTTCATTCGT AAACAAATAA GTATAAAAT TCAATATTTT TATTACTAGA ATATGGTTAA 120  
 ATACATTTAT TTCTTATAA AATTGTATGT TTAAGATATT TTGCCAAATT GA 172

## (2) INFORMATION FOR SEQ ID NO: 1601:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1601:

5 TTGGCACTGG CCGTCGTTTT ACAACGTCGT GCACTGGGAA AACCAAAACA CGACGTTGTA 60  
 AAACGACGGC CAGTGCCAAG CTGTCATGCC TGCAGGTCGA CTCTAAGAAG GA 112

## (2) INFORMATION FOR SEQ ID NO: 1602:

10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 679 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1602:

20 TGCAATGGTT AATCATCTCA TATAACAACA CATAATTTGT ATCCTTAGGA GGAAAACAAC 60  
 ATGACAAAAC ATTATTTAAA CAGTAAGTAT CAATCAGAAC AACGTTTCATC AGCTATGAAA 120  
 AAGATTACAA TGGGTACAGC ATCTATCATT TTAGGTTCCC TTGnATACAT AGGCGCAGAC 180  
 25 AGCCAACAAG TCAATGCGGC AACAGAAGCT ACGAACGCAA CTAATAATCA AAGCACACAA 240  
 GTTTCTCAAG CAACATCACA ACCAATTAAT TTCCAAGTGC AAAAAGATGG gCTCTTCAGA 300  
 GAAGTCACAC ATGGATGACT ATATGCAACA CCCTGGTAAA GTAAATTAAAC mAAATAATAA 360  
 30 ATATTATTTT CAAACCGTGT TAAACAATGC ATCATTCTGG AAAGAATACA AATTTTACAA 420  
 TGCAACAAT CAAGAATTAG CAACAACGTG TGTTAACGAT AATAAAAAAG CGGATACTAG 480  
 AACAATCAAT GTTGCAATTG AACCTGGATA TAAGAGCTTA ACTACTAAAG TACATATTGT 540  
 35 CGTGCCACAA ATTAATTACA ATCATAGATA TACTACGCAT TTGGAATTG AAAAAGCAAT 600  
 TCCTACATTA GCTGACGCAG CAAAACCAA CAATGTTAAA CCGGTTCAAC CAAAACCAGC 660  
 40 TCAACCTAAA ACACCTACT 679

## (2) INFORMATION FOR SEQ ID NO: 1603:

45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 85 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1603:

55 CATTTTAATT GATATAATTT AGACTTTAAC ATTTTCATGCT GTTCACGGTT TTAATTTGAG 60  
 ACGTCATTTG GTATAACAAC TATAC 85



## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1604:

ACTGGTGTGA ATAGCTCCAG CAATTTCTTT AACCGCGATC ATAATCAACG TCACCTTTTA 60  
 ATTTGCCA 68

## (2) INFORMATION FOR SEQ ID NO: 1605:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1605:

TGGGGGGTnT TTTTGGGTTG GGTAAAAA AGGGAATTGG CCCAAGGGGG GAATTCCTT 60  
 AAAAAAACCC CCAACCCCT TGGGAAATTA AAAATTGGGT TAACCGGGA 109

## (2) INFORMATION FOR SEQ ID NO: 1606:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1606:

GCTTATATAC ATGTTCCATT ATAAAGGAG TACGAACGAA AGTAACGCAT GACGTTAATT 60  
 TAAAAATATT GTAATAATTA TGGATTAAAT TAAAAACCA GGGGTATTCC AT 112

## (2) INFORMATION FOR SEQ ID NO: 1607:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1607:

GTTCAAGTTG GTAACCTAAC AACACGnAAT TAGTTTAAAC GTTTGG

106

(2) INFORMATION FOR SEQ ID NO: 1608:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 83 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1608:

CACACTGATA CCATAGGATT TATGATAGAT CAACAGCATG ACCAAATGTA TGACCTAAAT  
 TTAAAAATTT ACGTACACCT TGT

60

83

(2) INFORMATION FOR SEQ ID NO: 1609:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 132 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1609:

AAAAGAATAA AGTCACTGAA CAATGGTCTT TCACAATGAT GTTGCGTCAA TGCACAAGCG  
 CATTATGTnt GTGACTTGGG CATTITGGCT TATCAGCTGA ATATTATACG CATTACATC  
 CCAATTAACG TA

60

120

132

(2) INFORMATION FOR SEQ ID NO: 1610:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 107 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1610:

TTTAATGCAT ACGCTTCTCG CTTAGCAATT TCTTTGCACG TCTAACAAGC ATTAACGCTC  
 TTAntACTAT AATCACAACA AAACCAGCGA AATATAACAT GCGTATA

60

107

(2) INFORMATION FOR SEQ ID NO: 1611:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 84 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1611:

5 TTGCGCACCTG GTATCGTTCA AACCACCAAT GATGGCCCGT CTCGCCGTGG CAACAGCCGA 60  
 AGACCGCAGG TAAACCCTGA ACGC 84

## (2) INFORMATION FOR SEQ ID NO: 1612:

10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 127 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1612:

20 ACTCACATGT ACGATAACAC CCTTCGTAAA TCCATCTTTG GTTTGCCAAG TTCGTCGTTG 60  
 TAAACTGTCT ATACTCGTTA AACCGCTACA TGTTTTCCTA AAnCCTGTGC CTAAATGCTT 120  
 TACTGAA 127

## (2) INFORMATION FOR SEQ ID NO: 1613:

25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 129 base pairs  
 (B) TYPE: nucleic acid  
 30 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1613:

35 CGTTCAACTT TTTCAATTTT TAACGGCGTT TTACTATCTT TATCTGTAAC TAATTCAACT 60  
 CCAAACATTA AGCCTCGTCC TCTTACATCA CCAACATTTT GATGACGCTT CAGCGCATGT 120  
 40 AACTGTTTC 129

## (2) INFORMATION FOR SEQ ID NO: 1614:

45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 348 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1614:

50 nCAACTAGTG GATTTAAnAT AnACATAATT ATAAATGCAA ATGCTAATAG CTGAATACCC 60

55

GCACTAGGTG CATAATTTGT GTATTGAGCA AATAAAGCTA ATACAATGAT TGTAATTCCT 180  
 TTAATGACAA ATAAAGGTAA ATTTAATCGT TTAAAGGTT GGTAAATTAA AAATACAATT 240  
 5 GCAGCTATAT GCGAGCCACT AACTGCCAGC AAATGATATA TACCTATCTC TTAAACACGT 300  
 TCCTTAAATT GCTCATTAAC TTCTTTTACG TCACCAGTAA TCAATGCC 348

(2) INFORMATION FOR SEQ ID NO: 1615:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 72 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1615:

20 GAGCTCCACC GCGGTGTCGC CCGCTCTAGA ACTACTGGAT CCCCCGGGCT GCAGGAATTC 60  
 GGCACAGCAT AT 72

(2) INFORMATION FOR SEQ ID NO: 1616:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 63 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1616:

35 CATCACGTTA AATCATAACG CGTGACGTGC TTTTGCTATT TGTCTCTCGG TATCTCTATA 60  
 TCT 63

(2) INFORMATION FOR SEQ ID NO: 1617:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 113 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1617:

50 ATTGAATTCA AGGGTGGAAAC TCATGAATTG GCTGGAAAAA GGTAGATTTA ACTGGATGGT 60  
 TGnAGCCATA TATCGGTGCG TTTATTTATT TGGTATTTTA AAAATCAACC TCG 113

(2) INFORMATION FOR SEQ ID NO: 1618:

- (A) LENGTH: 80 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1618:

10 GTACAATAAA GTGGTAAACA ACATGCCAAT GGAAAAAGGG ATTAAAGGTG TTTATGTCAT 60  
 TCTTAAAGAT AGTAACGGTA 80

(2) INFORMATION FOR SEQ ID NO: 1619:

15

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 117 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1619:

25 ATCTTATGTT TTTTTCCTAA AACTTCTGCT ACTTCATTTA TTTGATGTAT GGTAGATAAT 60  
 TCTGTTTGGA TACTCATATC AACTTTTTCT ATCATATCTG AAATCTCTTT TnTGGCA 117

(2) INFORMATION FOR SEQ ID NO: 1620:

30

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 107 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1620:

40 CGATAAACCC TTCGTAATCA ATCTTTGGTT TGCCAAGTTC GTCGTTGTAA CAGTCTATAT 60  
 CGTTAAAGC TACATGnTTT CCTAAGCCTG TGCCTAATGC TTTACTG 107

(2) INFORMATION FOR SEQ ID NO: 1621:

45

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 63 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1621:

55 AATATCGTGT CTCTGTCCAG TGCTGTCCAA TCAATTTTGA TCCACCGATT GTCATACGTA 60

## (2) INFORMATION FOR SEQ ID NO: 1622:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 75 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1622:

ACCATCTGAC ATCATCAATT ATGAATTAAT GATGATATTA AAAATAAATT TGAACATTG 60  
CCAATTGATA GTGCC 75

## (2) INFORMATION FOR SEQ ID NO: 1623:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 78 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1623:

TACCTGTGTA TCAGCTCTAT TAACAACCTA ACATATGTGA ATAATTTGCG ATCCTTGTTG 60  
ATAATGCTGT AATTGAC 78

## (2) INFORMATION FOR SEQ ID NO: 1624:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 95 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1624:

GCAAGCTTTT GCGGCTTCTG ATGCACCATT AACTTCTGTA ATTAAACACA CAAAGTGAAA 60  
CAGGTAGGTA ATGCAAAACT GCAACGGACA ATCGA 95

## (2) INFORMATION FOR SEQ ID NO: 1625:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 76 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

ATTGCGATTA CACAGTAGTG AATGAGATAT TTGACATGAA AGCTCCTGCA GCTTCTAAAG 60  
 AAGAGTTAGC AGGTTT 76

5 (2) INFORMATION FOR SEQ ID NO: 1626:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 126 base pairs  
 (B) TYPE: nucleic acid  
 10 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1626:

AAAAGCTAAA AAAGATTATC AGGTGTATCA CAAACTCAAA TTCTCATTAC CATTTATCTC 60  
 AGTGTGAACG TCTTAATTGA GAACTAATCT NAATTGAGAT ATTAGTCATA TAAGGATGGA 120  
 20 CAAGCA 126

(2) INFORMATION FOR SEQ ID NO: 1627:

(i) SEQUENCE CHARACTERISTICS:  
 25 (A) LENGTH: 116 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1627:

TGATACGATA GAACATAGTT CAGCACATTG TTTGTTGAAA TTGGATATTA CCGCCATTTT 60  
 35 TTCACAATAT CAATAATACC TGAACGTGTT GGTThTTCCA CATTATGATT GTACAT 116

(2) INFORMATION FOR SEQ ID NO: 1628:

(i) SEQUENCE CHARACTERISTICS:  
 40 (A) LENGTH: 91 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1628:

ATTTTGTCTT ATCTTGAACA AATCCGATTT TTCTCAGACA CTGAATCCAA AGTATTCATG 60  
 50 TACCATAAAC CATCTGCATG TTGATTTATG C 91

(2) INFORMATION FOR SEQ ID NO: 1629:

(i) SEQUENCE CHARACTERISTICS:  
 55 (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1629:

	ACAGAAAGTC AAACAGTAAA AGCGGCAGAA TCAACTCAAG GTCAACACAA TTATAAATCG	60
10	TTAAATACT ACTATAGCAA GCCAAGTATA GAGTTAAAAA ATCTTGATGG TTTGTATAGA	120
	CAGAAAGTGA CAGATAAAGG AGTATATGTT TGGAAGGATC GAAAAGATTA TTTTGTGGC	180
	TTGCTTGGTA AAGATATTGA AAAATACCCT CAAGGTGAGC ATGATAAGCA AGATGCATTT	240
15	TTAGTCATCG AGGAGGAAAC TGTTAATGGA AGACAATATT CAATTGGTGG TTTAAGTAAG	300
	ACAAATAGTA AAGAATTTAG TAAAGAAGTC GATGTTAAAG TAACAAGAAA AATTGATGAA	360
20	TCATCGGAAA AGTCTAAAGA TAGTAAATTT AAAATTACTA	400

(2) INFORMATION FOR SEQ ID NO: 1630:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1630:

	GCTTTCCTTT TCGAAATCTA TAAATCTAAT CCATTGAAGT AAATAATTA TGATAATTAT	60
	TAATTCTATA ATTGTnGTIA TCTTTAAATA ATTTGGAAAC CTTTCATAAT CTAAACCAA	120
35	AAAGAAAGTT AGACATGAAA AAAGTATCAT AAATAATGAT GCTAAACTTA AGGCTTGTGC	180
	ACCTGGCTTT CGAAGAATGT CTATATTTTC CTTAGTAGTC ATATTTACCT ATCTCCTATA	240
	CATTGATTTT GTAATAGCAT ATTAAGTATT TAAAGTTATA AGTACTTAGA TTCTTTTCGA	300
40	TTAAAAGTAT AAAAGCCTAA AATTATCTTT ATATTATTAT TTGATGACAA CTTTATGGTC	360
	TCTATTGTTT TTTACTTAAA CGCTAAAAAG CTAnACAAAG	400

45

(2) INFORMATION FOR SEQ ID NO: 1631:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 70 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1631:

55



TCTAGAGCGA

70

## (2) INFORMATION FOR SEQ ID NO: 1632:

5

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 62 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1632:

15

CAACGAAGAT ATTCAAGTGT TCACTCATT TTTTGGACTG CTAATGAAAC TGATTCTTGT

60

GG

62

## (2) INFORMATION FOR SEQ ID NO: 1633:

20

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 81 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1633:

30

CTAATGATTA GATTCAAAC AATAAAGACT ACAAAAACAA GTTGATAATG GTAAAGATAT

60

TATCCAACCTT GACATCTAAA G

81

## (2) INFORMATION FOR SEQ ID NO: 1634:

35

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 63 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1634:

45

AATTCACCT TTGTCTAGTA ATTTATTTGT GTAGTGTAAT CATTAAATTGT TTAAATATCT

60

AGT

63

## (2) INFORMATION FOR SEQ ID NO: 1635:

50

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 579 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

55

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1635:

5 ACCAACTAGC TAAATGCCAG CGCGGnATCC ATCTCAnAAG TGCACAGCAA GACCGTCTTT 60  
 CCAACTTTTG AACCATGCGG TTCAAAATAT TATCCGGTAT TnAGCTACGG TTTCCCGAAG 120  
 TTATCCCACT CTTATAGGTA GGTATATCCCC AGTGTTACTC ACCCGTCCGC CGCTAACATC 180  
 10 CAGAGAAGCA AGCTTCTCGT CCGTTCGCTC GACTTGCATG TATTaGGCAc GCCGCCAGCG 240  
 TTCATCCTGA GCCAGGATCA AACTCTCCAT AAAAATTATG ATGTTTGATT AGCTCATAAA 300  
 TACTAAATAA TGTTTGTAAC TAATAGTTAC GTTTTTGGAA TTAACGTTGA CATATTGTCA 360  
 15 TTCAGTTTTC AATGTTCAAT AATGTTCAAT CTCTTTTATT CTACTTCATT TATTTCTTGA 420  
 AGTCAATAAC TTTTGAACG ATTACTTTAT TTATTCTATA TTGTTTTTAT AGTTATTTCA 480  
 ATGGLAAGTn TTACACTTTT GaaATTCTTC TTTAAAAACA ACTGCGTCGt TTTGaCGcT 540  
 20 TTATCaTATT ATCmACTTTG GGaATTTAAA GTCAATAAC 579

## (2) INFORMATION FOR SEQ ID NO: 1636:

25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 69 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1636:

TCGACATTAA GCAACGTTCT TCGCAAAGG TAGCGAGCGA CACGAGTTAA CTTTGCACGT 60  
 35 TTCATTATT 69

## (2) INFORMATION FOR SEQ ID NO: 1637:

40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 116 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1637:

CTGTGACTTC GTCGCGATGA CCTTCGCCGT TGTTCATCAG GTAAGCTTTA AGTATCGTCG 60  
 50 ATGCAGTCnG TTCGCCATGT GCGCCAGCAG ACTGGTTGTA ATGTCGCCTC GTCCGT 116

## (2) INFORMATION FOR SEQ ID NO: 1638:

55 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 71 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1638:

10

ACAACATTTA GGTACTTTCA CGCATATCAC TACAGCTCAA CGTGATGATT TACCAAATCA 60  
AATTTACAAA G 71

(2) INFORMATION FOR SEQ ID NO: 1639:

15

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 73 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1639:

25

GCGTGGCTTT GTGATTAAACA TTGACAAGCA CGTGCAACAA CATATTCGAC GCGATAAAGC 60  
GACATCTAAT ATT 73

(2) INFORMATION FOR SEQ ID NO: 1640:

30

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1640:

40

CGCGATCATT TTCATTTCTA ATTAATCTTC CAAGTCCTTG TCTAAAACGT GTAACGTCAT 60  
CAGGTAATAC ATATTCCTTG AAAGTTGAAG TGAATTCAGA ATCCATAAGC CAATATTTTG 120  
CATTATGCTT GTTCATAAAC GGTAACCTCG CTATCATCAC ACATTTAATA CCATTGCTT 180  
GAAAATCAAA ACCTTCAAAA AATGTTGACG TACCAAGCAG TATGGCCTTA TCAAAATTAT 240  
TAAACTGTTG TACTATTTTA TAATTTTGGT TCTGCTGTG TGTTAATACA ACATAATCTT 300  
CAAATCTGG CAATTCATTT AAGCATATCT TGTACCATAT GCATCATTTT ATAACGCTA 360  
AATAAGACTA AACATTTTGA TGACGTTATA GTCGTATATn 400

50

(2) INFORMATION FOR SEQ ID NO: 1641:

55

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 66 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1641:

ATTGTTGTAC CATGTATACT AACAATTGTA ATGTCTCATT TCAGTAAACA AAAAGCGAAA 60  
 GACATT 66

## (2) INFORMATION FOR SEQ ID NO: 1642:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1642:

ATTTGCTCGG GAATAAATTT TGCCATTACA TAGAAATATC TAATAGATAA CGAAAAAGTA 60  
 TCGTATGTAT TTTTAATATA GTGTAATAA TTATATGTAA AATAAAATGT AGGTTTTTAG 120  
 TTAGAGGCAT TATAAGAAA TTTTGAGTAT AGGTTAGCTT TTAATTATGA ATCTTATTGA 180  
 AATTTGATTA ATAAAAATAT GATAGGGGAT TAAAATGAAA CTATTTTATA TCGTATTTCT 240  
 TATTATTATA TGGCTGAATA TATTTTATAGG AAATGAAATC ATCCATACAC TGACTGTTTT 300  
 AATAACAACA TTGTATATTG TTAATTCACG AAGGGGATT AAAAATGACA GAGTTGAATA 360  
 ATATTATAAA CGCGCTGCA ATCTTGTTT GAGTCCGGAA 400

## (2) INFORMATION FOR SEQ ID NO: 1643:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 66 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1643:

AACTAGAGGA GGACATCCTA ATGGAAGCAA AACCCGTTGC TAGAACAATA AGAATCGCAC 60  
 CTCGTA 66

## (2) INFORMATION FOR SEQ ID NO: 1644:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 75 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1644:

TATCAATTTC ATATGCGATT TGGCCTTGCA ATAATTAGGT CTCACCTTGC CATATCTTTA 60  
5 CCTAAGCAAT ACTTG 75

(2) INFORMATION FOR SEQ ID NO: 1645:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 70 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1645:

CATTCTCCTG CATCATAAAA ATCAACAATT GTATCATCAA AGTGTATCAA AATATTTTAA 60  
20 TATCCCAATT 70

(2) INFORMATION FOR SEQ ID NO: 1646:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 73 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1646:

AGTGACACTT TCGTTCCACC ACATCGTAAA GAAGTACTTC AAGCACGTGA AGATGACATC 60  
35 AAAGAAAAAG TTG 73

(2) INFORMATION FOR SEQ ID NO: 1647:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 71 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1647:

CTGTGATTGG TGTGTGATT GTCTTGCTTC CTGGTTGTCC TTCTTGTTTC GCTCGCTCTT 60  
50 CGCCGGGTTG T 71

(2) INFORMATION FOR SEQ ID NO: 1648:

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 115 base pairs

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1648:

AACTATAGAA AAATTCGGAA TTATACCAGA AATGGAATAT GAAATGGAAG AGGTTAAACA 60  
 10 AAnCGAGCAA TATATTAGAG AGCAAGAAGA AGCTGGAACA ATAGAGGCCA TAACA 115

(2) INFORMATION FOR SEQ ID NO: 1649:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 59 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1649:

TGTTGTCATG ATCTGAAAAG TCAAAGTCAA TAGAACATTG GCTTTGGCTT TTTATTTGG 59

(2) INFORMATION FOR SEQ ID NO: 1650:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 125 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1650:

35 ACCGATAATA GTACACGGCA TAATGnAACA ACTTGGCATG CACCCTTTTT ACGTTCCTTT 60  
 ATCTCTGCAT GATTGTCATG TTCATCATGG TTTGGCTTGC ATTAATAGAG AGGGTTGACG 120  
 40 CAGAA 125

(2) INFORMATION FOR SEQ ID NO: 1651:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 71 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1651:

TGATTACGC GAATGCCACT TTTACTACCA ATGTTCCCAA AGCTGCTTCT GACAAACGCC 60  
 55 ATTGTACTCT G 71

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 60 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1652:

TCACTACATG CACCATAAAT ACAGTATGAA CGTATTGAAA TGGGCATTAC ATGATACAGA 60

(2) INFORMATION FOR SEQ ID NO: 1653:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 123 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1653:

TTAATTGAAA CAATTGACAA ATGCAATTTG ACGCCAAACT TTGAACTTTG AATGGATTAT 60

CACATTATGA TTGTTTCATCC ATGGnCAATT AGCATGGACG TATTACATTC TGGATTATCA 120

AGC 123

(2) INFORMATION FOR SEQ ID NO: 1654:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 76 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1654:

CTATGACGTC GCATGCACGC GTAAC TTGGG CCCCTCGAGG GATCCTCTAG AGCGGCCGCC 60

CTTTTTTTTT TTTTTT 76

(2) INFORMATION FOR SEQ ID NO: 1655:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 145 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1655:

TTTTAAATTT TCGTGAAATC GGAAATGTAC GATTAGTTAT TAAGCGTTAG AATGTGTGAT 120  
ATGTGAACCT GGTATTGACG GCGCT 145

(2) INFORMATION FOR SEQ ID NO: 1656:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 73 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1656:

TTTAGAATTC CAATACGCTA TTGCCAGCGA TTTAGCCACT TGTGGGTAAT GATATTGAAG 60  
GTGTTAGTCA AGT 73

(2) INFORMATION FOR SEQ ID NO: 1657:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 93 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1657:

CTTCTGAAAA GTAGTAATGT AACCTATTGG ATGCGAATGA ATCCCCAAAT TTAGTGGACG 60  
TATGTGGCTT CATCTTCAGA ACCTGTATCT GGT 93

(2) INFORMATION FOR SEQ ID NO: 1658:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 58 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1658:

AAGTTAACAT GCAAGTTGAC GATGTAATGA CTCAAAAAGA GTGGAAACAA AAACACGA 58

(2) INFORMATION FOR SEQ ID NO: 1659:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 65 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1659:

TTAATCCAC AAACAAATGT ATGAAATTGA GTCAGTGATA TTAAATATGG GCTTGAAAGT 60  
 5 GTCTA 65

## (2) INFORMATION FOR SEQ ID NO: 1660:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1660:

TGCATTTTTG TAAGAACGCA AAGCATTGTA AATTAGTTTT TATAAATTAG GATATTATCA 60  
 20 TGTGTATTGA AAACAATGAA GTGTGCTATG A 91

## (2) INFORMATION FOR SEQ ID NO: 1661:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1661:

ACATATCTGT CCACACAACA AGGACCATTT GTCTGAAGGG ACAGTGAGTG GGGAAATATGT 60

## (2) INFORMATION FOR SEQ ID NO: 1662:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1662:

TGGGGTTTTA ACCAGGGGAC CTAAAACCAG CCCCCATTTT CCAAGTTTGG ACCCCAAATT 60  
 CCCNAAATTT AAAAAAATT TGTTTGGGGT CTAAGTTGGG CCGGTGCCTT CCTGCCTAAA 120  
 TTTAGCCCAT GTCTAACATA GTACTTTGGG AACGTAAAAG TTAAATTTA 169

## (2) INFORMATION FOR SEQ ID NO: 1663:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 677 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1663:

	TGGCACAATT GCACCAATTA AATGAATAAC TTTATCATTT TTATATACAG GTACAACAAT	60
10	CGCTTCTTTT ACGAACTCAG ACTGGCGTAA TTGTGTTTCA ATTCTTCTA ATTCCATTCT	120
	GTAGCCATTC AATTTGATTT GGAAATCAAT ACGACCTTGA ATGAACCATT GACCATTTTC	180
	AAACTTCGCT TTATCACCAG TGTGATATGT ACGAATACCG TCATCGAAAT TAAATACTTC	240
15	AGCTGTTTTT TGGTCATTTT TTAAGTATCC TAAACTTACA CTTTGACCTT CGATAACAAG	300
	TTACACCTTCA TCTGTAGTAG ATAATCTTGC GCCTGGTCTT TCAACGCCAA CAGGTAATGT	360
	CGGATATTGA TCTAAGATTT CTTGTGTAAT TTGAATACTT GTAAGTACTA CCGTAGCTTC	420
20	AGTTGGACCA TATGTGTTGT AAATCGTGGC ACTTGGGAAA CGGTTTACTA ACGCTTTTGC	480
	TGCTCTGTGA GGTAGAATTT CACCACAGAA GAAGAATTCG TTAAGACTAC CATATTGTTC	540
	TTCAATTAAGC GTTGGTAATA ATAAACACAT TTCCATAAAT GATGGTGTTG ATACCCAAAT	600
25	GTAAATCGGT GTTGCTGTTA GCATTTTCATT TAATAATTTA GGTTTATTAA TCATGTTTTT	660
	ATCTACAAGA nTnAAnG	677

30 (2) INFORMATION FOR SEQ ID NO: 1664:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 62 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1664:

40	GTTACAACAA TAGTGGTATA AAACGGGAGC AATTAGAGAT CAATATATGA TTATTAAGAG	60
	CA	62

45 (2) INFORMATION FOR SEQ ID NO: 1665:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 342 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1665:

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GTTTACGCAA ATGATAGCTC GGTAAAACAT GAGCAACATG TTGAAGCCAA TTTGGAAATG 120  
 TGTTTATCGG AAACCACAAT CCACCTAATA CTGCTAAACC AATTGTTACG ATATTAGCTA 180  
 5 AAGCACTTGT TTTTGAATA TCATTTAACA AAGAACCATA ATATGCCAAA AGTTATTAAT 240  
 AGAGACGCAC CTAACCATAA AAATATTCCT GACTCTAACC ATTGAAGTGC ACTCATTGCA 300  
 ACACCTTTAT AAAAATGTCC AACCATAAAA ATAACATA TC 342

10 (2) INFORMATION FOR SEQ ID NO: 1666:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 102 base pairs
  - (B) TYPE: nucleic acid
  - 15 (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1666:

GTCCAAGAAT TCAAAAACGT TTTCAACTTC GGCCAAAGCC CAATTTnTCT TTGTGGTTTA 60  
 ACTTTTTAAT TTTGAACGTT TTAGGGCATA AAAAAAAAAA GG 102

25 (2) INFORMATION FOR SEQ ID NO: 1667:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 122 base pairs
  - (B) TYPE: nucleic acid
  - 30 (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1667:

TTGATAGTAG CCATAATCAT ACCACTTAAA TAATATGTTT GATCATCGGC ATAATTTTTTA 60  
 TTTATTGTCT GTTCGCAATA TTTGAGCAT TATCATAATT ACCACTAGTC ATATCATCTT 120  
 40 TG 122

(2) INFORMATION FOR SEQ ID NO: 1668:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 57 base pairs
  - 45 (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1668:

AGAGATGAAA TTAAAATCGC AATTGAAAAT TTCAAATCAC GATGAGAGTG GGACAGA 57

55

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 70 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1669:

AACTACTGCC AATATTAATA GCATTGGTAC ATCTTAGAGG CATTGAATTC CTTACTCAGA 60  
 CTCATAATGC 70

(2) INFORMATION FOR SEQ ID NO: 1670:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 73 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1670:

TTGTCTGATA TAATCCATT CGATTGGACT CCACACGTTA CACCGATACC TTCTTTACCA 60  
 GCCCCGACCCG TAC 73

(2) INFORMATION FOR SEQ ID NO: 1671:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 140 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1671:

GAAGAATTGT ACTGTTAAAG TGACTCTAAA CTATCGCGGA AATAACAGTG AAATCACCAA 60  
 TTAGACTAGC GAACTGAAG TCATTAAAAA CAGACATTTG TAGTGGTGCA CTTATCACCG 120  
 CAAATACAAG AGAGTTTCTC 140

(2) INFORMATION FOR SEQ ID NO: 1672:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 59 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

AACAACGTTT ACTATTGGCA CAGAACGGTT GGTACTTAGT CTAATACCAT TGTCAATCAA

59

(2) INFORMATION FOR SEQ ID NO: 1673:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 124 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1673:

ATCTCTTTGA CTTGAAGGAT TGGATTAAAA TCTTGGTGAT TTGGGCCGTG AAATATTTCC 60  
 AGAAAATTCC TCAGACGTAT TAGTATAATT GTAACGnTAC ATTCTAATAT ACCTTTCTTC 120  
 GATG 124

(2) INFORMATION FOR SEQ ID NO: 1674:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 109 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1674:

CACCACCACC ACACACACAC ACACAAACAC ACAACCCCCC CACACACAAA CCACACCACC 60  
 AACACACCAA CACnCACAA AAACCCACCA CACACACCAC ACACCAACC 109

(2) INFORMATION FOR SEQ ID NO: 1675:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 101 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1675:

TnGTCAACTG ATTTATGAAA TGGCAGAGCA TATGGCGTCA AAGGTTCTTA ATCGTTAAGC 60  
 CAGACCACTG GAGGACCATT AGATGCAGCG TTGCTTTCAA G 101

(2) INFORMATION FOR SEQ ID NO: 1676:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1676:

TTTTTAAAT TTGnAAATTT TAGACCTTAT TTCACGTGCG ATTTAATCGA TGTGTTAATA 60  
 5 AAACAATACT GGCATTCAAC ATGTAATCCG ATAATAAAAT AAGGTTGCAA TTATGTTATT 120  
 GCATATTTTG TTTATTACTT AGAATAATAC GATGGTTAAG ATGAAATATA TGACAAAGAT 180  
 AAATAATGAC ATTAAATTCA AGATGTTTAC GCCTTTTAGA TCTTTTTTAA GCATTTTAAA 240  
 10 TCCTGTCACT TCKACATTAC CGACTAAGAG TAATAAGACG ATAAATACCC ACCAATTsTC 300  
 TTTTGAAAA CTCATCGTCG TTAATGCTAA GACGAATAAT AACAACACAC CCATAATAAT 360  
 15 TCTCAAAATG CGAGTAAATA CAACTTCCAT TTTAAAAATA 400

(2) INFORMATION FOR SEQ ID NO: 1677:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 64 base pairs  
 20 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1677:

TCTTACTCAT GCATATGAGT GCAAGGGCCT GAGCATTTCAT CAGCAAGATT AGAGCGATTT 60  
 TTAC 64

30 (2) INFORMATION FOR SEQ ID NO: 1678:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 65 base pairs  
 35 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1678:

ACAGCTGATT TATTAAATGA TACTAAGTCC AAAGGCATGC GCATTATATC AGTTGGTACA 60  
 TTTCA 65

45 (2) INFORMATION FOR SEQ ID NO: 1679:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 362 base pairs  
 50 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

55

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1679:

5 AGCGCCACCA ACTGACGAAT TAGGTGGTAG TTGGACACTA TGGAAAAATT TAGCGCGACA 60  
 AAGTCCTGAA TTGGTAATC CTGATAAGTT TTGCCAAAAT ATTCCTA~~n~~AA AAAGTTGGTT 120  
 TGTTCAGCA ACTTCTACAA CAAACAATAA AGAGATTATC GATACAATAG AAAGTATTTG 180  
 10 TAAACGTGAC CCACTTGGCA GGCAAAACAG TTACAGGCGG TATTATTACA ATCAATGATT 240  
 CTGcATGGCA AATGAGTTTT ACAATCAATC GTGCAGCAAC AGTTTGAAAG ACCAACCTGG 300  
 AAAATGGAAA TATCTACATG GGGTTTGATG CCTTATGATT CnGGnGTAAA CGGCGGTTGA 360  
 15 TG 362

## (2) INFORMATION FOR SEQ ID NO: 1680:

## (i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 69 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1680:

AGATACTTCA GATTTAGCAT CATGAAGCAA CTTTAAAGC AATCGCTGAC GCTGGTATTC 60  
 30 AGCCCGAGG 69

## (2) INFORMATION FOR SEQ ID NO: 1681:

## (i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 56 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1681:

40 TAACCATTTT TTTTGACGTT TTATGTTGTT TTAAGAAATA AATACCAGTT AATGTA 56

## (2) INFORMATION FOR SEQ ID NO: 1682:

## (i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 56 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1682:

55

## (2) INFORMATION FOR SEQ ID NO: 1683:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1683:

CCCCAACACA ACAACAACA CACCCACCAC CCAACCCAC CACACCCACC CACCACCCCA 60  
ACCCACCACA ACACCACnCA CCAACACACA CCACACAACA ACCCCACAC 109

## (2) INFORMATION FOR SEQ ID NO: 1684:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1684:

ATTATGTTTCG CGATAATTTA AGTAAAAGAA GCACAGATAT TGAATTTGAT AGGAGTAATT 60  
GT 62

## (2) INFORMATION FOR SEQ ID NO: 1685:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1685:

CATAAGGTAC TTAAATTAAG GCATATCTGC TGTCTAGCAG TCGCATAAAT CATTAGA 57

## (2) INFORMATION FOR SEQ ID NO: 1686:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1686:



## (2) INFORMATION FOR SEQ ID NO: 1687:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1687:

CTTTATAGTA TATTGCTTTT TGTTTTTCTT TTTCGTCATA TTTCACCTTTT AAATAGATAC 60  
 CTGCAACACT AATTAATATG ATTAACATAA TACTAGTTAA TATTAAnATT 110

## (2) INFORMATION FOR SEQ ID NO: 1688:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 214 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1688:

AATTACTAGT CTGCTTGTCC AAAGATTATT TATATTCTAG CTCAACATTA ATTTCTTTGA 60  
 TTTTGGTACC ATCTATCGTG TCACCCATGC GATGCGGTTG TAGTTTTTTTT GTAAGTTCGA 120  
 AAGTATAAAA CTTATCATCT TCCATTTTAA CTACAATTTT ACCTTTTCTA TTATTACAG 180  
 CACCATATAA TTTTCTTCT TCCATCAATT TTTT 214

## (2) INFORMATION FOR SEQ ID NO: 1689:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1689:

GCTAGTTGTA ACGTGCTTTT TCACCACCAG ATAAATCATA ATATCTTTTA ACATCTCTG 59

## (2) INFORMATION FOR SEQ ID NO: 1690:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1690:

CCAAACTTTA TAATATGAAA TGCTTGGTAA TTACAAAGAT AAAATCATAC TCACG

55

(2) INFORMATION FOR SEQ ID NO: 1691:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1691:

TAGACAGCAA TCCATTGCTA TAGGGGTGGA TATCTCATTT GCGTTTGGAG CTGTGCTTGT

60

TATG

64

(2) INFORMATION FOR SEQ ID NO: 1692:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1692:

TGCATGGGAT TGCAGCTAAG AGAATCATAA AAATATATTA CTTTAATAAG TGTTAGTA

57

(2) INFORMATION FOR SEQ ID NO: 1693:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1693:

CGATGTGTAC GTCTCACCTG ATTTGCGACG GTAAGCTAGT GCATATTCAG CACCGCTACT

60

CGCCCAGCCT AGAC

74

(2) INFORMATION FOR SEQ ID NO: 1694:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1694:

AACTTTTCAG ATGTTGATAG CTATAGATTT AGGCGCTATT CACCAAGTCT ACATGCAATA 60  
5 CGTACGTTAT AATGCACTGC AACGAATCGC GCGTTATGAG TTGGTAATTG TTGTTCAATA 120  
TTGGGTGTAT AGTTTTCAAC GTGGTTACAA GCAACTACCT AA 162

(2) INFORMATION FOR SEQ ID NO: 1695:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 55 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1695:

AATTATCTCT ACACCTTTTC TTTCACATAA TTGACGCAAT ATAATCCCTA TATCT 55

(2) INFORMATION FOR SEQ ID NO: 1696:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 56 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1696:

ATGCAACGTT GGCATTGGGA AATGGTCCTG CCTAAATTAA CACGCAATAA AATGTG 56

(2) INFORMATION FOR SEQ ID NO: 1697:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 57 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1697:

ACTGTGTAGA AGATGCTATT ATTGTAAAAC ATAGTTTTAA TTTTATTTTC TGATATA 57

(2) INFORMATION FOR SEQ ID NO: 1698:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 109 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1698:

AAAATTTTCC CCCGGGAACC CGGTTTTTTA AACCCCCCGT TTTAAAAAAA TTTTGGGGGG 60

5 CCCAAAATTT CCCAAAAAAA NAAAAAATTT TTTTTTCCC GGGGAAAAA 109

(2) INFORMATION FOR SEQ ID NO: 1699:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 100 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1699:

GTGTTAACGT GGATTATATC AAGGAGGCGG TCAGGTACAG TCCACACGCA CAGCGCACAG 60

20 AAGTATCACA TCCAGTAAAC AAGGCTAGTA CAGCATTGCA 100

(2) INFORMATION FOR SEQ ID NO: 1700:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 129 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1700:

AAGGTTAAAT GAATTAGGTT GATCAATGCT CTATACTCAT TGCTAAGTCA ACGCACCTTT 60

35 ACCACCTTTT CCCAACTCAG TAAGGCATTC GACGTATTTT TTAGCCAAGT TTACATATCT 120

ACTCTGCAC 129

(2) INFORMATION FOR SEQ ID NO: 1701:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 63 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1701:

50 CAAGAGGAAC AACTCGGTAC TGCGCATCAG CAGAGATGGC GAAATCACAC TTAGAAGACA 60

AGG 63

(2) INFORMATION FOR SEQ ID NO: 1702:

(A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1702:

10	TATTTAATAA ATCTTCAATA CCTTGTTTCAT CAGTTTGTG ATAAATAAGA CCTCTCCATT	60
	TTAAATCTTC AATTAATACA TTCGTCATTA TTATTTCCCTC CTATTTATAA TTATTTATTG	120
	AATACTTGTT AAAATACTTT AAAGKTTTTT GAACGTAAAA AAAACCCTTA CAACAAATAT	180
15	GTAAGGGCGC GATTGCACGT TACCACCAAA CTAAACATA ATCATAAGAT AATGTTCACT	240
	CTATTAATGA TACGTTTCATT AATAAACGTA GGACATGTTA GTTATAAAGG TGTATTCATA	300
	TTATTAAAAA CACTAGTTCA CAGCGACCAC TAGCTCTCTG ATGATTTCAT ATAATATTAC	360
20	TTGTCCTTTT ATCCTATTCT GTATGCATTT TCCCTAATTA	400

(2) INFORMATION FOR SEQ ID NO: 1703:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 208 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1703:

35	TCAATATTGA TATCGAAACG CTTTGCAGAT TGATATAAAT TATCAGAATC AAGTAATTCA	60
	TTTATTTTCT TTGGTGAAG TACTTGGAAA ATACTATACT GATGAAACT TAAAAATGAA	120
	ATGAAGTATG GAAGTTGTTG CTTTGGGTAA GCAAAATTC TAATACATAC TGATTAAACT	180
40	GTTTGTTTAT TGNGAATTGC AACGCATC	208

(2) INFORMATION FOR SEQ ID NO: 1704:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 67 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1704:

55	AAGCCGATGT AATTATTTAT GCAACACCTG TTCTAATGCA CAAAGAAATA TCTTAGCGAG	60
	CTTATAG	67

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 54 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1705:

CCAAGTTGCA TGTTATTTTA AGCTGACTTT CCACCAACTT CTGAGTTTGT GGCC

54

(2) INFORMATION FOR SEQ ID NO: 1706:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 61 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1706:

CAACTACACG AAAGGGTAGT GCTTCAAGAT AATAACGTCC AATTATTAGG AACTGTGGCG

60

A

61

(2) INFORMATION FOR SEQ ID NO: 1707:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 54 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1707:

ACCATTCCAA ATGAACCTAA ACCAATTGAT ACGTTGACGA CAACAGGTTG TTCA

54

(2) INFORMATION FOR SEQ ID NO: 1708:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 59 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1708:

AAATTTGAAT AACTGTACAC ATTTTTTTGA TCATAGTCTA TATACTTTGT GAATTAATT

59

(2) INFORMATION FOR SEQ ID NO: 1709:

- (A) LENGTH: 59 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1709:

10 GCACAATAGC CAATTAGATG GGGCCGGTGC GGTAACATTT TGCTTCATTC CTGCATTAT 59

(2) INFORMATION FOR SEQ ID NO: 1710:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 55 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1710:

TTACAATTCA ATCAAGTTCT TCATTATCAG ACGAAGAAAT CCACCGTATG GTAAA 55

25

(2) INFORMATION FOR SEQ ID NO: 1711:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 56 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1711:

35

TTTCTGCTTA TTGTCATTGC ATATCGAATT ATTAGAAAGT GCAGATTTTCG CATCAG 56

(2) INFORMATION FOR SEQ ID NO: 1712:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 55 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1712:

TAAACCTTTA GGATTGCTGG CAATAGTAGT GCAGTTGGCT GGACTTGTCA TGCCC 55

50

(2) INFORMATION FOR SEQ ID NO: 1713:

(i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 207 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1713:

5 CAAGAGGATT CGTGCAATGA ATTCATGGAG ATATTTAGAT CTTTCACTGG AGAGAAAATA 60  
 AAAAGAAGAA AAGAGTAACC TTTAGATTGC TGGAThTGTG CAGTGGCTGC TTGCGTGCCT 120  
 TTAGGTGGCA TAAGGAGGCT ATACGCAGAC AACCACCGTC CCGGGGTTTT ATTGTACACT 180  
 10 GTGTAGGACG CAGACTTTAT GTGGTTG 207

## (2) INFORMATION FOR SEQ ID NO: 1714:

## (i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 84 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1714:

TGGTTATCGA CTGCTCGTAT ATTTTGACTG TTTTGACTGT TGTTCGTA GCAATACTAT 60  
 25 CTCCTAAGCC TTTCATTGGC ATTG 84

## (2) INFORMATION FOR SEQ ID NO: 1715:

## (i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 54 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1715:

35 GTTTGAATTG ACTGACTTCG TTTTACCGCG TGTTTAATAT TGTTATACAT ATAT 54

## (2) INFORMATION FOR SEQ ID NO: 1716:

## (i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 77 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 45 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1716:

50 GAAGCCTGTC AGTGGATCAA ATTATTGAAG ATAAGTTGGG TGGCATTTTT GGAAAGTCCA 60  
 AATGCTGGGA ATGGTCA 77



## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1717:

GGGCCCTTTT TTTCCCAAAA AAAAAAACCC CCCCAACCCC AATTTTGGnC CCCCTTCCCC 60  
TTTAAAAATT TAAAAATTGG GCCAAAAGGC CCCCCCAAAA AAAACCCCCA ATTGGAATTG 120  
GAAAACCATT GGAACCAATT CCATTGAACC AGGA 154

## (2) INFORMATION FOR SEQ ID NO: 1718:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1718:

ATTGTCTACA CTGCCACTTT ATTTTCATTA ACCATTTTCAC AAATGTGTTC ATCATTCAAC 60  
ATGAACATCA ATTGTTCAAT TACATCGACA CCTGATGCCT AAnCACGCAC CTTTTCACA 120

## (2) INFORMATION FOR SEQ ID NO: 1719:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1719:

TTCATTTGTT TGTAAGAGTG GCATTTCTAT GTCTTAAAG TGACGAACT TCAC 54

## (2) INFORMATION FOR SEQ ID NO: 1720:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1720:

## (2) INFORMATION FOR SEQ ID NO: 1721:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1721:

TTTGGATTAT AAATTGACAT GTAAGTACGA GGCAGCTGTA CCGATATAT AATTGCTAAG 60  
 AGTTAGGGCT G 71

## (2) INFORMATION FOR SEQ ID NO: 1722:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1722:

TTTTATCTTT ATTACTAAAA CCAACTGCAC CAAAGTTTGC AGTCATTACC ACACGTTTAA 60  
 CACCCGCATG TTCTGCAGCT CTTAAAATAC GTTGTATACC TTCAATTGCA GGCTTCGCCA 120  
 TCACTTCTGC ATCGTCTGTT TTACCGAAAA ACACCGGAGA TGCTACACTC AAGACATACT 180  
 TGCAATCTTT CATTGCTTCA TCCCAATGTh CATCTTGTGA TAAATCCGCT TCGACAAACA 240  
 TTAAATCGCT CTGTGGAAAT GCCCATGTCT TGCATTGTTT nAATTACTTT ATCAGCTTTA 300  
 CTTAAATCAA GnATCGTCGT TTGTA 325

## (2) INFORMATION FOR SEQ ID NO: 1723:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1723:

CAGTATTGCA GTCACGACAA TGTGATGACT AAATTATCCA AAGTATGAAT TCCATGCGGC 60  
 ATTAATCCTA G 71

## (2) INFORMATION FOR SEQ ID NO: 1724:

(A) LENGTH: 53 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1724:

10 TTGCAACGAT ATTAGGCTAT CTAGTCGGCA TATTTGTAAA ACAAGATCCA ATT 53

(2) INFORMATION FOR SEQ ID NO: 1725:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 71 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1725:

ATCTATTCAT CTTCTACAC GGACAGGAAA TGAGTCCAGT AGATGCACAT TGGGAATTAA 60

25

TCGAAGCTAG C 71

(2) INFORMATION FOR SEQ ID NO: 1726:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 71 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1726:

CATCTTGCAG GTCTACATTA TAAAATGTGA AGTTTTCTAC GATAACAATT GGGAAACTCA 60

40

GGGGCATCTC C 71

(2) INFORMATION FOR SEQ ID NO: 1727:

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 235 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1727:

TTCnTTTTTA AAAATTC CCC ATTCTTTTT AAATTTCTTT CCCGCTGGAT TAAATGGATT 60

55

TAAAAAATTC CACCCCAACT TAAATTAAA TGGCTTGTGG AAAATTAACG GGATTGGCAT 120

TCCAGCTTAA ATGGTTTTTT TGGAGGCTTC CACGTAAAAA ATGGCGGGTG GCTTT

235

(2) INFORMATION FOR SEQ ID NO: 1728:

5

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 61 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1728:

15

TAGAGTGGCT ATAAAGCTAA GTTCAATTGA CCAATTACA ACAGGTATT GAGGACAATA

60

A

61

(2) INFORMATION FOR SEQ ID NO: 1729:

20

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 54 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1729:

30

ATCACCAAGA AGTTCTAATG CTTGGTATAA ACGTTGAATA CGACGTCGG TATT

54

(2) INFORMATION FOR SEQ ID NO: 1730:

35

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 59 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1730:

CGTCCCGAAG CGTTGGAGGC GGGAAACATCC AGAGTAATTG GCACAGATTA TGACCATAT

59

(2) INFORMATION FOR SEQ ID NO: 1731:

45

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 60 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1731:

55

## (2) INFORMATION FOR SEQ ID NO: 1732:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1732:

TATGTGGTGT TCAATGCACT GGTCAATTATG GTGCATCTTA CCAGATTCCG CATTCTTATT 60  
ATAACTATAC TTGTAATAAA TGGCGACATG CAGACACGnC AATAC 105

## (2) INFORMATION FOR SEQ ID NO: 1733:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1733:

TTTACGTTCC ATAGCAAAGT GATACAAACG TCAGCATCAA TGTAAGGCAT AGATCATAGT 60

## (2) INFORMATION FOR SEQ ID NO: 1734:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1734:

TTCCATCATA CATTGCGGTT TTACTTTTCT TCTGGTATGA TCAAATATTC ACATAA 56

## (2) INFORMATION FOR SEQ ID NO: 1735:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1735:

AAATGGGGAT GAAACAGTTA GTGTACAGGT GAAAGCTTAA CAGCAGCTAC AATTGCA 57

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 61 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1736:

GATTTGCAAT TAAACTTAAA TGTAATTTTT CGGAATGTGT ATTGGTTTA CTAAAGTAA 60  
 A 61

(2) INFORMATION FOR SEQ ID NO: 1737:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 57 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1737:

AAAGAAGCTA AAGAAAAAGT TGATAAAACA GCAAAAGTGA TTATTAGCTA CAGCATT 57

(2) INFORMATION FOR SEQ ID NO: 1738:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 54 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1738:

CAATAATATC GCTAAAACCG CCATTTGTAC CAAATGAATT TGATAATGCT GCAG 54

(2) INFORMATION FOR SEQ ID NO: 1739:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 59 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1739:

TAGAGCCCAA CCGGCAACCC ATCCATGGAA ATTCACCAA ATAATACATT GACCCCAAG 59

(2) INFORMATION FOR SEQ ID NO: 1740:

(A) LENGTH: 136 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1740:

10 CCTTTTGGn AATTTAAGGG GGTTCCCAAC CAAATTCCCC CAAATTTTTT TGGGTAAAA 60  
AAACCCGGCC CAAAATTTA AGGAATTTG GAAAAGGTT TGGTCCCTT TTTTCCCAA 120  
GGCCCAAAT TTGGAA 136

15

(2) INFORMATION FOR SEQ ID NO: 1741:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1741:

25

CATTCAACCA ACGACTGACA ACAGAACATT TAAGACTCTA GGACATTGAT TGA 53

(2) INFORMATION FOR SEQ ID NO: 1742:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1742:

GCTCGTCTGA TTCAGTCACA AAATTGTCTT GTTATACTTG TCACCTATCA TC 52

40

(2) INFORMATION FOR SEQ ID NO: 1743:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1743:

50

TGTTATTTAA AGAGGCTCAA GCTTTCATAG AAAACATGTA TAGAGAGTGT CAT 53

(2) INFORMATION FOR SEQ ID NO: 1744:

55

- (A) LENGTH: 94 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1744:

10 TCTGAGTTAA AGACGTCTCA CTAAAGCTT TAGCAATTCC AACAATCAGA TATCTTCACA 60  
 CGTGTTATAT GTGTCCATTA ATATATCCTG TGGC 94

## (2) INFORMATION FOR SEQ ID NO: 1745:

15

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1745:

25 GGAAAAAann TTTTAAAAA AAGGGAAAAG GGAATTGGGG TTCCCGGCC CTTTTTAAAG 60  
 CCCCCAAATT AAGGAAATTT TAAATTTTGG GGAAGGGGAT TTTCCACCGG TTAATAAACC 120  
 GCCGATTTTG AGGGGGTTGA ATTAATTGGC CCAAATTTAA AAACCTGGAT GCTGGGTCCA 180  
 30 ATTTTTTACC GGGACCAATT GGTCTGTCAT GA 212

## (2) INFORMATION FOR SEQ ID NO: 1746:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1746:

TATCTTCCGA TGAAGAACAA GATGCACAAG AAGTACGCCA ATGATTTAAG AAAGTGGT 58

## (2) INFORMATION FOR SEQ ID NO: 1747:

45

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1747:

55



AAAATTAAGn CCTTTTITAA CCTTTCCTT CCCCAATTGG GGCCT

105

## (2) INFORMATION FOR SEQ ID NO: 1748:

5

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 52 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1748:

15

AGTGCCTATT ACTTTGATTG ATGTCCAAGT TTCCTATCAC ACAACTTAAT TT

52

## (2) INFORMATION FOR SEQ ID NO: 1749:

20

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 95 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1749:

AAAGCATCAT CCGAACTCCA ATGATTATAC TCCCTAGATA TTATTATGTG ATGCTTTGAG

60

30

CATTAAATTAG AGATGGGACG ATTCCATGAA AGATA

95

## (2) INFORMATION FOR SEQ ID NO: 1750:

35

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 63 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1750:

TTGACACATC TACTCACATT AAAAGTAGAT GAAGCGTTGA GATTAACATT TCCACATTTA

60

45

CAA

63

## (2) INFORMATION FOR SEQ ID NO: 1751:

50

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 116 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

55

TCGATATTTG AGACACGCTG CTGTAATAAA ACATCCTATA AAGTATATAC CAAGATCTAC 60  
CAATATAAAC AGCGGCTATA TGATATAAAT GCTCAGACAC ACCCnCTGCG ATCCAT 116

(2) INFORMATION FOR SEQ ID NO: 1752:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 114 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1752:

TATGATTAAAG CTTAGTGCAG ATTTGATTTA TThAACAAACG CTTCACTACA TTAAAAATAG 60  
GGCACTCGCA CATATAGTTG TATCAATAGC CTTTATCAAT TTTTGGGAA GGT 114

(2) INFORMATION FOR SEQ ID NO: 1753:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 52 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1753:

AACTTCAAAT GTGCCAAGTG TTGAATCACA TCAAATCAT TTTTATTTAA CG 52

(2) INFORMATION FOR SEQ ID NO: 1754:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 75 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1754:

ACTAATCCCT TCGTGTTTC CAATCAATTG CATTATTAGT GGCCATTGT TTGATATAAC 60  
TGACAAGCTT TAACC 75

(2) INFORMATION FOR SEQ ID NO: 1755:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 53 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1755:

GTGAACAAGG GTAGATGTAA ATAGTTGATG CATGTGTACA CATCATAACA AAA

53

## (2) INFORMATION FOR SEQ ID NO: 1756:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 66 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1756:

TTATTTGGGC AGGCAAATAC CCTTAATATA TTCAAATCAT GTTAATATCA TTGCTATTGC

60

TAAACC

66

## (2) INFORMATION FOR SEQ ID NO: 1757:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1757:

ATTAATCGGA GCACTTGGGT TCGCAATTTA TGCTGAAATG GATCATTCTA CATCATC

57

## (2) INFORMATION FOR SEQ ID NO: 1758:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 399 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1758:

CGAACAATAA CTCTAAGTAT CCAACAAATG CTGCAAGTGT ACCTACTGTG ATTGATCCAG

60

AAATAGCAAG ATATGCACCA ACACCGATGA CAATAATTGG TCCAATATCT GTAAGTGTAT

120

TAATTGCGGC AAAGGAATag GCATTCCATC TTGTATGTTT CAACGCACGT GTTAGGAAAT

180

TAGTATTCTT TTTATCAAAG TTTTTCGCTT CATTGTCTTC AATCGCAAAA CTTTTAACGA

240

CTGAAATACC TTGAACACGT TCATGCAAGA ATCCTTGAAC CTCAGCTAAT GCTTGAGATC

300

TTTCaNGTGT CAATTTTCTT AATCTTCCAA AGAAAACGTA CACCGTTAAA ATGTAAAATG

360

## (2) INFORMATION FOR SEQ ID NO: 1759:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1759:

DATTATGTCA TGCTAGGTCA CTTGCATCAT CCATTTAGTA TAGAAGACGA CAAAATTAAA 60  
 TTATAGTGGG CTCCTTGATT GGCAGTATTC ATTTTCGGGA AGCGGGGTCC AGGCTTAAAG 120  
 GGTATTAGAC GTGGTTACC 139

## (2) INFORMATION FOR SEQ ID NO: 1760:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1760:

TCGCCCCCTCC AGGCTATTAT TTCATCTATA TCATTGTCAT CAGTTAAATT CAGCCTCGAC 60  
 ATTTCCATTT CAATAGACTG TTCATTCAAT TCTAAGTCAT TATTGTAAGT TTCTAGTTGA 120  
 TTTTCATAAT GATTTAGATT ATTTTGCTCA ATTAACTTTC TTTGAGACAA TTGCATTAAC 180  
 TTATCTTCAA TCTCCTTTGA GAGTTCTTGA TGCTGATTCA CATCTTGAAC ATACTTCTTA 240  
 TAATCCACCT CAAAATTAGT GATATTANTA TATnTCGAGA GTGTTTCAAA TTCAGTGATG 300  
 AGATCTCGAC ATAAT 315

## (2) INFORMATION FOR SEQ ID NO: 1761:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1761:

TAAATCCTCG AGATTCTTAA TAGGGTAGAT ATCTAACGTT TTCGCAAAGC TCTTTTTGAT 60  
 TTGTTCTTCT TTTGAATCTC CAATGATCTT ATTATCACCA TCACAAGATG TAACAAAGAT 120

CCATCCTCAT CATTTCATCAT CTTCATCTAC CTTCGCGGCT GGAAATTCAA aGaaTCTATT 240  
 ACTGACAAAT CGCTTTTTCC ACCTTTTGAA AAGTCAATTT CCAACTTTTT ATAACCCACA 300  
 5 GAACTTCCTT TCAAATTACC ATCAATATGC ATTTTAAATA CCGGTGCTTT ATCAGTAGGA 360  
 ATATTATAAC GACTTCTTAA TTGCTTAACA TTTTCATCT 399

(2) INFORMATION FOR SEQ ID NO: 1762:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 224 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1762:

20 GTATAGAAGA CGACAAATT AAATATAGTG GCTCCTTATT GCAGTATTCA TTTTCGGAAG 60  
 CGGGTCAAGC TAAAGGGTAT AGACGTGTAC AATTAATGAT GGCATTATTA ACGATGTATT 120  
 TATTCCTCTT AAGCCACTTA GACAATTGGn AATTATCTCA GCGGAATATA ATGATGTTAT 180  
 25 TAATGAAAAA GTTCATGTGA AAAATAAAGA TAATTATnTA CATT 224

(2) INFORMATION FOR SEQ ID NO: 1763:

- (i) SEQUENCE CHARACTERISTICS:  
 30 (A) LENGTH: 54 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1763:

AGCAACCAAC GCCAGATAAA GCAGAAGATA ACGCATTTC CCCCATCACC ATAT 54

40 (2) INFORMATION FOR SEQ ID NO: 1764:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 59 base pairs  
 (B) TYPE: nucleic acid  
 45 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1764:

50 ATTCCTTAT CGCATTCTGT AAAATGATCT TCATCAGAAA TTGCTTCGAT ACGTTTATG 59

(2) INFORMATION FOR SEQ ID NO: 1765:

(A) LENGTH: 54 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1765:

10 GATTCAATTC ATCTGTATAG ACGATATATC CTGATATGAA TTGGAAATGG AATA 54

(2) INFORMATION FOR SEQ ID NO: 1766:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 85 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1766:

ATCGCATAGA AGCATTAGAC TCAAATATT TTCGGTTATG AGAATAACTC TGACATCCAT 60

25

ATGGATACTT AGTTTCCAAG TTAGA 85

(2) INFORMATION FOR SEQ ID NO: 1767:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 54 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1767:

CAGTACTGCT GAATGATGCT ATTGATTTTC TCATGAGACA TGGCGATAAC ATCG 54

(2) INFORMATION FOR SEQ ID NO: 1768:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 116 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1768:

50 GnCACTACTA ATCGTATCAG GATCACTAAT TAAGGCATCC AGCATCAGAT ACGAGCGCAC 60

GTCAGACTAA TCTACTGTCA TGATAAAGCA GCTGCTAACC TTGTAAGTTC GTGAAA 116

(2) INFORMATION FOR SEQ ID NO: 1769:

55

- (A) LENGTH: 82 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1769:

10 GTTCTATCCA ATATGGAAAT GAGGACATTA TGCCTGAAAG CTATGGACGA TGGACGATGG 60  
 TACACGCATG TTGTGTAAGC AG 82

(2) INFORMATION FOR SEQ ID NO: 1770:

15

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 152 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1770:

25 TATCTGTATT GTAGTAATCC GCTTCTCCCA TCTATATAGG GATCTTTCGT AGATATTCAC 60  
 TTTATGCCTA GGATCCAAGA TGTGTAAGCA GCACTTTGCA TTATCTAATG CAAAGGGnAC 120  
 ATGCGGCTGT AAGCCCTGTT CTGATAATCA TA 152

30 (2) INFORMATION FOR SEQ ID NO: 1771:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 51 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1771:

40 TGGAGGCGAA GTAAATGAAA AGTATTACGT TTGAAGAACA TTATGTCATT G 51

(2) INFORMATION FOR SEQ ID NO: 1772:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 232 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1772:

50 nGAAACAAAT ATCTGATGAG ATATGCAATG ATGACTATAA GTAACATTAA AATGAAGCCC 60

55

CGTACACCAA TTATATCTTT GTGGnTGTTA TATTAAATCT ATATTATGTT CATTTAACAG 180  
 CATATGTTAA AAATTGACAG TTAACACATG TAGCTATTTG ATGTGAATGT GC 232

(2) INFORMATION FOR SEQ ID NO: 1773:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1773:

TAATGTCCCC CAGAATGTAG GCAAATGCAG AACCTGGTTT TAGGGTCAAC TGTTTnTTCT 60  
 CCAAGCAGAA ACAAAGTTCT TGTGTCAGTG CACTTTTGGT CCACCATT 108

(2) INFORMATION FOR SEQ ID NO: 1774:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1774:

CGCAATTGAA GGATACACTA TTTTAAGAGC TGCAAACATG CGGGTGTAACT GTGTGGTATA 60  
 CTGCAACTTT GGTnATTGGT TTAGTATAAG ATAAAATCAT CACAATGAAT C 111

(2) INFORMATION FOR SEQ ID NO: 1775:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1775:

CAGGTTATCA GCTAATAGAT ATGTTGAAGA GGCAGTTGCA GGCCAAATGA AACTGCAGAT 60  
 GTAGTTCAGT ACC 73

(2) INFORMATION FOR SEQ ID NO: 1776:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1776:

5 TAGACACAGT GCAAAATCTG GTACAGCTTA TGAATTAGA CGGGTAAAGC AAATTACTGA 60  
GTACCCA 67

(2) INFORMATION FOR SEQ ID NO: 1777:

10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 127 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1777:

GTATGCCAGT GTCATTGCTG AAAACATCAA CCATTCCCTG CACCAAAATT TTTTGGTAGA 60  
20 GTTTGATGCT GGCCATCCTC CAAGGGACTA AGGGTAATTT TGTtTAAAAA GAGCCAAAGG 120  
CCCAATG 127

(2) INFORMATION FOR SEQ ID NO: 1778:

25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 236 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1778:

35 GAACCCAAAA ATTAGCAACA GTGGCTACAA TAGTTGGGCA CTGAAAGCCA GCCAAGTGGG 60  
ATTTTtagCC CTTGATTtGA AAGCGGGGTC CCCAGGATTA AAAAATTtTAA ATTAGCCTAA 120  
TAAGCCCAAA ATTCCCATTt GGAAAAGGAA ACCTCCTTAA ATTGGGTTGG AAAAAAGnTT 180  
40 AAAAAAAAAA AGGCCcAGnC CTTGGAATTT TTTGGAATTG GAAAAGGAA TTAAAA 236

(2) INFORMATION FOR SEQ ID NO: 1779:

45 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1779:

## (2) INFORMATION FOR SEQ ID NO: 1780:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1780:

GACGACTCGC TTCTATTTTA AAATCCGGCG TACTTgGTTA TATAAATATC ATAATGGTTA 60  
 AAATTAAAAA GCAATGTCAG TTCACACTAT TACTGACATT CTTTtagTTA TGTGTATATT 120  
 ATTCATTCAC AAGCTTTTGG TCTATAAATC GAGTGATTG CTTTGTTTGT ATATAACCAT 180  
 CTGCTACATA TTCATCGTTC ATTGTAATTA ATGGATAAAA TAGTTCATCn n 231

## (2) INFORMATION FOR SEQ ID NO: 1781:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1781:

GTCTCCCTGC CCCACATTTA ACATTGTAAT TTTGTGATGT GAATTTGTTG GAAACGTTAT 60  
 TAATAATGTC AGAATAATTA TAGTCCAAAA CGTAACCAAT ATATATTTAC GTTTAGCCAA 120  
 TAACCAAAAT ATGTAATAAA CAGAAATTAT AAATACTATA AATATCCAAT CATTAAACTT 180  
 GGGAACAGAA AAATGTGATT GCTTGATT 209

## (2) INFORMATION FOR SEQ ID NO: 1782:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1782:

GTTAAACTTA GTTAGATAAA ATGCAAAATCA CATTATTGTA GATAGTCTCT TTTC 54

## (2) INFORMATION FOR SEQ ID NO: 1783:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1783:

TCTGGAATGT CTCCTTGCT CTCTATATAG CTATAGTCCG TCGCAAGCGG ACGTAATGTT 60

10 CATTTCATA ATGATTATAG TATGAAAGCG CTTTCTTGTA TATGTGACAT GTGCGTGtng 120

(2) INFORMATION FOR SEQ ID NO: 1784:

(i) SEQUENCE CHARACTERISTICS:  
15 (A) LENGTH: 57 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1784:

CTACCATTTA CATAAGACC GTCTAATTCT TCAGTTTCAA TGGCATTITG GAGCAAT 57

(2) INFORMATION FOR SEQ ID NO: 1785:

25

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 54 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
30 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1785:

35 TCATAACCAT TACCAAGTAT CCAAGCAGCT TTAAACAAT ATGGCATAAA CATT 54

(2) INFORMATION FOR SEQ ID NO: 1786:

(i) SEQUENCE CHARACTERISTICS:  
40 (A) LENGTH: 84 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1786:

GGATGGGTGA TTTTAGCAGG TTTGGCTATG AGTACCGTAT TTGCATTAGG ACCGATTTCa 60

TTTAACAAAA TCATAATTTT GGGC 84

50

(2) INFORMATION FOR SEQ ID NO: 1787:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 134 base pairs

55

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1787:

CCGGTTTACC CTAAAAATTA TTTTGGGG GGTTCATTA AACCTTCAA TTCCAATTA 60  
10 ACCCCnACCC CCCTGGGTTT TCCTTAAAA CCAAAGGCC CTTTTCCTC CCAACCCAAC 120  
CTGGGGGAA TTGG 134

(2) INFORMATION FOR SEQ ID NO: 1788:

15

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 70 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1788:

TATATCAACT AAAAAGCGCA TCTGCAACCG ACGGTTGAAA ATTTGGACAG GAGACAGATA 60  
25 ATGTAATATA 70

(2) INFORMATION FOR SEQ ID NO: 1789:

30

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1789:

AATATCCAAT TATACAAGCA GGTATGGCAG GAAGTACGAC ACCGAAATTA 50

40

(2) INFORMATION FOR SEQ ID NO: 1790:

45

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1790:

50

TGATTTACTA GCTGAATCCG ACATGCTTGA TGATACACTA TGTGAATTCA 50

(2) INFORMATION FOR SEQ ID NO: 1791:

55

- (A) LENGTH: 58 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1791:

10 CCGGACGCTT TACTTCCAAC TTTAGGTGGT CAACACAGGT TTAAACATGG CGATGTCA

58

(2) INFORMATION FOR SEQ ID NO: 1792:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 58 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1792:

CATCATCCTC TAATTTAGTC CAAACTCCTG GATGATATCC AAATGAAGTT CCAATTGA

58

(2) INFORMATION FOR SEQ ID NO: 1793:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1793:

35 CACAAGTTTT AGAAGGAAAC CAATAACAAA TGACGAGATT AATTGCCACA AACATTAACG

60

AC

62

(2) INFORMATION FOR SEQ ID NO: 1794:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1794:

50 AAGGCCCGGG GGGTTTAAAA AAAAAGGTTT AAAAAAGGnT TTGGCCCTTT AAACCCAAAG

60

GGAAATTTTA ACCCCAAAAA AAAAAACCC CTTTGGGAAA GGG

103

(2) INFORMATION FOR SEQ ID NO: 1795:

55

- (A) LENGTH: 121 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1795:

10 TATCGATCGA TCATGTCGAA TCGATCTGTC GATCGATCGT ATCGATCGAA TCGCGTCGAA 60  
 TCGAATnCGT CGAATCGATG CTATCGATCG AATGCTATCT GAGTCGAATC ACGTCGATCT 120  
 G 121

## 15 (2) INFORMATION FOR SEQ ID NO: 1796:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

## 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1796:

AATTCATGTT AAAATCCTCC TGATATTAGA TGGCCCATTT TTATTTTTTTT CGTTTCCATA 60  
 TA 62

## 30 (2) INFORMATION FOR SEQ ID NO: 1797:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 397 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1797:

40 CATACTCGAC AATTTAGATG GTGAaTACTT ATCATTTAAG TCCTTTGaCA CCTCATCTAA 60  
 AATTCTAGGA CTTTTAACAA TTTCTTTATA CGTATTTACA AGTTGAATAT TACTTTGAAC 120  
 CTCTTGCGCC ATAAACTGAG GATTGTCACC CTTAGTTTGA TTCACTAAAA TTTGAGTATT 180  
 45 AGCTTGATAT TTAGGTGATA AGACGAAAAA TGTAACAATA GCGCTAATAA TTAAAAATAA 240  
 TAGCGGTAAA ATAATTAAAA TCTTCAAGTT TTTTGTGAAT ACTTCITTAA TTTTGTAA 300  
 TTCTAATGTA CTTTCCATTA TTTACCTCCC TTAAAAATTT TCATTAAAAT TGGTATTATA 360  
 50 TATATAGTAT TTACATATTA CATATCGTTT AAACAAT 397

## (2) INFORMATION FOR SEQ ID NO: 1798:

55

- (A) LENGTH: 66 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1798:

10 CGGGTAACAG CGAATGGTGT GTCACCGTAT ATAACCTTAC TATTTAATAT TTGGCCTGTT 60  
GCTTTC 66

(2) INFORMATION FOR SEQ ID NO: 1799:

15

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 77 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1799:

25 GTTGCTAAGT TTGTATTACA ATTTAAATGA TTTTTCAGCTT GAGTAAGTTT ATTTAAAGAT 60  
GCAGTAATTT CGCTAGG 77

(2) INFORMATION FOR SEQ ID NO: 1800:

30

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 172 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1800:

40 TAATGCTATT TAATTTTCTA CTTCTAAGC TTCCACCCAT AACGAGTAAn ACTTTTTTAT 60  
TTTCATTAAA GCCTGTTAAT TGATAACCAT TATGTGCATT ACCATTTTTT AAATCTTCTC 120  
GAATTGTTGC TCCAATAAAA TCAGCTTTCT CTTTAGGTAA GTAGTTTAGC GT 172

45

(2) INFORMATION FOR SEQ ID NO: 1801:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 140 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1801:

55

AGTAAATTT GTCATCACGA TCAGCAAAAG CTTTGTGATC TGACGTATCT TCCATAAATG 120  
ATCTAAAAAT TGGTAGTTCG 140

(2) INFORMATION FOR SEQ ID NO: 1802:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 60 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1802:

ATCCCCCGTA CAGACTTCAG CTTACGTAAA CATGCTGAAC ACTCTAGTGA AGATTTCAAA 60

(2) INFORMATION FOR SEQ ID NO: 1803:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 60 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1803:

CAATTTAAAT GCATCTTTCC CATTAATTTT ATTGTGTGTC GCTTTAGCTG TGTTAATTAA 60

(2) INFORMATION FOR SEQ ID NO: 1804:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1804:

ACTTGATCGA AAAGGTTTCA TACCGGTAAA CGATAAGTT GAAACAAATG 50

(2) INFORMATION FOR SEQ ID NO: 1805:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 53 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1805:



## (2) INFORMATION FOR SEQ ID NO: 1806:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 70 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1806:

AAGAACTGTC TATGAATATT GGATGACGCT TTGATGAGAA CATTAGTAAG CCATTTGTTC 60  
 AAGGAGTACA 70

## (2) INFORMATION FOR SEQ ID NO: 1807:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 77 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1807:

TAGCATTCTTCT AATGGAATCC AATCTTACCG AATGACAATT GGAATATAAC TGGTGATAAT 60  
 GTTGAATGGT CCTGTGA 77

## (2) INFORMATION FOR SEQ ID NO: 1808:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 121 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1808:

CCCGGCCCAA AACCCCTTTT TTGGGTAAAA AATTTTTTTT AAAAAGGGAA AAATTTCCCC 60  
 TTTTTTGGTT CCCAAATTTT AAATTAGAAA GGGCCCCCCC TTCCCCCACA AATnTTTCCC 120  
 A 121

## (2) INFORMATION FOR SEQ ID NO: 1809:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 60 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1809:

AAGTTTGGTG AAGGAACCAC GTGCATGATG GTGTTCAAAC AATGCGTTAC GATGTTGACG 60

(2) INFORMATION FOR SEQ ID NO: 1810:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1810:

TGTTGAGAA AACACAGCGT TAAAGTTGAG GTATTTCAAA AGACAAGTTG GAACATTA 58

(2) INFORMATION FOR SEQ ID NO: 1811:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1811:

CTTAAATAGC AAGTGGTTTT ATAACAAC TT TGAGTTATCT CAATATAGTT ATCGC 55

(2) INFORMATION FOR SEQ ID NO: 1812:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1812:

TAAGTCTTCA ATTTTTTCAG TTGATACACC TAAGTGATAC AGCCATTCTT 50

(2) INFORMATION FOR SEQ ID NO: 1813:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1813:

## (2) INFORMATION FOR SEQ ID NO: 1814:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1002 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1814:

TGGTCATGCG	GGAAATACTA	GGACATGAAA	ATTATGCTAA	AGGCATCAAA	GTAAGTGAAG	60
ATAATGGCGT	AGTGGATATA	GATATGTACA	TTATTGTAAG	TTACGGTGTG	AAAATATCTG	120
AAGTTGCCAA	TAATGTACAA	TCAACAGTGA	AATATACTTT	GGAAAAATCA	CTTAATGTAT	180
CAGTAAATTC	AATCAATATA	TATGTACAAG	GTGTACGTGT	GAATAATACA	GGCAAGAAAG	240
CTTAGGAGGA	CAACTTGAAA	TGATTAGCAA	AATTAATGGT	AAATTATTTG	CCGATATGAT	300
TATACAAGGG	GCACAAAATT	TATCTAACAA	TGCAGATTTG	GTAAGTCTT	TGAATGtGtA	360
TCCAGTGCCA	GATGGtGATA	CAGGAACAAA	TATGAATCTT	ACTATGACTT	CAGGTGCGGA	420
AGAAGTAGAG	AATAATTTGT	CGAAAAATAT	CGGCGAATTA	GGTAAACAT	TCTCGAAAGG	480
TTTACTAATG	GGTGCAAGAG	GTAACnCTGG	TGTCATCTTG	ncACAATTAT	TCAGAGGATT	540
TTGTAAAAAT	ATTGAAAGTG	AATCTGAAAT	TAATTCAAAA	TTGTTAGCTG	AAAGTTTnCA	600
AGCTGGTGT	GAAACGGCAT	ATAAAGCTGT	TATGAAACCA	GTTGAAGGTA	CAATACTTAC	660
AGTTGCAAAA	GATGCTGCGC	AAGCTGCAAT	AGAAAAAGCA	AATAATACTG	AAGATTGTAT	720
AGAATTAATG	GAGTACATTA	TTGTAAAAGC	CAATGAATCA	CTTGAAAACA	CACCAAACCT	780
ATTAGCTGTA	CTTAAAGAAG	TTGGTGTGTG	TGATAGTGGC	GGTAAAGGTT	TGTTATGCGT	840
TTACGAAGGA	TTCTTANAAG	CGCTTAAAGG	TGANAAGTT	GAAGCCAAAG	TTGCAAAGAT	900
AGATAAAGAT	GAATTTGTAC	ATGATGAACA	TGATTTCCAT	GGTGTAATTA	ATACTGAAGA	960
TATTAATTTA	TGGCTATnGT	ACTGAGATGA	TGGTTCGTTT	TG		1002

## (2) INFORMATION FOR SEQ ID NO: 1815:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1815:

5 GACAACGCTA TTATTTTTAG TTTTCAATT CTATTATGTC ATAATTATGT CACTCAAAAA 120  
 CTGTTTTCCA ACATTGATTT ATTGTTGGAA AATCTCGAAA ATCTAGTCTA TTTCTCCAAC 180  
 AATCGAAGAT TTATGCCCTT TTTTCTCCCT TTaATAAGT CATAATACGA GGCATACATG 240  
 CAACATTAC AATAAAATAT GTTCCTACAT CGTATTATAC GAATGCTCAC ACTTATAGTT 300  
 10 GTTTAGTAAA CCCAGATGTA TTGCTAACAT ACCCATnAnc nCTATATAGT T 351

## (2) INFORMATION FOR SEQ ID NO: 1816:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 62 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1816:

ATATCGTATC CCATGCGGGA AGGGCTTTAT TTATACTGTG CACGATGAAT GCGCACAACG 60  
 25 GG 62

## (2) INFORMATION FOR SEQ ID NO: 1817:

30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 70 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1817:

AAAGGGGGGA AATTTTTTTT TTTTGGGTTT GGGGGGAAAA TTTTTTTTGG GTTTGGGAAA 60  
 40 TTAAATTAA 70

## (2) INFORMATION FOR SEQ ID NO: 1818:

45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 51 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1818:

CAAGTTCGGA ATGCGAACGC GTCTTAATCT ATATACAAGT GATGCACTCC A 51

## (2) INFORMATION FOR SEQ ID NO: 1819:

55

- (A) LENGTH: 52 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1819:

10 TCGCCATACT ATCGACAGCT GCTAAAATTG CGCTCTTCTT GTGTCGCAAT CG 52

(2) INFORMATION FOR SEQ ID NO: 1820:

- (i) SEQUENCE CHARACTERISTICS:  
 15 (A) LENGTH: 58 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1820:

CAAATTGGGG AAATTACTAG AAATGAAGAT ATTTATAAAG ATGACTGGAC GTCAACTT 58

25 (2) INFORMATION FOR SEQ ID NO: 1821:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 58 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 30 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1821:

35 ACTGCTTCAG CACCTGTATT CATTGGGGAA AGCTTTATCG TTGACCGGCC AGTTTACA 58

(2) INFORMATION FOR SEQ ID NO: 1822:

- (i) SEQUENCE CHARACTERISTICS:  
 40 (A) LENGTH: 190 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1822:

ACCTGTTGCT CGTGTCAATA ATAGGTGACT ATAAATCTCT GTTCAATATA CTTTTCGTTT 60

50 TTCCAATCTT AAAGGTCGAT GTTCGTGAGT AATCTTATCT CTGGnCCAAT TTTAATGTCA 120

TGATATGTTT ATAGTATCAC CCCTTTGTTG TGTAATAATA ATCAGGTGGG TGGTTAGAAC 180

55 GGTGTGAATA 190

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1823:

AGCnTTAGCn TATGGTTT TAG ACACAACTGn TAAAGATGcA AAGTTCTTGT

50

(2) INFORMATION FOR SEQ ID NO: 1824:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 102 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1824:

AAAAATTGGA AAAAAGGGGC CCAAAGGTTA ACCCAAATTG GAAAnAAACC CAAATTTTTT

60

GGAAATTAAC CCAAAAATTG GCCCCCAATT GGAACCCAAA AT

102

(2) INFORMATION FOR SEQ ID NO: 1825:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 57 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1825:

ACGTACCAAT GTCATAATCA GTCATTTTAC CACTCTTAAT AATCTGCTTC CGGGCAA

57

(2) INFORMATION FOR SEQ ID NO: 1826:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 61 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1826:

ACCATCTTGT ACAAAGTGA TGTCATATGC ACCATCTTGT GTTTGAGCT GCATTTAATT

60

G

61

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 56 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

10

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1827:

ACCGTTTCGC CAAGCCGACC TAATTTCTCA GCAATATTTT TTTCTACGCC ACCAAT

56

- (2) INFORMATION FOR SEQ ID NO: 1828:

15

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 62 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1828:

25

ACTTATAGGG CGCACTTATT TTCGCTTCC ATAGCGAAAC TAGTGTCCT TATACGTATG

60

TG

62

- (2) INFORMATION FOR SEQ ID NO: 1829:

30

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 54 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1829:

40

GCTACACACG ATTTACCTTT CTTGTCACGT TTTGCGACCA TCATTGTGAT GATA

54

- (2) INFORMATION FOR SEQ ID NO: 1830:

45

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 67 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1830:

GTAATGACCA TCGCTGATTT ATGACATTGT TAGATCTCAT GTGCCATTTA GTCTGCTGAA

60

TCTTGGG

67

55

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1831:

ATAACTCTTC GACAACTCC TCAACAACT TCTGTGTTC CATCTTCTGG

50

(2) INFORMATION FOR SEQ ID NO: 1832:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 101 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1832:

AAACGThAGA ATATTTAATG GAGCCAAGAA TGGTTTACAG ACGGAGAAAT GGGATATGTT  
 GAAGCGAGGC GTACGCGGAA AGCGTACTAG GCTAGAACAC T

60

101

(2) INFORMATION FOR SEQ ID NO: 1833:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1833:

TCGTCATCAT GTCTGTGTTA CCAACGTTTG ACGATTTANT TCATGCnGAA

50

(2) INFORMATION FOR SEQ ID NO: 1834:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 55 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1834:

ATAAGTTAAT TGATTTATTG ATAAAGAGAA GCCAGATTTA AATATTATTA AACGT

55

(2) INFORMATION FOR SEQ ID NO: 1835:



- (A) LENGTH: 58 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1835:

10 AAACAAGAAC CCCCATATGG TTAAGCTGCG CGTTTCAACA TACGGGGGGT TTTCATAT 58

(2) INFORMATION FOR SEQ ID NO: 1836:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 125 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1836:

TACGTTTTAT AAAACAAGA ACTAAAGTAT GCAGTGTGAA TTGTTCACTT TcTGGCGTT 60

25 GGAATTGATT AAAACGAGAT ATGGTGTGT GGAAGTTGTT TGTGTTGCA TATTTTAAAC 120

CGATT 125

(2) INFORMATION FOR SEQ ID NO: 1837:

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1837:

40 AATCTACAAT CCTGAATCAC TCGTTAAGAT TAAAAGTATC GACAATGAGT ATCTGAACAT 60

GAGCTCATCT GCCGTTTTTA ATGCnAAAAA CCGGCGGCGG GATATTTTTG ACCACGGC 118

(2) INFORMATION FOR SEQ ID NO: 1838:

45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1838:

55 ATTTGGGGTT TTGGGACCCT TACCCAAAAA TTGGGGTTTG GTTATTAAAA AAAAGCCATT 60

GTCCCAAGTTT TTGGGATTGC C

141

(2) INFORMATION FOR SEQ ID NO: 1839:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 54 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1839:

TCTGGGGACT AAGTATGTCT CAGGCTTTAT GCTGTTATGT TTGAAAATGA AAGG

54

(2) INFORMATION FOR SEQ ID NO: 1840:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 133 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1840:

ATTAAAAAAC CTTTTTAAAC CGGGAACCCA AGGAAAAATT CCGGGTTTTA ATTAAACCT

60

TTTGTTAATT GGTTCCAAAC CAACCTTTTG GGTTAATTTT AACCAGGAAT TTTGGAAAAC

120

nGTTTTATTT GGA

133

(2) INFORMATION FOR SEQ ID NO: 1841:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1841:

AAAGTATGGA TTGATCGTGG AGAAGTTCTT CCTACTAAGA ACACTAGTCG

50

(2) INFORMATION FOR SEQ ID NO: 1842:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 60 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

CGGTTTTCCT GGGATATGTT TGATGAATGG ATGTTGTAAC ATGTTAATAA ATCGTTGGTA

60

(2) INFORMATION FOR SEQ ID NO: 1843:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 60 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1843:

CTGAGATGAA TATTGTGTTT CGCCATACAT ACTGGGTAAT ATCCCAACCA TTGCTGTAAA

60

(2) INFORMATION FOR SEQ ID NO: 1844:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 125 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1844:

CATTACCTGT AAAAGGAAGC TAAAGACGAT GAGTATTTAT AGAAACCAAT TGCCGACCAT

60

TTGCAGCCAT TAGGAGGGTA GGAGGGCAAT CGCGnCCAAA GGTTATTAAC CGTCAATTAC

120

CTTGA

125

(2) INFORMATION FOR SEQ ID NO: 1845:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 126 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1845:

ATCCACCTGG GTTTGTTCTT AATTTAACCT GntAATTAAT TGGGTTGGGT CCGGCAAAAG

60

TCCGGACCTG CAAATCGGAT TTTATCGTTA AATCTTGAAT TCTATTGCCC ATATTAAATC

120

GCAAT

126

(2) INFORMATION FOR SEQ ID NO: 1846:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 57 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1846:

5 TTTTGGGAAT AAACCAATTA ATCATGGGCA AAAAATAAGC AATCCAAGTA CTTACTA 57

(2) INFORMATION FOR SEQ ID NO: 1847:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1847:

TGATAAATAT TTCATCTAAA GAGAGGGAGT CATTATGACA CTACTTACTG 50

(2) INFORMATION FOR SEQ ID NO: 1848:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 65 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1848:

30 ATCTAGGCAA TGAATGGACG GACTTAATAT TGATGTGCAA CAAGAAGAGG AGAAGCGAAT 60

CAATA 65

(2) INFORMATION FOR SEQ ID NO: 1849:

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 244 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1849:

45 CGTGTGAAGT CATTACTTTT AATCCCATGA TGATGGTGAT GGATGAGACG ATATCTCTCT 60

GTCTTTAACA GTTAAGTCCA ATTCTTCCAA CGAAACTTTT CCATAGGTTG TTTTATAAGT 120

TGGAATACTT GCACAAATCA TaCCTAATTG CTTATCAATT TTCTCAAGAC TGTCATCAGT 180

50 TATAAGATCA ATTTTATTAA TAATAATCAT GTCACCTAGT TTCAACTGAT CTTCCATCAG 240

GCGA 244

55

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1850:

TTTAAAGGTT CCCGGAAAGG TTTGAAACCA AACCTTTGCC CCGGCCCCCC GGGAAAAAAA 60  
AAAnTTGGTT TAACCCCGG GGGGGGGGC CCTTAAAAA ACCCAA 106

## (2) INFORMATION FOR SEQ ID NO: 1851:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1851:

TTTTTTAAGG CCCTTGGGGG GCCAATTTTC CCCCCCCCC AACCTTCCAA AGGTTGGGGG 60  
GCCTTTTTTT TTAAATTGGG GGGA 84

## (2) INFORMATION FOR SEQ ID NO: 1852:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1852:

TCATGATTAA AATTCAACAA TTACAACATC ACTTTGGATC ACATAAGAGT AA 52

## (2) INFORMATION FOR SEQ ID NO: 1853:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1853:

ATAAACATT TCAAGATGCG CTTGTAATTG TATGTGATAC TGCCAATGCT CCACGA 56

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 54 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1854:

AAAAGATCAT GCGCATAATG ACATGGTGAT GATATGAGTA TGATGGTGGG TACA

54

(2) INFORMATION FOR SEQ ID NO: 1855:

- 15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 52 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1855:

ACAACAAATG GTAATGCATA AACATACAGC CAATAGCTAC AATTGCACGA CG

52

25

(2) INFORMATION FOR SEQ ID NO: 1856:

- 30 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 57 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1856:

ACGGCTGCAC TCATCATGGT CTGTGGCGTG ATTGTTAATG TTTTAGTTGC CCGCTTC

57

(2) INFORMATION FOR SEQ ID NO: 1857:

- 40 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 192 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1857:

GCAGATAACT TCCTTGATCC TAACAAAGCA AGTTCTCTAT TATCTTCAGG GTTTTCACCA

60

50

GACTTCGCTA CAGTTATTAC TATGGATAGA AAAGCATCCA AACAACAAAC AAATATAGAT

120

GTAATAnACG AACGAGTTTCG TGATGACTAC CAATTGCACT GGACTTCAAC AAATTGGAAA

180

55

## (2) INFORMATION FOR SEQ ID NO: 1858:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1858:

CGCTGCACTT CCTGAACGCA GTGAGACCAG AACGTGGTGT CACTTTCGGT CTATTCGGT 60  
TAAGTGTTGG TCTCGGA 77

## (2) INFORMATION FOR SEQ ID NO: 1859:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1859:

TTTGCGTTC GTGATTTTCT CTAGACGTAG TAACTTTCCC ACTCTTTGCG TCC 53

## (2) INFORMATION FOR SEQ ID NO: 1860:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1860:

TTTCTCACTC GCGCATTTCA GTTTGTTTTG ATTTACCGGT CTCTTCTATT TGTCTTAAT 59

## (2) INFORMATION FOR SEQ ID NO: 1861:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1861:

AATGAATGTA TGCACATTAA CATCATCAAT TAATCCTTTT AATAAATTGA GTTGTAATTT 60

## (2) INFORMATION FOR SEQ ID NO: 1862:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 54 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1862:

ATTAACTAGT AGCAAATGTG CATAAGACAT CATGAATTAG CACCAATTTA CAGG 54

15

## (2) INFORMATION FOR SEQ ID NO: 1863:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 89 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1863:

25

TTTAACCATC ATTCTATGTC AAAGTTTGA AATGATGGTT ATTTTTTATT GCTTAAATTT 60

ATTATTGCTA CTACTATACC AATGAAAGT 89

30

## (2) INFORMATION FOR SEQ ID NO: 1864:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1864:

40

AAAGCTGGTA CGCCTGCAGG TACCGGTCGG GAATTCCTGG GTCGACCCAC GCGTCCGGAA 60

CCTAAATGTC ATCTGATGGT CTCAAGGGTC GTGTGTTTGA AGTGAGTCTT GCTGATTGTC 120

AGAATGATGA AGTTGCATTT AGAAAATTCA AGCTGATTAC TGAAGATGTT CAGGGTAAAA 180

45

ACTGCCTGTA CTAACCTCCA TGGCATGGAT CTTACCCGTG ACAAATGTG TTCCATGGTC 240

AAAAAATGGC AGACAATGAT TGAAGCTCAC GTTGATGTCA AGACTACCGA TGGTTACTTG 300

50

CTTCGTCTGT TCTGTGTTGG TTTTACTGAA AAAACGGCAA CAATCCAGAT ACGGGAGGAC 360

CTCTTTTGCT GCAGCACCAA CAGGTnCCGC CAAATCCGGA 400

## (2) INFORMATION FOR SEQ ID NO: 1865:

55



- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1865:

10 AAATGGCGTA TCTTTATGTA TCAACTAAGT AATCACCAAT TTCTTTCGGA T 51

(2) INFORMATION FOR SEQ ID NO: 1866:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1866:

GTGTTGCGGA TAATCCGTCG ACATTAGCGT CTGAAGGTAT CATGAGGCAA CTGCGCAA 58

(2) INFORMATION FOR SEQ ID NO: 1867:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1867:

35 ACAGCAACTG ACCCAGTTTA CTACCGTCAC TCAAATCACA CAGGTGGTAT CAAATCAATC 60

(2) INFORMATION FOR SEQ ID NO: 1868:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1868:

CAATCTCTTA CCATTTATCT CAGCTGGTGA AAACGGTCCA TTACACTTAG AATAAA 56

(2) INFORMATION FOR SEQ ID NO: 1869:

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1869:

5 GCTATAGACT AGAGGTACAG CAAATTCATG TGTACAGTGA TTAGAAGGCG ATGAGCAAAA 60  
GTAAT 65

(2) INFORMATION FOR SEQ ID NO: 1870:

10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 173 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1870:

20 GCTACTGGCG GGGGATAGTA ACACCCAATG TTACACGTAT ATACGTACGG CTTCTTGATA 60  
AAAAGATGAA GCCnTTACAA GTAGAGAGCG TAAGAACGTG ATCATCTAAA TGGTAAGGGT 120  
AGACTATCCC ATGCCATTGT GGGCGGTTGC ATAGGTACCA CGGCACATAG CGG 173

25 (2) INFORMATION FOR SEQ ID NO: 1871:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 104 base pairs  
(B) TYPE: nucleic acid  
30 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1871:

35 GCTGTGGGAT TGTCTTTGG CATGGGGTTA GGGAGAGCGT TTCTAAGGGG CGTTTGAAAG 60  
CCATTGATCC GTAAAAGGAC CATTGTTGGA AGCnGCCTTA AGAA 104

(2) INFORMATION FOR SEQ ID NO: 1872:

40 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 64 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1872:

50 CCATTATCTC AAGAGGTTCT AGTAAGGGGA TGGCATTGTC TTCTTATGAA TTTGACCAGA 60  
ATAA 64

55

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1873:

GACAACCTAT TGTTCCTTA CCATACTGTT GTCCGGTTTG ACAAACGGC GTTCCACAAT 60  
 CCATACATCG TGCACCTTGG ATAGAGGCAT CTTCTTTAGT AAATCGTTGT TGATATGCTT 120  
 TATGATGCTT CAAACGGTCT ACCAGTGATA ATTCACCTAA GTACTGTTTG TCATACTTCA 180  
 TAAATCCTTT AAATTCACCC ATCGTATCTC CCCCTTTCCT TAATACACAA CGGCTGGTTT 240  
 ATGTTTAGCA TCGATTGTTT TGA CTGTnCA TCGTAAATG CAGCTAACAT CGCTTCATCT 300  
 TCCATTGTCA TGTGAAGATT TTGTGGCAAA nGGAATTTTT TGCATCAATG AATnGGTGAA 360  
 CCTTTGGGGG TGACCTT 377

## (2) INFORMATION FOR SEQ ID NO: 1874:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1874:

ATTATCTGAA TACGCAGCAG TTGCAGCACT TGATGGATCA GCAGTATTTA AAAGAGGTTA 60  
 ACACATTACC CAATAGTG 78

## (2) INFORMATION FOR SEQ ID NO: 1875:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1875:

CTAAAAGAAG TTAAAGAGTG TGATGGTAGA ATTATATTAT TTATTGATGA AATgCCATAT 60  
 GCTTGTAGGT GsTGGTAAAA CAGATGGTGC CATGGATGCa GGCAACATGC TAAACCAAT 120  
 GTTAGCACGA GGAGAGTTAC ATTGTATTGG TGCAACAACT TTAAATGAAT ATCGAGAATA 180

TGTGAAGAT ACAATT

256

## (2) INFORMATION FOR SEQ ID NO: 1876:

5

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 286 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1876:

15

AGCGCGAAAT TGAGCAAGCG GAACATGCGA CTGATGAAGA AAAACAAGTT GCTTTAAATC 60

AATTAGCGAA TAATGAAAAA CGTGCATTAC AAAACATCGA TCAAGCAATA GCATAAATG 120

ATGTAACGT GTTGAACAA ATGGCATTGC TACTATAAAA GGTGTACAAC CTCATATTGT 180

20

AATTAAGCCT GAAGCACAAC AAGCAATAAA AGCAAGTGCA GAAATCAAG TAGAATCAAT 240

AAAAGATACA CCACATGCAA CAGTTGATGA ATTAGATGAA GCGAAT 286

25

## (2) INFORMATION FOR SEQ ID NO: 1877:

30

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 74 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1877:

35

ACTTCCAAAC ATGATAAAGA CAGACTACTT CACAGGTTTA AGGGAAGCAA CCACATTAGC 60

GGGATTACCC CTAT 74

40

## (2) INFORMATION FOR SEQ ID NO: 1878:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1878:

50

TTTCATTAAG TTCAAAAAAT CTCAATAACT TTAAGGATTG GTCCGCATAT TA 52

## (2) INFORMATION FOR SEQ ID NO: 1879:

55

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 60 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1879:

ATACCCCTGA GATTAATTAC TTGTCCTTTT TTTAGAACAA CATCTCCTGG CTTTGTTCG 60

10

(2) INFORMATION FOR SEQ ID NO: 1880:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1880:

20

AATATCATTATAATATCAT TGATGCAAGT CCTATTGTGC ACAACTGGGG TGATTGCCTT 60

(2) INFORMATION FOR SEQ ID NO: 1881:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 56 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1881:

ACAATGGCAC ATGGACTTAT GCCTGGGGTG TCCTGTTCGT CGCAGCATCA AAATGA 56

35

(2) INFORMATION FOR SEQ ID NO: 1882:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 121 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1882:

TGCAAAGCAT TGGCACATGG CCAGTCAGTT TTACAACGTC GTGACTGGGA AAACCCGAGA 60

NGCGACGTTG TAAAACGACG GCCAGTGCCA AGCTTGCGATG CCTGCAGTCG ACTCTAGAGG 120

50

A 121

(2) INFORMATION FOR SEQ ID NO: 1883:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 56 base pairs

55

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1883:

ACATTTAATG TATAACCACT TTCAACATTG CCGATTTAGT GGCAGCAGTT GCAGGA

56

10

(2) INFORMATION FOR SEQ ID NO: 1884:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 52 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1884:

20

TGCATCCATT TGATTGAATT TTATGTTTTG ACCAAAGCCG GTTGCAATGT AC

52

(2) INFORMATION FOR SEQ ID NO: 1885:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 51 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1885:

TGAAAAGTGG TGGAATGGTG TTAAAAGTTG GTGGGTAATT TTAGAGAAGA G

51

35

(2) INFORMATION FOR SEQ ID NO: 1886:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 95 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1886:

45

TACACGAACC ATACTCACCA GGTTCGTCG TCATGAGGCG ATATTTTTTG TCATTTTATA

60

TACATTTATC CAAATTCATC TTTTAAATGT TGAGT

95

50

(2) INFORMATION FOR SEQ ID NO: 1887:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 65 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1887:

GCTACCAAAG GCGTTTACC TATTGCTAGT CACTGCAAGT GGCTTAGCTA TGCAGATCAA 60  
 CTGGT 65

(2) INFORMATION FOR SEQ ID NO: 1888:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1888:

GTGGGACCAA CTGGCCGGTG ACGGTGGTAA AGGTGCTTCA GTCGTATTGA AGTGGGATGA 60

(2) INFORMATION FOR SEQ ID NO: 1889:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1889:

TGTTGGAGAA ACAGTTAACG AGGTTTAATG TTAAAAAGC AACGTATCAT GGGTATA 57

(2) INFORMATION FOR SEQ ID NO: 1890:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1890:

TGGGATCTGC TTGCAAATAC ACAAACCTT CTGGATTTTA TTACAATTGC AATATAATCA 60  
 AACA 64

(2) INFORMATION FOR SEQ ID NO: 1891:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1891:

GGCATCCACT CAGATAAAAT AAAGATGTCA AAAAGGCCAAA GATGGTGCTA AAAAAACAA

59

(2) INFORMATION FOR SEQ ID NO: 1892:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1892:

GGTATCTCAA CGATCCTTTA GGTAAATTCG GAAATTTCTA CACGTGAGTT AGCA

54

(2) INFORMATION FOR SEQ ID NO: 1893:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1893:

TTGTCTTGGC AATGGCAGAG CAACAGAAGT TTAAAGTGCT TGCTGATCAT AT

52

(2) INFORMATION FOR SEQ ID NO: 1894:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1894:

TAAACCTATA CCCTGTAAAA AGAAAAATCG TGGATCGAAA GAACATGTAT GTGGCATTTA

60

TGATTGATGC TCAAGCAGA

79

(2) INFORMATION FOR SEQ ID NO: 1895:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1895:

TTATAAAGGA GAGAAATCCT TAATTATGAA TAAAGCATCA TTTGATAAAA AAGTTAAAAA 60  
 5 GCAATTATGG TTTTGAACA AGAAGGAGAA ACAAGCATTG GATCAACGAT TGTCTTCTAT 120  
 ATCTGATGAT GACAGCGTTA ACTTAAATAA GCCTGTTACC TTTGCTAATG CTTACTTAAG 180  
 ACAAATGTA TTTCGAAATA AAGAAACAAA AAGTTATAGT ATGTTTGTTA CATTAGTAGT 240  
 10 GATGATGTTT GCTTATGTTG CTTTATTAGG TTTGTTTATA TTTGGGCTAA TTACAAGTCT 300  
 ATCTGGCGTA CAATTTTTTCG TTAGTCCTAA GGTAGATTTA TCTACnACTG TTGTTATTTT 360  
 15 AACAAThATT GGAGCGA 377

## (2) INFORMATION FOR SEQ ID NO: 1896:

## (i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 58 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1896:

TTAGGATCCG TCTTTGCCGC AGCGTGGGTG TTCCGCGAGC GCTTCTTAGA GGTTTTGC 58

## (2) INFORMATION FOR SEQ ID NO: 1897:

30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 445 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 35 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1897:

40 ATCGCTCAAA CCGAAATTGA AAATGCATCT ATTACTTCAT TAAGCCGTTT ACCAGACGTT 60  
 ATATTAGCAT TGAAAAGTGG AAAGGTTGAA GGTGCTGTAG TTGAAAACC TGTAGCAGAA 120  
 GCATATTTAA AACAAAATCC TAAATTAGGA ATTTCCAATG TGAAATTTAA TGAAGAAGAA 180  
 45 AAAGATACAG TGATAGCAGT GCCAAAAGAT TCACCAAAAT TATTGTCACA AATTAATAAA 240  
 ACGATTAAGG AGGTTAAAGA TAAAGGATTA ATCGATAAAT ATATGACTAA TGCTGCAAAT 300  
 GCGATGAATG ATGACAGTGG TTTTATTCTT AAGTATGGTA GTTTTTTCTT GAAAGGAATT 360  
 50 AAGATTACAA TATTAATTTT ACTTATCGGT GTTGCAATTAG GTTCTATTTT AGGTGCATTG 420  
 GTTGCGTTAA TGAAATTAAG TAAAA 445

55

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1898:

ACCTTTTCAA TGTTGCTTTG ATATAAATTC ACAAAGTTGA CTTTThAATT CTTCAATAGA 60  
TTCTCTACTG CGATAGCTGA ATTGCCATCT TTTCTACTAC T 101

## (2) INFORMATION FOR SEQ ID NO: 1899:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1899:

TGCCCTGGAT GCCTTTAACT TGATTCATGA CCTGTGGTTT TATTTCAATT TAGATGAGCT 60  
ACCTTCAAGA CCTTC 75

## (2) INFORMATION FOR SEQ ID NO: 1900:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1900:

AGCAATACGG AACTGATGAA CGGAATTGTA ATACGAGAAT ATGAAGCATC AACG 54

## (2) INFORMATION FOR SEQ ID NO: 1901:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1901:

AGTACCTGAG TATCGCAGAC CGGCTTCAGG TCGTAGAATT TCTATACGTG GAGCTAGAAG 60

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 51 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1902:

GTCTAACTAC AGCATGCCGG CTTATTGTTG CACTTCTCA ATATTTCAT A

51

(2) INFORMATION FOR SEQ ID NO: 1903:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1903:

GGATTnAAAC GTGCATTAAAC GCGTGTnTTA AATAGTTATG GTTTAAGTAG

50

(2) INFORMATION FOR SEQ ID NO: 1904:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 53 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1904:

ATCGTATTTA TTTCAGCGAG TAGCGGTAGC CTTCAATACA CAAAGATTTT ACC

53

(2) INFORMATION FOR SEQ ID NO: 1905:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1905:

ATAAGACGCT AGATCTGGTC AATTTATTTT CGATTTTTTC AACACTATTC

50

(2) INFORMATION FOR SEQ ID NO: 1906:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 51 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1906:

TTCATCTGAA TCGTCGGCTT TCGCGATTAC TTCTTCGTCA GGGTTGCTAT C

51

10

(2) INFORMATION FOR SEQ ID NO: 1907:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 55 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1907:

20

CAATTGCTAA TAATCCTTTT AAGTCATTAA TGATTGTATC TTCCGTAATG TTGAA

55

(2) INFORMATION FOR SEQ ID NO: 1908:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 53 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1908:

TTGCCAAACA GACATGACTT AAATTTCAAT ATCTTCTTTG ACTGCATCGA TAT

53

35

(2) INFORMATION FOR SEQ ID NO: 1909:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 94 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1909:

TGAATTTCTA TACAATTATG GGAAGGGTA TTGGTGAATT GGAATGGGCT CCTAAGTTTA

60

CAAGCCCCCA TCGATGGCC GTTAAAGTTT TTAA

94

50

(2) INFORMATION FOR SEQ ID NO: 1910:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 66 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1910:

5 AACATGATCG TGGGGGGATG TTATGTTTGT TCATATATTT AGGAAGTCGT TTGTAGTTAT 60  
TGTTTG 66

(2) INFORMATION FOR SEQ ID NO: 1911:

10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 55 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1911:

20 ATCTTCGCTC CACTTACTGC AATAAGGATT TCGGGAATC CTAAACCGTT TTTCA 55

(2) INFORMATION FOR SEQ ID NO: 1912:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 59 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
25

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1912:

AACAATCGTA ACGATACAAC GCAATCTTCG AAAAATAATG CAAGTGCAGA TTTCCGAAA 59

(2) INFORMATION FOR SEQ ID NO: 1913:

35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 51 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1913:

45 ACACCACACA CACACACACA ACACCCACA CAACACACAC AAACACACAA A 51

(2) INFORMATION FOR SEQ ID NO: 1914:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 111 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
50  
55

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1914:

TGTTACGACT TGGTCGACCT GGCAAGCGCT TCGCGCACGT TCTGCAGCnT CTCACCTTATT 60

GGTATCGCGA TCGGACGTTA AGAAATTTTCG GAGTTCTGGT CACCTTATGT T 111

## (2) INFORMATION FOR SEQ ID NO: 1915:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1915:

TGGTCCGCTC TCAATCGCAT CTTCAGGTTT TACTTGGCAA AAGAGCGCGG TGCTCA 56

## (2) INFORMATION FOR SEQ ID NO: 1916:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1916:

GCCGACAGTA AAATAAAGGT ACTTGATATA ACATATAACG GAAAGCAACA GTTACTGTCA 60

CA 62

## (2) INFORMATION FOR SEQ ID NO: 1917:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1917:

ATGATATTTA TTTGATTGAA GAGATGTTGC TTAAACAAGA AGACGTACAA TTGATANAAC 60

GTAAAGATTA TATTCAGCAC CCTAAAGAAA ATGTTACCG CAG 103

## (2) INFORMATION FOR SEQ ID NO: 1918:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1918:

5 CAGTGTAGCG TGTGTCATGC CGTTTTACCA CAATTGAAGA CTGAGCTCTA TCCCTGTGCC 60

## (2) INFORMATION FOR SEQ ID NO: 1919:

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 117 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1919:

15 TCAAATTAAC TTCCAACAAA AACAAATGCA AGGTGAAGAA ATTGCTGAAG AAGATTTACA 60

AAAAGCGCAA GAACAAGCGC AAGCAATTGA AAAAGATGAA AACATCTCTn CATTAA 117

## (2) INFORMATION FOR SEQ ID NO: 1920:

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1920:

30 TGCCTAATGA AACATTTAAA AATATTTTTTA AATATATCTA TCAACACATC GTTCTATTAA 60

TTGGGATTGT TAGTTTTCTC AAAGGATTTT TAGGATTTTT CATGGAAAAA AATGGAAGTA 120

35 ATTTATATTT TGTTCATTC CCGTTTTAG TAGTCGTTGG ATTCCTTTATT GTCTTTTTAT 180

TTATATGGTT TAGTTTTAAA ACAATACAAC TGCAGTGTTC TAACAATTCA AATTGGATAT 240

GGATATTCAC CTATTTAGCA ATCATTCTAC TAATTGTAGG ATTTTTCTAT GTATTCTTTA 300

40 TTCCACAATC ATTACTTGCC TTTGGACCAT ATATTCAGGT AAGCAATTGG GTATTTATTA 360

TATTTTCATT TATAGTTATG CCTATnGGAT TACGCATTGA 400

## (2) INFORMATION FOR SEQ ID NO: 1921:

## (i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 122 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear
- 50
- 55

TCACAGTCAT CATTThATTT TCGATTTTCA ATAATTGTAT TTTTAATTTA TCTTGATATT 60  
 CATTAGATT TATACAAGCT ATCTTTAACA TTGCCTTATC TTTGATATAT TTCTTGCATT 120  
 5 CG 122

## (2) INFORMATION FOR SEQ ID NO: 1922:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 410 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1922:

AGAAGATACC ATACACATTT aATTAGTTAC AGCATAAATC AATTTATACC CTTAATTATT 60  
 20 ACATTGTTTA TATTTTAAAT TCGGGGGAGT AATTTTAAGT AATATCTTGT TGCTGCTAAT 120  
 TCTATTGTTA ATAAATTGAT ATTAGATGTA GAAATTGAGT GTGAAAGTTA ATAATAGATG 180  
 ATTTAGCTAG TAACATAATT AATTCATATA TAGTCAAAAA GTTCTGTAG ATACTGTTCT 240  
 25 TGATGAATAT TCTTTGATGT TAGGTGTTAG CTATTCTAGA TGAGTTTCTT AGATGTGGAT 300  
 GCCTGTCTTG ATGAAGTTAT CTATGATGTT AATATAATAC TTGATGTTGA TTCTTAGATG 360  
 TTAGTGCGAT TTCAAGATGC TGATTCTTTG TTGTTGCACT ATCTTGGTGA 410

## (2) INFORMATION FOR SEQ ID NO: 1923:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 348 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1923:

TTTCTATGGT TTATCAGGTG ATTTTACGGA AAACAGTGAA GATTATGGCG TATACCGCTT 60  
 TAAACGTGGA TTTAATGTAC AAATCGAAGA ATTAATAGGG GATTTCTATA AACCAATTCA 120  
 45 TAAAGTGAAA TATTGGTTGT TCACAACATT GGATAAATTA CGTAAAAAAT TAAAGAAATA 180  
 GATGTAAATG ATGTTAGGGC TTATAGThAT TGATACTATA GGCTCTTTTT TATATGTTTT 240  
 TTAATAAAGC CTCGAATAAT GATATATTAA ATGACAAGTT TAACAAGTGA TTGCAATAAA 300  
 50 TATAAATnTG AATTGCACAA CCGATTThnA AATGATTGAG TTGAGGAA 348

## (2) INFORMATION FOR SEQ ID NO: 1924:



- (A) LENGTH: 253 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1924:

10 AGGGCAGATT TAAGCTAACT TGGAAATGTTT TCGAGTTTTT GAGTTAGTTC TCTATCCATT 60  
 TTTTCAGTTA CATGAGTATA TATGCGAATG GTTGTGTTGTT CATCTACATG TCCTACCCCTT 120  
 TTCATAATTG CTTTAAAGA AACATTCATT TCTACTAATA AAGTTATGTG TGTATGTCTA 180  
 15 AATGTGTGCG TGCTAACTTT CTTATTCATA TTAAAGCTT TTGTACGTTT TCTTAACGCA 240  
 CACCGGCCAT TTC 253

## (2) INFORMATION FOR SEQ ID NO: 1925:

20

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 52 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1925:

30 GGTATAGGTG CAAGTCCTAT CTTCCGCTCC ATGGTTTAAT GATAATGCGG GA 52

## (2) INFORMATION FOR SEQ ID NO: 1926:

35

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 84 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1926:

TGGTCACTGT TCCTGATGCT TACGTTAGAA TGTAAGATTC CCGATTTATC AGTTATATAC 60  
 TGTTTGCTTC ACTTTGGAGA TCTG 84

45

## (2) INFORMATION FOR SEQ ID NO: 1927:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 56 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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CTTCTAAAT AATTCTAGTA TAGTTTTTAT TCAAATACGC TAGGCTCAGA GCTATT

56

(2) INFORMATION FOR SEQ ID NO: 1928:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 138 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1928:

GCAAATTGTC ATTAGACGGA GTATTATTTA GAATTTTCGG TGATATCCAC CGGCACAAGA 60  
TCGATGTTGG ACAATATCTA ATATACTGAT ACGCATTTAA ATAGAAGAAG GGAATTAGAG 120  
TTTGGTTnTG AATGCAAA 138

(2) INFORMATION FOR SEQ ID NO: 1929:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 52 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1929:

ACATCTTTAT ATGCTTCAAC ATCAAATACA CCACATATTG GTAAACAACA AA 52

(2) INFORMATION FOR SEQ ID NO: 1930:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 51 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1930:

TTTAATGTTT ACAACACCGG AATAATAATA ACTAAAGCGC CGCTAATAAA T 51

(2) INFORMATION FOR SEQ ID NO: 1931:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

ACGAAAAATA AATAATCATT TCACCTTTAT AGCCAGTATT TTTAATTAAT ATATTTTCAT 60  
 CTATTAGCGC TTCTAAAAAT CTATTGACT TTTGAACATA CTCTTTAGCT ATATTATTAA 120  
 5 CAACAGTATA GGATTCCTCA TAATTTAGTT GATTAAATTC TGAGTCGTTT ATTAATTCAA 180  
 CTAATCCTTT TATTACTTTT TGTACAACAT TAATATTTTT ATCAAAATCA AATTTATCTT 240  
 CCTTAGATAA ATTAATAnnn AAAGTCTTAA GAACATTTGT AAATAGCTCT GCAACACTTA 300  
 10 TAGTTTGGnC AAATTCCTTA AATTTATTTA CACAGTACTC ACACATTAGT TTTAAAAATA 360  
 ATGGATTGTT GAATTCCTGA TTTAATATAG GTAACCTTAGG 400

(2) INFORMATION FOR SEQ ID NO: 1932:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 100 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1932:

25 ACTTGCGGAA nGACGCAACG TTTATGTACG TTGGAAGAAA AATTCAGGAC TTACGTTCAA 60  
 AACTACCATA GCAATATGCA TTGAAAGATG ACAGTATGCG 100

(2) INFORMATION FOR SEQ ID NO: 1933:

- 30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 61 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1933:

40 CGCTCTGCTT TAAGCGTTGG GACTTTGTCA ACGGTAGTGG ATGGGAAGTG GTTCTGCTTT 60  
 G 61

(2) INFORMATION FOR SEQ ID NO: 1934:

- 45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 53 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1934:

(2) INFORMATION FOR SEQ ID NO: 1935:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 56 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1935:

ATGTATTACG GTTTAATTAA GCCACATACC AACAAGATTG CATTTATGGT ATCTCA 56

(2) INFORMATION FOR SEQ ID NO: 1936:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 61 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1936:

TCGCACCAGA AACAAGGGAT TGTTAAATT GCGTAAATCC TTAAATTTAT TTGTAAATAT 60

A 61

(2) INFORMATION FOR SEQ ID NO: 1937:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 51 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1937:

ATGAATAATC ATATTTCTAA TCAAAGTAAT AGCATTTATA TTGTGTTTAA A 51

(2) INFORMATION FOR SEQ ID NO: 1938:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 56 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1938:

TTGCTGAAGA TAGAGGCTTC ATGAAGGTGG AGAAGTTAGC TGATTTCTGG AACAGG 56

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 51 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1939:

ATCTCAATGT ATTCTCTAG TGTAGTTCT TCATAAATAA CCGGTGATT C

51

(2) INFORMATION FOR SEQ ID NO: 1940:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 318 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1940:

CTCAGGTCGA CTCTAGAGGA TCCCCTGTTA AATAAACTT CTTAAGCACA TACTTATTTTC 60  
 ACTATGCCTT TTACGTTCCC CTTATACTTT TCTCACATCT TTCTCTTAGA CTACTCCCTT 120  
 ATACGCCCCG CTCAATATCT TTAATCATTT CATCTACAGT TATTTTCGCA CTCGTTAAGA 180  
 CAATAGGAAC GCCTGGCACC TGGATGCGTA CTTGCACCTG CAAAATATAW ATCTTTATAA 240  
 TCTCGCGATA CATTyTGTGG ACGATAATAA TTACTTTGCG CTAAAGTTGG GCATTAAACC 300  
 GAATGCCGAA CCAAATTC 318

(2) INFORMATION FOR SEQ ID NO: 1941:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 57 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1941:

CCGGGAAAAT TTTTGAATT AAGTGGAAAA AAAATCCCCT TAAATTTCCC CTGGCCA

57

(2) INFORMATION FOR SEQ ID NO: 1942:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 378 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1942:

5 TGTTCCTCTT TTGAATCTGT TTTATTCGTT TGTTCTCTCT TTTTCTGTTC ATCTTTCATA 60  
 TTTCCACATC CCCCAATAAA AATGATTAAA AGTAATACAC TCATGTACAA AGCAATTTTT 120  
 TTTATATACT CCATCATTTT ACATCTCTCT GTTTTAATTT TATAAACATT TGAATATTTT 180  
 10 ATACAACTTA TTAATAAGT GATTATTCAA CTTTTATGTT ATCAAACAAA ACTAACTTAT 240  
 TCAATTTAAT ACATGTAATT CATTTTAACT TTATTATTAA ATGTTCTAAC GTnATTTTTT 300  
 ATATTAGTAA TTATATTTAT TTATCCTCGC TTGGATTAAA GTAGATACTA TCTGTGAAGT 360  
 15 AnATATTTTC TGCCTTGn 378

## (2) INFORMATION FOR SEQ ID NO: 1943:

## (i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 394 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1943:

AAGAAGAAGT CAAAATTCAG CTAAGTAAAA GCTCGAGTTA TAAAAAAGTC TAAATTGATT 60  
 30 CAACAGGAGT AGAAAAGGAA ATTAGTCTTG CATATTTTAG AAAATGAATA AAAACAGTTA 120  
 CTATATGCAA CTCAAGAATT AAATATTATT TAAGCCACAT ACCTATTAGA GTACAAAATA 180  
 TACAAGTTGT ACTTATATCT AGGTATGTGA CTTTGTGATT TAAGCGTAAA GTAAAAGTTT 240  
 35 TTATGTTTGT ATTAGTTCTA AATTATTTTG CACTTGGATG ACACGTATTT TTGAGTTTAA 300  
 GTGGTGA CTC AAGTTCAATA AAATAAATAT CAGATAGGAT AATTTGAnAA TnATATGAAA 360  
 40 GGGTTATCTC CAAAATnATC TCCATATTAT AAGG 394

## (2) INFORMATION FOR SEQ ID NO: 1944:

## (i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 52 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1944:

50 TATTCGTGAT GACGATTGTC GGTGACATGA AGTTCTATTT GCTGGCACTG AT 52

## (2) INFORMATION FOR SEQ ID NO: 1945:

55

- (A) LENGTH: 82 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1945:

10 CGTTTAAAAA ATGATATCAA TCTTTATTGT GGATTGCAAC ATCCGTGTGC TCCATAAAAC 60  
 GTGTGGCGAG ACTTGGGAAA GG 82

(2) INFORMATION FOR SEQ ID NO: 1946:

15

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 70 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1946:

25 GTATTATTGA TGAAGAAACA GCTCTCCAGT TGTAGATGCA TGCTACGTTT ACGTTACCAC 60  
 TGTATCAATT 70

(2) INFORMATION FOR SEQ ID NO: 1947:

30

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1947:

40 TATCACCAGC ACCAAGGATA ATGACATGCT GATCTTTTGC AGTTATGGTA 50

(2) INFORMATION FOR SEQ ID NO: 1948:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 117 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1948:

ATTGTATGAA TCTTTGGGGA ATGAACTTTT AACGAACGGA CATCTTGCAA TGACGCATCA 60  
 55 AAATGGTTTT AACACATGTA ATCGGCTCTC GGTACTATTC GTGTGATGTA CACATGG 117

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 64 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1949:  
TTTGATGATT TCGGGATGGA TTGGTATTGT GGTGAATGAA TTTTITAGCT CATCATCAAA 60  
TTAG 64

15

(2) INFORMATION FOR SEQ ID NO: 1950:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 57 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1950:  
CTCTAGTGGC CATTCAATTT TGTCGCTGAA TGATGTTGGT ACATCCATTG CTGCTGT 57

(2) INFORMATION FOR SEQ ID NO: 1951:

30

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 68 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1951:

40

CTGTCCTTCT GAAACTTGGG TATTTAATTA GGAATAGTTA AAAAAATCAT TCACAGAAAC 60  
ATTTAATA 68

(2) INFORMATION FOR SEQ ID NO: 1952:

45

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 106 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear.

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1952:

55

TTAAATTAAC CTTAAGGTTG GATTTTTTTAA CCCCCAAATT TTTGGGGTGG TTAAAATTCC 60



## (2) INFORMATION FOR SEQ ID NO: 1953:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1953:

GACATTTACA CCTGCTTCAA TCTGGTCCAG TGCAGCATCT AATTCTTCGA 50

## (2) INFORMATION FOR SEQ ID NO: 1954:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 107 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1954:

ATTGGCCAA CTGTTTCAGCA CGGTATTGGT TCAATGCAAC ACTTTATCAT TGCTTCAGGG 60

CTATATCGGT GGTATGGGtT GTATCACTTC TTAGAACGTG GTATTAA 107

## (2) INFORMATION FOR SEQ ID NO: 1955:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 54 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1955:

GAAGTGAATA TGAAGCTGCT AAAGACTCCG GAATGCTACC TCAGACAACT GATG 54

## (2) INFORMATION FOR SEQ ID NO: 1956:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 365 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1956:

ATGATTATTT TAGTTCCATT TGTGAGTCG ACTGCTAAAG TTCCATTTAA ATGTTGTACA 60

ATAAGCAGTA ATTTATGATT GTTTACAGTT TTTAATTTAC CATGAACTTT TGAAGCATTT 180  
 GCATGTTTAA TAACATTATT TATCGCTTCA CGCGTAATCA TAACTAACAT AGATTGTTTA 240  
 5 GTAGGACTTA ATACTTGCGC TAATTCCTTA TTTTCAAATG TAAATCAAT ATCAGCATCA 300  
 nTnAAAACTT TACGTATACT ATCAATCTCT TCAATAAATG ATGGTAATTT TACATCATCA 360  
 ATAAT 365

(2) INFORMATION FOR SEQ ID NO: 1957:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 346 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1957:

AAATAATGTC ACAAAGTTA AAGATACTAA TATTTTCCA TATACTGGTG TAGTTGCTTT 60  
 TAAAAGTGCA ACTGGATTG TAGTTGGAAA GAATACTATT TTAACAAATA AACATGTGTC 120  
 25 GAAAAATTAC AAAGTGGGCG ATCGTATTAC TGCACATCCA AATAGTGATA AAGGTAATGG 180  
 TGGTATTTAT TCGATTAAAA AGATTATTAA TTATCCAGGT AAAGAAGATG TATCAGTCAT 240  
 30 TCAAGTTGAA GAGCGTGCAA TAGAACGTGG ACCAAAAGGC TTTAATTTTA ATGATAATGT 300  
 AACGCCATTC AAATATGCGG CAGGGGCTAA AGCTGGTGAG CGAATT 346

(2) INFORMATION FOR SEQ ID NO: 1958:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1958:

TTTTCCAGTT AATTTTCCA GTTCACTAAA TACTTTATTG ACTGTACCAG ACCCAATAAT 60  
 45 AATTTGGTAT TGTCCCCCAG TAGAAAACGT CCCTTTAACT ACATCCATAT TGTTTAGCGC 120  
 CTCTTCATTT ACTAACTTT CATCATTTAA AACTAATCGT AGTCTCGTTG CACAATGCGC 180  
 50 CATTGCATCT AAATTCTCTT CTCCGCCTAT CGCGTTCAAA ATTTCTTCTG CGGATTGCTT 240  
 ATAATTCATA TATTTAGCCT CTAATTAGA ACCGGTTCCA TTTATTCCAC TTTATTGTAA 300  
 CCGGTTCCAA AAATATTTGC AACACTCTAT TATCATTTTA TATAACACC TACACCATTT 360

## (2) INFORMATION FOR SEQ ID NO: 1959:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1959:

GATTGCATAT AATAGTAAAA ACATTACATC TTGAACAGTA CTCGTTTGT

## (2) INFORMATION FOR SEQ ID NO: 1960:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 57 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1960:

AATTGAACC AGACACTGAT ACAAGTCACA CCCAGAAACT TTAAAGGACG TAAATGT

## (2) INFORMATION FOR SEQ ID NO: 1961:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1961:

AACGCTATAT TAGCGATATA CAATGATGCC ATTATCAATA nTACAnCTGn

## (2) INFORMATION FOR SEQ ID NO: 1962:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 60 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1962:

TACAACGTCA GTTGGCAGAC ACCAGAAGAA GGATTCATAA GTATATTCAG GAACTTGTTA

## (2) INFORMATION FOR SEQ ID NO: 1963:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1963:

10 AATTTTTCCTCCTTTTTTAAATTTCCCAAAA AAAAnCCCCC AAnAAAAAAA 50

(2) INFORMATION FOR SEQ ID NO: 1964:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1964:

CAACAAGTAG ATGCATCAGA GAGTAGTGTT CAAACGTTAA TAGATGTGGC ATG 53

25

(2) INFORMATION FOR SEQ ID NO: 1965:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1965:

35

AGCAAAGGCA TAACTGCTAA TGACCATGTA AATGAGACGA GTCGATCGTG GCCA 54

(2) INFORMATION FOR SEQ ID NO: 1966:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 252 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1966:

CTCAAATAAC TGGCTCAACT CAACCGGTCT ATAACACCAT AACACCGCAT GCCACTCTAG 60

50

CATACTCAAT CGCTCTGGTA CCAGCnCTCA AATAACTGGC TCACGCCAAC TGTCTATAAC 120

ACTAACACGC ATGCACTCTA GCCTACTCAG AGCTCTGGTA CAGCACTCAA TAGCTGACTG 180

55

TCACAGTCCA CACACACTCA ATACTGGCTG ACACAGTTCA CACACnGCTT ACTCGCTCTC 240

## (2) INFORMATION FOR SEQ ID NO: 1967:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1967:

CAGTTTAAAC TCGATGTTGT GTACTACTGT GCCAGCTGGA ATGTTTATA ATGGTGATG 59

## (2) INFORMATION FOR SEQ ID NO: 1968:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1968:

GTTACATGGC ATCAGCCAA ACCTGTCTAT AACACCATAA CACGGCATTG CC 52

## (2) INFORMATION FOR SEQ ID NO: 1969:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1969:

ACAATTTTAA TTATATACT CCAGGGGCTA CAGTAATACG ATTTCTCCAG ACTCCAAA 58

## (2) INFORMATION FOR SEQ ID NO: 1970:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1970:

TGACGTATAA TGGATGAAAG TCTATTAAGT TTAAGAAGCT AATACTGTGA AATCTTTCT 59

## (2) INFORMATION FOR SEQ ID NO: 1971:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1971:

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TATCATGTGA TCTTCAATCG TTCACCAACA GTCATTGCT GCATCAGTAA CG

52

(2) INFORMATION FOR SEQ ID NO: 1972:

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1972:

TTGCTGGTGC CATAGACTAC ACTTGTTTGA TATCAGAAAT GGGATCTGTT CCATTACC

58

25

(2) INFORMATION FOR SEQ ID NO: 1973:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1973:

AGTTAAACCG AGTCCAACCC AAACCTCCAA TCCACCTAAT GGTAAAAATT CCAAACCAAT

60

ACCAGGGAGG GACCAAAAAA CGGAATGGGG CCTATTGGTA GGGTACCTAT CCCATTTAAA

120

40

AATCCATCCA AAAGCCCAaA TTATCGGACC ATTTTCGCCA AAAATAATTT AAGCGGAAAT

180

TGAATACCTT AAAATTCTCh GGGCCCACT

209

(2) INFORMATION FOR SEQ ID NO: 1974:

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1974:

ATCTGAGTAT TTATAACATA AATCACTAAT ATCGTTATTA CATAGGGATA GGGTAAAAGT

60

55

## (2) INFORMATION FOR SEQ ID NO: 1975:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1975:

TTCCTGCATC CGAGTCTGAA TCGCTGTGCA ATCACGTGCA GTCGATCGCT ATCAGGTCGA 60  
 GTCGCGTCGA ATCGTTCGCT ATCGAGTCGA TCGCGTCGAA TCGAATCAGG TCGAGTCG 118

## (2) INFORMATION FOR SEQ ID NO: 1976:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1976:

TTGCAACHTT TGATCTAGAT ACTACCTTAG TTGGATTGTA CTAATTGATT CTAATTACCC 60  
 TTTAGTTGGT TTTGTAGCAG GCGTTTTGTC TTTACCTGAC TCACTAGATG CGTCATTTTC 120  
 TTTTTCACAA CTTGGTAATT GTTTATTGTC ATCTTTTGG CTGTCTTGT TTTGTGATTC 180  
 TTTTTCACAA GGTGATGGTG TTGGTTTGCT AGGCGTACTG GAGTAGCTTC CTTCTTAGCT 240  
 GAGTTATCIT GTTGTTCITT TTTGTTAGAT TTATCGGTAT TGGCTTTTGT AAATGCTTCT 300  
 NTATCAACGA TTCTGACATG GTATTGTCCA TCATAATCAA TCGTTTTTAC GTGAACITTA 360  
 ACGATAGCAT CATATAGAGT TTACCTTCAA CATATGGGAA 400

## (2) INFORMATION FOR SEQ ID NO: 1977:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1977:

TAGACAAAGA CAGTAACAGT AAAGTACGCT TCAGAACTGA TGGCTCACTG CGAGTATAAA 60  
 AACITGTAGT GTCC 74

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 72 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1978:

ACTCAAAAAC TCGGAAAACA TTCCAATTGA GCTTAAATCT GACCCTTTTT TTGACCCTTA 60  
TATTTTTTAC AA 72

(2) INFORMATION FOR SEQ ID NO: 1979:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 69 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1979:

ATGTCATTGG CTTTGAACCT TATCTTCAAG CACCCAATCG TTTTAACTTT TCAAAATTTG 60  
GCACCATAA 69

(2) INFORMATION FOR SEQ ID NO: 1980:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 109 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1980:

CAGAGAGTTG TCGCTCATTA AACGCCACCT GATGAGTTTT CGCTTACGAA GTGCCACGCG 60  
GTATGGATAA TTTTCACCTG TTGCTGAGTC TTTGATAAGC CTCGACTGT 109

(2) INFORMATION FOR SEQ ID NO: 1981:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 55 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1981:



## (2) INFORMATION FOR SEQ ID NO: 1982:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 53 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1982:

GAATCTGTTT AAGTTAGAAT TATCCCGGCA TAATGATAAA GGCGAGTAAA TGG 53

## (2) INFORMATION FOR SEQ ID NO: 1983:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 252 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1983:

GnCTTTTGAA TAAAGAAAA TTCATCAATA GAAAAACCGT CTTTATCGTC TATTTTTTTTA 60  
 ACTAGTAAGT TCGGCGTTCT TAGAGACTCA AATATTGATT TTACGTTTTT CTTTGTTACA 120  
 CCACTAACAC TAAATATTCT TCCATCTAAA TCTACTAATT CTGGTACCGC AAAGACATCT 180  
 AAACCATGTG TTTTTTCTTT GTATTTATTT TCATCTTTTC CCAATAAAAA CACTTGAAC 240  
 TTTTGATTTh GT 252

## (2) INFORMATION FOR SEQ ID NO: 1984:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 63 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1984:

CGTGTTAATC AACTAATTCT TAGTTTTAAC TGTCGTAATA ATCAACTGAA CACTTTCAAT 60  
 CTA 63

## (2) INFORMATION FOR SEQ ID NO: 1985:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 63 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1985:

5 TCCTAAAATG ACCGCTAATG CCTATGGATT GTTATCACCG ACCGCAGGGA CAGCAGGACC 60  
 TAC 63

## (2) INFORMATION FOR SEQ ID NO: 1986:

- 10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 112 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1986:

GGCATATAAA AATTAGAGAA ATTATTTCAA ATGAACAGAT AGAGGCACAA GATGAATTAG 60  
 20 TTAAACGATT AAACGATTAT GNTTTAAATG TCACTCAAGC AACTGTTTCT CG 112

## (2) INFORMATION FOR SEQ ID NO: 1987:

- 25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 106 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1987:

TTTATCAATT TGTAACGAAC ATGAATTACA TGTTTCAGGA AAATATATTT CATCCCATT 60  
 35 TTAAAAAGTA TAAGATTTTA TGAAAAATTA AACCAATTGA GTATAA 106

## (2) INFORMATION FOR SEQ ID NO: 1988:

- 40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1988:

45 AATGGCGTAG TTACAGCATT TATGATTGTG TTAATCTTTT CTTCTGATAA ACATAATCTG 60  
 50 TTTGACCAAA AGTATTTAAG TGTTCATTA ATTAGTTTTA TTATTTACGT CGTATGGCAA 120  
 GTTTTATTGA TAATGTTTTA TTATCATTCA AAACCAAAAA ATAATTCATT TTCAAAATTT 180

TGGTTAGGTG GACATCAGAT TCACTTCCAT GAAAGTAAAT TAATTGAATT TGTTGGTTTC 300  
 TTAGGAATTT CTTATGTTAC ATTCAAAAGT GTGCAGTTAA TTATGGAAAT TCGTGATGGT 360  
 5 TCTATCAAAG AAATTAAAGT ATGGAAATTA ATTCAATTTA 400

(2) INFORMATION FOR SEQ ID NO: 1989:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1989:

TTCAGCTTAC AATAATGAGC AGGTTGGGGT GGGCTCCAAC GCAGAGAATT TCGATAAGAA 60  
 20 ATTCCACAAA TAATACAAGT TGGCCCACTC CCATTCTGTA ATAAATATAG GAGGTCATTG 120  
 TTATGCAAAT AGAACTTACT GATGCAGCAG TAACTTGGTT TAAAAATGAA CTTGAGTTGC 180  
 CTGAAAATAA TAAAGTGCTC GTGTTTTTTT TAAGATATGG TGGCGAATTC CAACTCAAGC 240  
 25 AAGGATTTAG TCCTGCTTTT ACAGTTGAAC CAAAGGAAGA TGTTGATATT GGCTATGAAC 300  
 AACAAATGA CGATTTAAAT GTTGTCGTAG CGGAAAAGA TTTGTGGTAC TTTGAAGATG 360  
 ACCACATTAT TGTAATGTA GTTGTCACGA AGATGAATTT 400

(2) INFORMATION FOR SEQ ID NO: 1990:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1990:

CAATTTATTA TGTAATAAT TATAGCATTG ATGAACAAGG CGCTCAACGT AATANTACAA 60  
 TTAATGGATT GTTTCACAAG ATGGTAAAGC TAGGATGTCT TTTTATTAAG A 111

(2) INFORMATION FOR SEQ ID NO: 1991:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

TAAACAAATT CATCAATTGT TAGTGGCATA TCCTAATGTA ATTAGAGAGG AGTT

54

(2) INFORMATION FOR SEQ ID NO: 1992:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 59 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1992:

GAACGATAGA TTGATGAAAA GTTTAAAAAA GTACGTATAT GTTTATTAAAG TTTGAGTTT

59

(2) INFORMATION FOR SEQ ID NO: 1993:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 73 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1993:

CGAGACCAAA ATATTCGAAC GAATAATTTTC AGTGTTTTGC TCCTTTATTA TAGATTCAAG

60

CTATGGATAA TAG

73

(2) INFORMATION FOR SEQ ID NO: 1994:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1994:

ATCCATACAA ATGTAACAAG CACAATTGCh GCCATACTTn GCATGACAGT

50

(2) INFORMATION FOR SEQ ID NO: 1995:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 57 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1995:

## (2) INFORMATION FOR SEQ ID NO: 1996:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1996:

TCaTTAAaA TTAATGTnCG TTGGGGCTCT AATAAAATTT GTTTACAACG

50

## (2) INFORMATION FOR SEQ ID NO: 1997:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1997:

TCATGATTTG AAATGACTTT CAATGACTTG GGTGGGACAC TTGTTGCACA GCTGGATGTG

60

C

61

## (2) INFORMATION FOR SEQ ID NO: 1998:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1998:

CATGCATTGA TGnTCTCAA GAACATGATG AAACAGGTCA nCACATGnCA

50

## (2) INFORMATION FOR SEQ ID NO: 1999:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1999:

GGTTCGCTAC TGATTGGGTA TACATCTGAT TTAGCAATCT TGCGCACTTG TT

52

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2000:

ATGTGTTAG ATATCTGCAC ACTTGAACGT TATTGTGGGA TATACTTGGC CAT

53

## (2) INFORMATION FOR SEQ ID NO: 2001:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2001:

ATCTCAGTAA GGGTAAGCGT CAAAGTCTGC ACGGATGCTA ATGTTTACCA GGTT

54

## (2) INFORMATION FOR SEQ ID NO: 2002:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2002:

CTAAAGATTG TAATGCTTGA ACAATTGGTT CAGTGAATTT TTGGAAATTG TGGAAACTGT

60

TACCATCATC ATCTGTTATA AAATAAAGT TTAAATTGCC AGTATCATGA TAAACAGCGC

120

CACCACCAGA AATTCTTCTT ACTACATCGA TGTGTGAGC ATCGATATAT GTCTGATTTA

180

CTTCCTCTAT CGTATTTTGA TTCTTTCCAA CAATGATAGA TGGTCTATTT ATGTAAAATA

240

AAAAGTAACT TTCTTCTGCT GGTAATTTT TTAAAACATA TTCTTCCATT GCTAAGTTTA

300

AAGTTGGATC TGTAATATTA TTATTACTAA TGAATTTTCA TACAATCTCT CCCTTATATC

360

TATATATATn CTCTACTTAT TTATGCCTTA ACTTTGCTCA

400

## (2) INFORMATION FOR SEQ ID NO: 2003:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2003:

CCGAAATAGG ACGGGCAGTT GGATTTATTC GAAATGGGTG GCGTTAATAT ATACAGT

57

(2) INFORMATION FOR SEQ ID NO: 2004:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2004:

AGTAGTTGA AGGCGACCGC GGTCCACAAG CTGCAACGT TGTTAACTA TAATTCTTAG

60

ATTTGAATCA TTGATTTTAA CTAACACCTT ACCAAGAAGT AAGGTGTTTT TA

112

(2) INFORMATION FOR SEQ ID NO: 2005:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2005:

AAATCTTGAC ATAGGCACAG GAATGTATAT TGATCTCGAT CACTTAAGTC

50

(2) INFORMATION FOR SEQ ID NO: 2006:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2006:

AAGGTGGGTT TAAATTTCCC AAAAAAAAAA GCCTTTTAAC CTTTGGGGG GTCCCCCTTC

60

CTTGGAATTG GAAAGGGGCC AAAATTGGAA TAAGGGGnTT GGAAAAACCC AAGCC

115

(2) INFORMATION FOR SEQ ID NO: 2007:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2007:

TGAAGAAATA GCAAATGAAC TCAATATTTTC TATTGAACGT CAATATTTCA ACCAATTATA 60  
 5 TCGCTTCAAT AATCAAGATT TAAAGCATCT TGAACAAGAN TTTGA 105

## (2) INFORMATION FOR SEQ ID NO: 2008:

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 67 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2008:

ATTGGCTACT AAAGTTAAGG ACATGATGGA TTGGATTAGT GGTATGCGCT TTGAAAAGAT 60  
 20 CAATTAT 67

## (2) INFORMATION FOR SEQ ID NO: 2009:

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 73 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2009:

30 TATAAATTAG CGTCCTTCAT ATCACAACGA TGATGCTCTG TCGGAAGATC TGATTTATTT 60  
 CAATGTGCGC ACG 73

## (2) INFORMATION FOR SEQ ID NO: 2010:

## (i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 51 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2010:

45 CTTTGTTTAT GTTTCGTTTA ATTTGTAACC CTCTCTTTGG ATACCGAGGT T 51

## (2) INFORMATION FOR SEQ ID NO: 2011:

## (i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 88 base pairs



(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2011:

TAACGACCAA GCTTAAAGAG ATACGCTCTT ATGCGATTGG ATAGGTCGTT AAAGTTAACT 60

10

ACAATACCTC ATAAGTAGAT TTAGAATC 88

(2) INFORMATION FOR SEQ ID NO: 2012:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 56 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2012:

GTCAACCCCTT GCCAAGCTTA TATCAGGATA CTGGGATGTG ACTTCCGGTG AATTAC 56

25

(2) INFORMATION FOR SEQ ID NO: 2013:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2013:

35

AGCTTATAGT ACTTGTGACT TCATAATGGA TGAAGTTGAA GTACCAAAG AATTAACACA 60

ATTACACGAA TAATTAAAT AGAGAGTGTG ATAGTAGGTG GAATTATTAA ATAGTTATAA 120

TTTTGTTT TCGTATTAA CTCAAATGAT ATTAATGTTT ACAATACCAG CTATAATTAG 180

40

TGGTATTAAG TACAGTAAAC TTGATTATTT TTTCATCATA GTAATTCGA CATTATCGTT 240

ATTTCTATTT AAAATGTTTG ATAGCGCGTC CTTAATCATA TTAACITCAT TTATTATTAT 300

AATGnATTTT GTCAAAATCA AATGGnATTC nATTTTGTG ATTATGGCTT CGCAGATTAT 360

45

CCATACTGGT GCCAACTACA TGGATATAGT TATATATGCA 400

(2) INFORMATION FOR SEQ ID NO: 2014:

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2014:

TCTTTTCGAGG ACAGTAGAGG GTCCACCCTA TTGGACGTGG TACTGTACTA CTTTTAAA

58

5

(2) INFORMATION FOR SEQ ID NO: 2015:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2015:

TCTACCTGCA GGCATTCAAG CTTGGCACTT GCCGTCTTTT TACAACGTCTG TGA

55

15

(2) INFORMATION FOR SEQ ID NO: 2016:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2016:

TACTCTTAAG CTAACAACGG CGGTTATGAG TCCTTTGACA AGGTATCGGA GGAAAGACCG

60

30

TAAAGC

66

(2) INFORMATION FOR SEQ ID NO: 2017:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2017:

CCAATAAGCA CACTGCCATT ATTGAGGACG GTACATATAC GGTTAGACCC AATTGTTTCAT

60

45

GGCGGTGGGC ACATAGTGTT TGGCTTTGAG GAGGTTACCA TTGCC

105

(2) INFORMATION FOR SEQ ID NO: 2018:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

50

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2018:

CCTTCCAATA GTAATTGATT GATGTATGAG TATATTAGGT GTGAAATCAA GAGGATTC

58

(2) INFORMATION FOR SEQ ID NO: 2019:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2019:

TTTCCTCGTA GGTGGTTCTT CTTCATCTTC GTTGTTTTGT CCGAAGTTTG GA

52

(2) INFORMATION FOR SEQ ID NO: 2020:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2020:

ATAGTTTAGG TGAGGATGTT GnGGTACGAC AGGAAGAAAG ACGGCAAACA

50

(2) INFORMATION FOR SEQ ID NO: 2021:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2021:

TTGTCACAAT AATTTCTTCA GGATCATAGG AAAAATGATA ACGATTTTTG AAGTATTGAC

60

TAATTGCTTC GCGAGTTTCT AATAACCCTT TATTGTGAGA GTATGATGTC TTGTCATTGT

120

TAATAGCATC AATATATGCC TTTTTCACAA CATCAGGCAT CGGGAAGTCT GGTGGCCAA

180

TAGTTAAATT AACACAATCA TCCAAATTAT TCATACGATT TGAAAATTGG CGATACTTGG

240

GTGGCTCCTA AAATAATTAG GAAATGAGGA nTTnAAGGAA GGTTTCCATT TnGTGGACAC

300

(2) INFORMATION FOR SEQ ID NO: 2022:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2022:

TCATCCAAAT TATTCATACG ATTTGAAAAT TGGCGAATAC TTGGTGCTCT TAAATATTTA 60  
 10 GAATTAGAAT TTAAGAAAG TTTCATTTGT GACACCTCAA ATATAAATCA AATATTGTCT 120  
 AAAAATTTAG AAATTAATAA TATCATAACA TACTTTTAAA GCAAAAAAGG GTAAATTACT 180  
 TAAGCTTTAT TTGAAAAACG AAAAATGTCT AAATACACTG TAGTAACTAC TTTTCAAAT 240  
 15 GAATAAAGTG GTTACAGTTA ATGTACTTAG ACAGTATAAA ATTATGAATC TTTAAACTGT 300  
 GATGGTCTTT GTAAATTAAT TATTGGATTT GTCCATTAC AAACAAAGTT TGTAGATAAT 360  
 ACATATACGA TGATTACAGA TATACTTATT AAATAAAGAT 400

20

(2) INFORMATION FOR SEQ ID NO: 2023:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 25 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2023:

TTnAAATATA CCAATCACGT TCATCCACAG TGATCCTAGA CCAATCCAGA 50

(2) INFORMATION FOR SEQ ID NO: 2024:

35

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 66 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 40 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2024:

TTTTTAATGG TTAAAAAATT CCCTAATAAA ATTTTGAAA ACCTAAATTC CAAGGGGTTA 60  
 AATTCC 66

(2) INFORMATION FOR SEQ ID NO: 2025:

50

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 64 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 55 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2025:

GTAAGAGCAA TGGCGCAAAA TGCCTGTAAT GATATTGTGA ACGTAATTGA ATCAGTAGAG. 60  
5 GACC 64

(2) INFORMATION FOR SEQ ID NO: 2026:

(i) SEQUENCE CHARACTERISTICS:  
10 (A) LENGTH: 53 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2026:

CTGTCGCTGC GTGACTTAAT TCTTTTGCCC CGTTGGCATA TGAGGAAATG TCA 53

(2) INFORMATION FOR SEQ ID NO: 2027:

(i) SEQUENCE CHARACTERISTICS:  
20 (A) LENGTH: 53 base pairs  
(B) TYPE: nucleic acid  
25 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2027:

CATTCACTA TTATTGGTTT AGGGTTGTTT ACGTTCATCA TGACCGCACC ACA 53

(2) INFORMATION FOR SEQ ID NO: 2028:

(i) SEQUENCE CHARACTERISTICS:  
35 (A) LENGTH: 73 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2028:

CAACTAGACA TAGTATTGCT GCATTAATCA AGTCAAGCTG CCACACTAAG AATCGATGCA 60  
45 AACGGAATCG TCA 73

(2) INFORMATION FOR SEQ ID NO: 2029:

(i) SEQUENCE CHARACTERISTICS:  
50 (A) LENGTH: 127 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2029:

AATAATAATT CTGGAATAGT GTTTAATACT TATTnTCCGT TTAAGATTTC AACTTAATAT 60  
 5 GGGTTACAGC GCGTAGCTCG TCTAATTCAT CATCACGTGT AGAGTGCTCT GCCTTATCAG 120  
 ATCAGTT 127

## (2) INFORMATION FOR SEQ ID NO: 2030:

- 10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 61 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2030:

20 GCAAGTGAAT TGAAGTGACA TGTGGCTGGT GCTTCATGGT AATGATAAAC CAACACCATG 60  
 G 61

## (2) INFORMATION FOR SEQ ID NO: 2031:

- 25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 78 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 30 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2031:

35 ATAAATATCT ATTTAGATAT AAGTATTGAT AAGTTGCTTG AATTTATAAA GTGAAGGAGT 60  
 AGGTGTCATT AGTATAGT 78

## (2) INFORMATION FOR SEQ ID NO: 2032:

- 40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 229 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 45 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2032:

50 GAATAGTGTT TATAAAATGT TGACACTGTA GTGGCATATT GTAAATTAAA TATTATTATG 60  
 TGATCATTTT GTTTAAATAT TAGTTATAAG AAGTGAAATA nTCATTTTAA AAGGAGACTT 120  
 AAAACTTGAA ACGATCAACG AATCAAGAAA AATTTCTTGA TACACTAATT AGACTTAATA 180

## (2) INFORMATION FOR SEQ ID NO: 2033:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2033:

TTTTGTCATC TGTATAGGTA TGCGCGCCGG TGTCTTTATT CACTTTGAAC TGTGCGT 57

## (2) INFORMATION FOR SEQ ID NO: 2034:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2034:

AAGGCATTGG ATATAAGACT TGATGTTGCA TGGCAATCAC ACTGCCTAAT CCTTGCATAT 60

AA 62

## (2) INFORMATION FOR SEQ ID NO: 2035:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2035:

ATGGCAAATA CTATACATCG TCCAATTGAT TGAAAAATAT GGTTATTAAA GA 52

## (2) INFORMATION FOR SEQ ID NO: 2036:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2036:

AAGGTGTTTT TATATGCTTA TTACAAATAC TTAACGCGAT GAGTTTCTCA ACCAAATTGA 60

## (2) INFORMATION FOR SEQ ID NO: 2037:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 71 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2037:

TACCCACCCC CAAACCCAAG GTTTTAAAAA ACCCCTTCCA AAAGCCCGGA AAAACCAAAA 60  
 GGAATTATTT T 71

## (2) INFORMATION FOR SEQ ID NO: 2038:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2038:

GAATCCCGGA AGTACAATTT GGTACGTGAA GAAAATGGTA GTGGAATTAC 50

## (2) INFORMATION FOR SEQ ID NO: 2039:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2039:

CAGTATCTCT TGGTATTTTA ATTGGTGCTT TATTAAACGT AATTTTACCT TTATATATCG 60  
 ATGGAGCGAA GAGTATTTTC GTATACGTTT ATAGTGCCTC TATTTTACCA GGTATGATTC 120  
 CTTGGTTTAT GATTTTATTC AGTCATTTAC GTTTTAGAAA ATTACACCCT GAAGAATTGG 180  
 AAGGTCACCC ATTCAAAATG CCTGGTGGCG CAGTAACTAA CTATTTAACA ATCTTATTCT 240  
 TAATATTAGT ATTGGTTGGT ATGGTATTTA ATGTTGAAAC TAGAATATCA GTGCTTATTG 300  
 GTGTCATCTT CTTAACGATT GTAACGATTT ATTATTTTAT TAGATATAAT AAAAATAATG 360  
 TAAAGCAnAA TAGTATGTTA TAAnGAGCGn TACTTATGAC 400

## (2) INFORMATION FOR SEQ ID NO: 2040:



- (A) LENGTH: 79 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2040:

10 AAGCTGATTT TTCTAAATGT TGAAAATCAT AAAGTCTTA ATAATAAATA ACGAGATCTA 60  
 AGTAATAGTG CTCCATTAA 79

(2) INFORMATION FOR SEQ ID NO: 2041:

15

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2041:

25 AATTGAACGG ATCGTTCCCA ACCGTTATCA ACCCAGACCG GTGTTTGAAC CCAA 54

(2) INFORMATION FOR SEQ ID NO: 2042:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2042:

35 AATGGGATTG GTTCAAAGTG AAATGGGCTG TTAGTCCCTG TAAAACCAAG 50

(2) INFORMATION FOR SEQ ID NO: 2043:

40

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 109 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2043:

50 ATTGGnATAA TCAAAGCATT GAATCATACA TAGTCACATT GATTGTTTCC TCAGAGTTTC 60  
 AACACTCTAT AACTCATTTT AGTAATTTCG TGATTGCGCA CTTTCATGTG 109

(2) INFORMATION FOR SEQ ID NO: 2044:

55

- (A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2044:

10 TTTTATGGAG GTGATGAAGT GGGTGAAGCT GAAAGGAAGC AAAAGCTTGG 50

(2) INFORMATION FOR SEQ ID NO: 2045:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 101 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2045:

TTGGCCCCCT TCCAACCCTT GGAAATTTTA AAAGGCCANT TTTGGGGTAA AACCTTGGT 60

25 TCCAAGGACC CCCAAAAGTT TTTTAACCTT CCAATTATTA T 101

(2) INFORMATION FOR SEQ ID NO: 2046:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 100 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2046:

ACCCCTTTCCA AAAAGCCCAT TTTGAATTCC CCAAAGGGAG CCAAATTTAA GATGGCCGCh 60

40 AAAAAGGACC GGGGGGTCCA TGTTTAAATT TAAGCCGGAC 100

(2) INFORMATION FOR SEQ ID NO: 2047:

(i) SEQUENCE CHARACTERISTICS:

45

- (A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2047:

GTTAGTTATG AGCAACGTAT TAATGAAATT ATTGAGCAGT AATThACCAG 50

(2) INFORMATION FOR SEQ ID NO: 2048:

55

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2048:

10 TACGTATTTT CAAATGACGT TGGTGGACGT CACACTCCAT TCTTCTCAA CTATCG

56

(2) INFORMATION FOR SEQ ID NO: 2049:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 82 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2049:

TTTTCCCCC CCCCCCAAA TTGGGGGTTA AAATTTTAAA AAAAGGGGTT AAAGGGAAC

60

25 CCCAATTCCG GTTAACCTTT TG

82

(2) INFORMATION FOR SEQ ID NO: 2050:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2050:

TCAGATGGAT GGCAGTTATT TGGTATTCCA TGGGTATAAA GATAGCATAT T

51

(2) INFORMATION FOR SEQ ID NO: 2051:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2051:

50 TGAACGGGAG AAAGATGTTG TTGCATGGTG TCTCGGAAAC GTTTGTGTCC ACGTA

55

(2) INFORMATION FOR SEQ ID NO: 2052:

(i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 74 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2052:

ATACCTGGAT GCAAAGGCAA AGTCGCAATT TTCCCTGTTC TAATGTGTCT AACTTCTCTT 60

10

CTAAAGTTCA GGTT 74

(2) INFORMATION FOR SEQ ID NO: 2053:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 51 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2053:

AATCTTGTCT GATGTAATGT TCAGGTCCCT TGACCCTCAT ATGCATGAGG T 51

25

(2) INFORMATION FOR SEQ ID NO: 2054:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 52 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2054:

35

CATCGACTTA TAGCTTAATT ATTATAAAAA ATTTCTCCAG ATTAACTTT CT 52

(2) INFORMATION FOR SEQ ID NO: 2055:

(i) SEQUENCE CHARACTERISTICS:

40

(A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2055:

ACTGACACAT TATATTAGTG AATTATTAAA AAATGATGAG AAAATTAAAA TCATCATGAA 60

50

TGAATTCGGT ACTTTTGATA TTGATAGCAA TAGTATTTCA AATGAAATTG AAGTCCATTC 120

ATTGATTAAT GGTGTGTGTT GTTGCATCT TAAACAAGAA CTTGTCTATG AACTAAAAGC 180

CATTGCTTTA AAAGGGGACG TTAATCATGT CATCATAGAA GCGACAGGCA TTGCGCATCC 240

55

TTATTTATGG TGTATTAGAT GCGACTCGAT TTTTAGAACG TCATCAATAT ACCGAAAAAT 360

ACAGTTTCGC TGGATGGGGA GGATCCAGTT GGAAACTAAN 400

(2) INFORMATION FOR SEQ ID NO: 2056:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2056:

TCAAAACTTT GAAGTTGTGC TTGCTTTGCA CCATTTTAA AATGTTTCAGC TGAGAGTATA 60

TCTTCCGCTG TAAAATTAC TTCTCCTGGA CTAAAGATT CAATTAACAA CCAAGCCGAT 120

AACGTATCAT TTAGCAATTG ACTCATGAAA TCCCACCTTG TTCCCTATTT GTTTTTTACT 180

TAATGCTATT TTAACAAATA ATTTAATCAT ATTAGTGTTT TTTCAAAAAT ATTCATATAT 240

TATCATTACC ATATTTATTC AACAAATGTT TGTAAAATCC TCACTAATAA AATTAATCGA 300

TATGACCATA ATTCATTATC CAATAAATGA CTATAAAAAT TTCTnCTATG CCTTCATTTG 360

CAACTAAATT TGGACATCAA AAAAGAGCAC TCCTGAATGA 400

(2) INFORMATION FOR SEQ ID NO: 2057:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2057:

TTGTTGTTGT GATTTCACAT TTTCAAAATT TTGTTGCATG TTGTTAACTT CATAAATTAG 60

TGATTCGACT ACATCATTCA TGAGGACGCC TCCTACATTT TTTAATTTAT CACAATATAC 120

TGTATTCGTC ATGTTTTAAC ACTCTATATA ATTTGATTTA ACTATTTTTT CAAATGTGTT 180

ATCTGTTAAA TCAAGTAAAT CTAAAACTT CCTATATAAA TACAAAATTT TATCGTGTAT 240

GTTGTTATAC GATGAAAATA CTTTTAATCT AATAAAATCA TTTAAATCAA ATACACCTCT 300

GCTGATTAAC AACACATACT TGTACTTGCC TCAAAAATAA AAATTACTAA TCATGATTTG 360

ACTTTTATAA CAAAATTCAA AAATATTGTA ATGAGTATTC 400

(2) INFORMATION FOR SEQ ID NO: 2058:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2058:

10 TCTTTTACT CGCAATTTTA GGAAAATGG TTGGATCAAT TGATAAAACC GGAAAATTAT 60  
 TAACAATAAT CAATAAAATA TCAAGCATAA TAATTATTAT TGTGCTCTG ATGATATTAC 120  
 AAAAATTAT TCAATTATTA TTCTAAAGCG TTATGTAGTT GTATTTTAAA AGCGTTATAC 180  
 15 AAAAGACATA CTTGTGTCTA TGTATAACGC TTTATTTTATT ATAAATTTGG ATCAATTAAC 240  
 TCAACAAATT TAAATGTTCC ATTGTCATAT TCAAATTTCA GGATATTACA ATTACCGATA 300  
 TTATGCTTTA ATGCTTCATC TAGTTTAAGG CAATATCTTA AAAATACCnC CCTTANTGGT 360  
 20 CCATGACTCA CGACTAATGC ATTATTCTTT GGTGAGAC 400

## (2) INFORMATION FOR SEQ ID NO: 2059:

- 25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 51 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2059:

AAAACAACAC AATCAAAAAT ATTGGATACA ACTGAAAAGT TATCAAAGCT A 51

35

## (2) INFORMATION FOR SEQ ID NO: 2060:

- 40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2060:

TTATCATGTT TAGTAGATT TAAGAAGCTA GAACATTGTA GATATGATGA 50

## (2) INFORMATION FOR SEQ ID NO: 2061:

- 50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2061:

5 AACGTCGThA TATCAnCTTG CCAAACAAAG ATATTGTCAC CTTTTATCGG 50

(2) INFORMATION FOR SEQ ID NO: 2062:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2062:

ACCATGGTGn ATATGGTCAT GATGATCGTT TGTGCCGGGA GCTTGAGCTG 50

(2) INFORMATION FOR SEQ ID NO: 2063:

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2063:

30 TTTCCCTTGG TTTTGGGAATT TAACCAAATT TGGGAGGGAT TTGGGACCAC CCCAGGATT 60

TTAÀAAAAAA AAAATCCCAG G 81

(2) INFORMATION FOR SEQ ID NO: 2064:

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2064:

45 TTTTGGGGAC CTAACTGGG TGGGTCTGGA ACTGTTTCCC TTCAAACAC A 51

(2) INFORMATION FOR SEQ ID NO: 2065:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 52 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

55

ATGATGTATT CAAAAGGTAT CTATAAATA GCTTTAGTTG GAAAAGATGA GA

52

(2) INFORMATION FOR SEQ ID NO: 2066:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

10

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2066:

15

TTTCATCACT GGCATCTTGT AATTTCTTGG TCTCATATCT GGAATTAATA GGT

53

(2) INFORMATION FOR SEQ ID NO: 2067:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 63 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2067:

AACCATTAAG AAATTGGATA CACAGAGCAA ATATGGTTAT GATTAGGAAC CATGGCATT

60

30

ACC

63

(2) INFORMATION FOR SEQ ID NO: 2068:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2068:

AAAGGCAGCG ATGTTACTCA TACCGAACCT GGTTATATAT GAGCGATGAT GCAATGTA

58

45

(2) INFORMATION FOR SEQ ID NO: 2069:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 67 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

50

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2069:

55



AACAGGA

67

## (2) INFORMATION FOR SEQ ID NO: 2070:

5

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2070:

15

CATTTAACCC ATCTTCTTTT TTTAATTCTT CTATACTACG GTTTAAAAAC TCTACAATAA

60

CTGCCATTTT ATCATCATCA AAGACT

86

## (2) INFORMATION FOR SEQ ID NO: 2071:

20

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2071:

30

GTTTCTTCAA AATATGTGTA TTACCTTTTT GTATGGTTAA ATCTTTTAAT TCTATCATTC

60

TTGTCTTACC TCTTTTGGTG TATCCTCTTT TCAACATAT GTGATCGATA TGACATATTG

120

CCCTTTATGC TTTATTTTGA CATACGTTCT ACTAGGTGAA AATCCATTAA ATGTTAATTT

180

35

ATAATCAAGC TTTTCCCCTC TTTCACTATA AGCCGTAATA TTAACATATT GTTGCCTACC

240

TTTTGGCACT TTGGCATAAC TATACTCCGT TTTTAAGAAA GGATTAAAAC GATCAAGTAT

300

AGGATGATGT ATGANTGTAA AAGCAATAGT AATGGATAAT ATTAATCCTA ATAATATTGC

360

40

AATGATAAAT TTCATAGTTA A

381

## (2) INFORMATION FOR SEQ ID NO: 2072:

45

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

50

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2072:

ATCCCCGAAT TGCTTCGCAA ATGTATCATC TTCGAGGCTA CGTTACTTAA AT

52

55

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 82 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

5

10

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2073:

CCAAAAACAG CATCACTGTG ATTATGGTTT TCATCTTCTA TAACTAAGAA TACATGTTTT 60  
TTTGTA AAAA TTTTTTTGAT CA 82

15

- (2) INFORMATION FOR SEQ ID NO: 2074:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 82 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

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- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2074:

TTTATCGCAA TGAGGGAAGA TAAAGGATCC CGAAAGCGCC GTATGGGTTG GCAAACATTG 60  
GGGACCAAGA CCGTTCCCCA TA 82

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- (2) INFORMATION FOR SEQ ID NO: 2075:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 66 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

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- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2075:

CTTGTTGCT CTTTATTTAT TTAATTGAGA CCTAGAAATA AGTTATTAAG CACAATCATT 60  
CACTTT 66

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- (2) INFORMATION FOR SEQ ID NO: 2076:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 57 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

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- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2076:

## (2) INFORMATION FOR SEQ ID NO: 2077:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2077:

TACGTTCTAT CATAGAGCCT GGAGATGAAA TTATAATACC GGGACCAATT TATGCAGGCT 60  
 ACATACCACT CATCGAAGTA CTAGGTGGTA AACCAATTTA TATTGATACA ACAGCAACAC 120  
 AATTTAAAT TACACCTGAT GCATTAGAAA GTCATATTTC TCCAAAGACA AGAGCTGTCT 180  
 TGTAAATTA TCCGACTAAT CCAACTGGCG TAGTTTTAAA AAGAAATGAA GTTYTATA 240  
 TCGTAAATGT ATTAAAAAA TATCCGTTAT TTATTATTAG CGATGAGATT TATGCTGAAA 300  
 ATACATTTAG TGGTAAACAT GTATCC 326

## (2) INFORMATION FOR SEQ ID NO: 2078:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2078:

ACCCCTTAAT TTAATTGATG TTTTGTTATT TTAAATGA ATAGTTGAAG AAAAAT 56

## (2) INFORMATION FOR SEQ ID NO: 2079:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2079:

CACGTACTGC CATGTATGCA CAAGCCGGCA TTCATAAAGC CTTCCATGGC AGTCGTTATC 60  
 A 61

## (2) INFORMATION FOR SEQ ID NO: 2080:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 base pairs

- (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2080:

TGGGACAGGG CGTACCATT CAAAATGATA GTTCTGAGCT GCTAATTAAT ATGCCTTCGA 60

10

AAAAGATGAG TTAAATTGA GATGATGAGA CTGA 94

(2) INFORMATION FOR SEQ ID NO: 2081:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2081:

AAGACGACAT GCAAGACATT GCCTTATCTA ATGACAATGT TAAAGCGAGT 50

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(2) INFORMATION FOR SEQ ID NO: 2082:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2082:

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TTGTTGGCT AAAAATAAAG TGGCATTGAC GTGACCGCAA GTTGACGTAC 50

(2) INFORMATION FOR SEQ ID NO: 2083:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 133 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2083:

CTTCCCAACA TTGCGCACTG AATGGCGATG GCGCTGATGC GTATTTCTCC TACGCTCTng 60

50

CGTATTCAAC CGCTATGGGC ATCTCATACA TCTGTGATG CGCTATTAAG CAGCCCGAAC 120

CGCACACCGT GAG 133

(2) INFORMATION FOR SEQ ID NO: 2084:

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- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2084:

GGTAGGGGCA CTATTTTGTA TGTAAGGTT TTGTCGGCA GTGTGAAATC AACGACT

57

(2) INFORMATION FOR SEQ ID NO: 2085:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2085:

CCCCCCCCAA AAACCGCCCC CCCCAATTTG GCCTTTTCC AAGGGGGTG TTTTAA

56

(2) INFORMATION FOR SEQ ID NO: 2086:

25

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 114 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2086:

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AATAGCGAGA GCCCGACCAT CGCCTCCAGA TTGCGACTGA ATGGCAATGC GCTGATGCGT

60

ATTTCTCCTA CCATCGTGGT ATTCAACGAT ATGGGCACTC TCATACAATH GCTC

114

(2) INFORMATION FOR SEQ ID NO: 2087:

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(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 80 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2087:

AAGGGGGAAA AGGAACCCAA GGCCCCCTTC CCAAGGAAAT TGGGGGGTTG GAAAAAACCA

60

AAAATTTTTT AAAAACCCGG

80

(2) INFORMATION FOR SEQ ID NO: 2088:

55

- (A) LENGTH: 66 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2088:

10 GGGGTAAGTG GTTGAGACAG GAACTTTACA AGAGGTGTTT CGTCATCCTA GAACGACGCT 60  
TGCTCA 66

(2) INFORMATION FOR SEQ ID NO: 2089:

15

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 62 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2089:

25 ATCAATGTAT TACGTATCGA AGGTGAATTA TATCATACTG CTAAATATGA CGGTTTCACA 60  
TC 62

(2) INFORMATION FOR SEQ ID NO: 2090:

30

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 50 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2090:

40 GAATTCGCTA TCCTGAAATC CTGAGTCGCT GTCCTGAAAT CTGAAATCGC 50

(2) INFORMATION FOR SEQ ID NO: 2091:

45

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 74 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2091:

CGGGGTTCCC CCGTTCAATT CCCTTTGAGT TTTCAACCTT GCGGGTCGTA ATTCCCCAGG 60  
CCGGAATTGC TTAA 74

55

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2092:

ATTGTTGGGT ACGGTGGTGG GTTAATAATC CAAACACGTT AACTACCCG TTTTAGATAT 60  
ACCTATACAA 70

## (2) INFORMATION FOR SEQ ID NO: 2093:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2093:

GTTTTGGGTC TTGGGTATTA GTTTAATCTC CATCATGGTT AATTGGTATG GTATTGGTAT 60  
TAGTAATCAT GTATGATGGG CTGGGCGG 88

## (2) INFORMATION FOR SEQ ID NO: 2094:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2094:

TGGCCATTGA GGCGCATTAC GTACTACGGC TTGTCGTAGG GACAATTATT AT 52

## (2) INFORMATION FOR SEQ ID NO: 2095:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2095:

AGTTGATGCA ATGAGTGATG CAAGGCGACT GAAAAGTTGG TATGAATGAC AAAACTTTAA 60

## (2) INFORMATION FOR SEQ ID NO: 2096:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2096:

ACTTAAATC TAATACGGTA TTTTCAAAAA CGAATAAAAG TTACCTCTTG TCT

53

## (2) INFORMATION FOR SEQ ID NO: 2097:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2097:

AACTTAATAT TGCTACGATA TGAACGGCAT NAACATACTT AGCGnTGnTC

50

## (2) INFORMATION FOR SEQ ID NO: 2098:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2098:

CAAAATAAGA AATTAAATTAA GAAAATGCCA AGATGCCAGA TGCCATCGGC GGAAAGGAAA  
TTGCACGTAC GG

60

72

## (2) INFORMATION FOR SEQ ID NO: 2099:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2099:

CCACCCAAAC CCAAAAAATA AAGCCCAAAA AATTGCCAAG GAAGGAAAAG GAAAATTGTT

60



## (2) INFORMATION FOR SEQ ID NO: 2100:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2100:

CACCAATTTTCTGGGCT GGATCTCGAC CTAAGTCCTG TAATAATTGA CGTTGAACAC 60  
 GAATTAATTT ATTAATTGTT TCTACCATAT GCACAGGGAT ACGAATCGTA CGTGCTTGGT 120  
 CAGCAATTGC ACGAGTGATT GCTTGCTCTAA TCCACCATGT TGCATATGTT GAAAACTTAA 180  
 ATCCTTTGTT AAAGTCAAAT TTTCAAC 208

## (2) INFORMATION FOR SEQ ID NO: 2101:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2101:

TAATGAAATT AAGTAAAATA AAAATTATTT CATGGATTGC TTCTATCTAT ATCGAAATAT 60  
 TAAGAGGAAC ACCAATGTTA GTTCAAGTAT TTATCGTATT CTTTGGTATA ACTGCTGCAT 120  
 TAGGACTAGA CATTTTCAGCT CTTGTTTGTG GAACAATTGC ATTAGTTATT AATTCCTCAG 180  
 CTTACATTGC TGAAATTATT CGTGCAGGTA TAAATGCTGT TGATAAAGGC CAAATGGAAG 240  
 CCGCACGTAG TCTAGGTTTG AATTATAGAC AAACGATGAA AAGTGTAATT ATGCCACAAG 300  
 CAATTAAAAA TATTTTACCA GCTTTAGGTA ATGAATTTGT CACTTTAATT AAAGAATCAT 360  
 CTATTGTGTC AACCAATTGGA GTTGGCGAAA TTATGTTTAA 400

## (2) INFORMATION FOR SEQ ID NO: 2102:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2102:

## (2) INFORMATION FOR SEQ ID NO: 2103:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2103:

TTTAAGGAGA AAGGTCATTG GTATAATCTT GAGAAAGAGT GGCAAGAGTT CTTAAACTCT 60  
 GGGAAAGAGG TGAAAAATAT TAAAATGGAA GTAAAATATA GCGGTAATAG TCAAAGACCG 120  
 ACTATATTTA AAGTTGAATA TGAAATTAAT GGTGAAAGAA ATATTAGAAG AATATTAAAT 180  
 AAGTAGAGGT GCCAACATGA CATTGGAAGA GAAGCTTAGC AAAATATACA ATGAAATTGC 240  
 GAATGAGATT AGCAGTATGA TACCGGTAGA GTGGGAAAAA GTATATACAA TGGCTTATAT 300  
 AGATGATGGA GGAGGTGAAG TATTCTnTAA TTATACTAAA CCAGGnAGTG ATGACTTGAA 360  
 TTATTACACC AATATACCTA AGGGTATAAC ATTCCGGTGC 400

## (2) INFORMATION FOR SEQ ID NO: 2104:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2104:

AACCATCATA AAATGTTATT AAACCGTCAT GGACCGCGTC ACCATTTAGT CCT 53

## (2) INFORMATION FOR SEQ ID NO: 2105:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2105:

AAGCACAAAT TAGCAGAGTG TTTTAATTTA AATGAACAAG TACCTTTACA ATTTTGGAT 60  
 AATGTAAAAG TTGGTAAAAA TAATATTTAT GnTGCTTTGG AAGAGTTTGC CAACAA 116

## (2) INFORMATION FOR SEQ ID NO: 2106:

- (A) LENGTH: 61 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2106:

10 AATTTGCAAA AGAATCATGG ACAATTGAAA GCAAAAAGGA TCATCATTAA AATTGAACTG 60  
C 61

(2) INFORMATION FOR SEQ ID NO: 2107:

15

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 60 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2107:

25 GAACCAATGT TAAGCTAATT AATGGAATCC TAACAGCGTT AATCTATTTA AAAAAGTTAA 60

(2) INFORMATION FOR SEQ ID NO: 2108:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 126 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2108:

ATTTGAAAT GAATCTGTGG AACATTTTGC TAATCATGAG GATAAAATCA TATGATGTTG 60  
40 AAAGCGAGAA TGGGATTACG TTAAACGTGG GCGCTGCTAA TTAAAGCACC TTATTTAGTG 120  
GAAGAT 126

(2) INFORMATION FOR SEQ ID NO: 2109:

45

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2109:

55 ATAATGTTAA AAAAACGGCA ACTAATCTTT TCATACTAAC AATGATTATA TGTACAATAA 60

CGTTAATAAT GCTAGATAAT TTTAAAAAAA TGAAAAACCG TGAATATCAA AAAGAAATAG 180  
 5 CAGAAAAAAA TAGACATATT AATACATTAA TTGCTGAACA AGAGCGACAT AGAATTGGTC 240  
 AAGACTTACA TGATACGTTA GGGCATGTGT TTGCAAGTTT ATCATTAAAA TCAGAATTAG 300  
 CTTATAAACT AATAGATGCT GATGTAGANA AAGTAAAAGC TGAATTATTA GCAATTATA 360  
 10 AATTATCTCG TGAATCATTG nACAAAAGTC GAGAAATTAN 400

## (2) INFORMATION FOR SEQ ID NO: 2110:

(i) SEQUENCE CHARACTERISTICS:  
 15 (A) LENGTH: 61 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2110:

AAGATTTAAT ATCGGGGGTA ATGTTGATTT TCAAATATCG CGATGTGCTT GTACCACCAT 60  
 25 T 61

## (2) INFORMATION FOR SEQ ID NO: 2111:

(i) SEQUENCE CHARACTERISTICS:  
 30 (A) LENGTH: 55 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2111:

TATACTAAAT TATGGCAACT TGGCTCATAT AGGTCGAGTT ACCAGACATA TTCGG 55

40 (2) INFORMATION FOR SEQ ID NO: 2112:

(i) SEQUENCE CHARACTERISTICS:  
 45 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2112:

CGAATAAGTT CTGGGCCTTT TGTTGTTTAT TAGCTTGTTT CTGTTTTGAT TGTCTGCCA 60  
 TTTGAACTAC ACCAACCTTT TAAATTTATT CTAGTGACAG GATAACTAAA ATATATTTCT 120  
 55 TATGCAATAA TTCCTATTG ATAAGCATTT TCAGATTTTA GTTGTAATT TTGCCCTAAT 180

AATTTATAAA GAATAAATTC GTCTCCTCTT TGACCTATAA TATATTGAnC ATTATAAGCC 300  
 ATGCGATTCA TTCCAGACAC AGCCATAAAC TCTTGTATTAT CTATCATTTT AAATACCATT 360  
 5 TTTAATTGGG CTTAATGGGA CATTCCGTAT TAAATCATT 400

(2) INFORMATION FOR SEQ ID NO: 2113:

(i) SEQUENCE CHARACTERISTICS:  
 10 (A) LENGTH: 87 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2113:

TGTTTTCAAA GCATGGTATA AATGCTTTGT AACATAGGTT TTGCCTACAT CAGTATTCGT 60  
 20 ACTTGTAATA AAAATCCTCA TAAAAAT 87

(2) INFORMATION FOR SEQ ID NO: 2114:

(i) SEQUENCE CHARACTERISTICS:  
 25 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2114:

TTTACAAGTT AATATAnCA CTAAAAATTT TTAAGTCAAT AAGAATATAT 50

35 (2) INFORMATION FOR SEQ ID NO: 2115:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 52 base pairs  
 (B) TYPE: nucleic acid  
 40 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2115:

45 TGTGCATAAA ATCCTTTTAC TTTTGTGAAT TGATTGTTAT CTTTAACAAT TA 52

(2) INFORMATION FOR SEQ ID NO: 2116:

(i) SEQUENCE CHARACTERISTICS:  
 50 (A) LENGTH: 113 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2116:

ATTTAnAACC CAATTCCCCA TTATTTTTTA AAACGGATTC CATGGGTGGA CCATTGGAAA 60  
 TTTTAAAAAA ACCATGGCCC CATTCCAAAA AGTTAGGATG GCCAAAAAGC CTT 113

(2) INFORMATION FOR SEQ ID NO: 2117:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 93 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2117:

GATTTATCAA CTATTTCCGT ATTTTGATTA TCTCCATACA ATTTCCAATC CTCTGGCTTA 60  
 TCAATAAATA ATGATAATGG CTTATCTTTC GAT 93

(2) INFORMATION FOR SEQ ID NO: 2118:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2118:

TGATTACCTT GAnACATGAC TTTnCTGAn TGGTAAATAT TTACAGTTGT 50

(2) INFORMATION FOR SEQ ID NO: 2119:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 217 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2119:

AGATATAAAA TATAAAAAAT TATTAAAAGC TATATCCAAT CAAGACTTTA AAGGGTTAGT 60  
 TCCAATATC AATCAGAATG ATAATTATn TGAAATATAT ATAATTAACA ATACTAAAAA 120  
 CTTAATATAT CATTTATATG ATGATAGAGG TCTATGGCTA GCTTTTAATA ATAATGAAGA 180  
 TTATGCAAGA TATnCTGAAA AATATAATGA TTTAATA 217

(2) INFORMATION FOR SEQ ID NO: 2120:

- (A) LENGTH: 75 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2120:

AGACTTAGTA AAGTTAGATC ATCTAAAGAT GAGCGTAAAA TTTATATTTA TTAAATAAT 60  
GGATGATATA TCTAA 75

(2) INFORMATION FOR SEQ ID NO: 2121:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 87 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2121:

CACCACCTAC ATTTACTATA TAAATGTAG GAATGGTAGA TTGATTAGA TAACTGGAC 60  
GTATCACTTT AAGTGCTTTT TCAAAGA 87

(2) INFORMATION FOR SEQ ID NO: 2122:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 70 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2122:

TGTTCTTTAG CTAAAGCTTT AGCTTCTTCA TCACTTTTAA CTTCAATAAAA ATCTACACCA 60  
GTAGCTTCTT 70

(2) INFORMATION FOR SEQ ID NO: 2123:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2123:

TAAATCTAAA AGGAGAAATG CTGAAGATGA GAGAGGTATT TTTGAAATGT 50

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2124:

10

TTAAAGGGTA ATTGTTTAA AAAAAGATTA AACCGAGGAC TTTTAATTGT TAAAACCATC  
CCT

60

63

15

## (2) INFORMATION FOR SEQ ID NO: 2125:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2125:

25

TGTAAACGAC TATTACATGA TCACAATCCA TTCAGCGCCA TTATATAAAG GTACTTAATA  
TAGGACATCA TTCGCAGC

60

78

30

## (2) INFORMATION FOR SEQ ID NO: 2126:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2126:

40

TTTGGTCGTG TGCAAGACAG AAGTCGACAT ACTCCAATGA AACATCATGT

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## (2) INFORMATION FOR SEQ ID NO: 2127:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2127:

TTTGTGTCGA TGCGCTTTTT CACTTCTTCT GAATGCTCGA AATCATTCGT

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- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2128:

TGTCTGAAAT GATCATTAGG ATTGCTCCAG CTCAATGTCA GTnGnAATGA

(2) INFORMATION FOR SEQ ID NO: 2129:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 65 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2129:

TCCAATTACC TACAAAGTGA GTGCTTTCTT GACCAAGTCA AAACGAACTT TTATATTTGT  
 CCAAC

(2) INFORMATION FOR SEQ ID NO: 2130:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 61 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2130:

TTCCAAGGTG TCGCTGACTT TCAACACACT GAATATATAC CTGCCAGTCG GCTGGTCATG  
 C

(2) INFORMATION FOR SEQ ID NO: 2131:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 92 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2131:

AGTTCTTCAG TCCAAATGCG GCATGTTGAC CCACCATAGG CGAGGGCATT TTCACCACGG

## (2) INFORMATION FOR SEQ ID NO: 2132:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2132:

CCCCTCGAGT TTTTTTTTTT TTTTTTTTTTA CTGGAGCAAA ATGAATTTTT TTTATTGTAC 60  
TTCAGGGCAA CAAGTCAACA GCTGCAGGAA AACAAAACCA GGTCCAATCT ATGATCTAAG 120  
AGGAAGTCAG GAAAGGCTTG GAAGAGAGAT CCAAAGGCCA TCCTGGCAAG GGAATCCCA 180  
CATGAGAATT CCTGGGAGAG AGCAGGCCCC AGGCAGCAAG GTCATCTTGC CTGCTTCTCT 240  
GTAAGTTAAT CCTTCACAGG GAGCCAAGGC TTCTCTTGAC TGCTTGGACA AGAGGGTAAG 300  
GGCCCTGGTT GCAGGATTG CCAAGTGAAGT CATCCATGTC AATAGACCAG ATCATGGCTC 360  
CTCCCAGGTT AAATTCCTTA AGAACTGAAC CTTGnCTCCA 400

## (2) INFORMATION FOR SEQ ID NO: 2133:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2133:

TTCATCATAC AACATTACAC TTTGTATGAC TAAACCCAAA TTAACGATAT 50

## (2) INFORMATION FOR SEQ ID NO: 2134:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 59 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2134:

GTGGCAAGCT TTTTAAAGT CTGACTGCCA TCGACGGATC TATGTTAACA GGTGGATCT 59

## (2) INFORMATION FOR SEQ ID NO: 2135:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2135:

ATCAAAGTCA TCTnCATGGT CnATCACACC ACGCTTTATA TGGTAATTCT

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(2) INFORMATION FOR SEQ ID NO: 2136:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 52 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2136:

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CGGGATCTGA GGTGCTATC TGCAATCTGC AATCGCTATC TGCAATCTGG AG

52

(2) INFORMATION FOR SEQ ID NO: 2137:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2137:

nCTCAACCAC CCACACAACA ACACAACAAG CAGCACCCAC ACACCACACA

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(2) INFORMATION FOR SEQ ID NO: 2138:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 87 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2138:

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TGTATTGTCA TTGTAGACGT GTGTAGCCAA ATCATAAGGG CATGTGATT ACGCATCCAC

60

CTTCTCGGTT TGTACCGCAG TACTTAG

87

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(2) INFORMATION FOR SEQ ID NO: 2139:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 77 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2139:

TTCACCGTTG CGCAACGTTT AAGTTTGAAG TTCGTTTGGC ATGTTGAAAT AAGCACCAGT 60  
 5 TACACCAAAA CGCCAG 77

(2) INFORMATION FOR SEQ ID NO: 2140:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 148 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2140:

ATCTTCTAAC ATTCACCTTAG TAGCGTnATT TTTCGCTTAT AATGAAATGT TAAGCATATG 60  
 20 CGGGATTTAT ATTTTAAAGA GACCTTTAGA TACCATATAT ACCTAGGTTA TTGAAATAT 120  
 GGATACCTTA TATAAGTGAT TTGCAATA 148

(2) INFORMATION FOR SEQ ID NO: 2141:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2141:

GCTGGCACAT AGATGATCGT CAAGTCGATC TCGCCAGTCT GAAGTCAAGA 50  
 35

(2) INFORMATION FOR SEQ ID NO: 2142:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 60 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2142:

TTGTTGTAAA TACTATCACT GTACATGGGT GCTATCAAAA TATTGTCAGT TCGTAAAATA 60  
 45

(2) INFORMATION FOR SEQ ID NO: 2143:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 135 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2143:

GTAGTATATC TTATTAATTG TATCATGAAG CAATTTAAAT ATCATGACAA TTTAGTTTGA 60  
10 AAAACACACT TTGTGTTGAC GTTGTGTTTT ATGGGATATA GnATAGTAAG GAATGTAAAA 120  
TGAAGGAGTG AATGC 135

(2) INFORMATION FOR SEQ ID NO: 2144:

15

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 57 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2144:

25 TTTTAAGGTT TGAAGAAAAA AAGTTTTTAAA AATTCAAGGA AACATTAAAT TAATTTA 57

(2) INFORMATION FOR SEQ ID NO: 2145:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 148 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2145:

TTTCGAAAGT TTGATAGTCC ACCTTACATT CTCCTACTAT TTTCTGATGT CCCAATACTT 60  
TATATTATTT AAAGTAATAT AAAAGCAATC TCTTTTGAAG ACATGTTAAC CTAAATATTT 120  
40 TTATATATAA TATATATATA AAATATA 148

(2) INFORMATION FOR SEQ ID NO: 2146:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2146:

55 GTTAATACAA TACGGTTAAC AGCACCTTTA CGnTAGTTGC TTTnCTGCAn 50

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 68 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2147:

AATCCCCTCT TTTCTCTATT TCCTAAATCA TAGAACTTTT AACAGTAAAA TTCAATCATT 60  
AATACATG 68

(2) INFORMATION FOR SEQ ID NO: 2148:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 92 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2148:

AGGTCCATTT GTAATTTATA ATGTTGACTA ATAACATCTA CAGAATTTAA CGTTCCCAT 60  
CCTCGCCACT GATTGTAAAT AAACAAACCA TA 92

(2) INFORMATION FOR SEQ ID NO: 2149:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 69 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2149:

ACCATCCATT AAATCAGGAT CTTCACTAAT AAGTGCTAAA TTAGCAGCGC CACGTTTAAC 60  
GTAATCCAT 69

(2) INFORMATION FOR SEQ ID NO: 2150:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 384 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2150:

TCAAAATATA TACGATCACC TTTCTGTAAA ATCACACTAT TTTTATTTGC CGCTTCTGGA 120  
 TGTGTGTTTAA AAAATTGTTG GCCAACTTCA CCTTTTAACG TGGCAAATTG ATAATTTCTT 180  
 5 GGTAGGTCAT GTTGAATTAA CCAAATGACA TAGTTATAAC AATATATACA GTTTCATCA 240  
 TAATATACGA TTGGCATAAT TTATTCGCTC CTTTAATAGT ACTTATAGTC ATTTTTCCTA 300  
 10 ATTTAAAAAC ATTTAAACAA GGTGTGCTACT TGATAAGTCC TCGCGACACG AAATTGCCAT 360  
 AAAATTTATT TTTCAGnTTh ATAT 384

## (2) INFORMATION FOR SEQ ID NO: 2151:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 83 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2151:

TGTGTGTTTAT CACTATATTT TAAAAATAGT CTATAAGGCT TATCAGATGA AGTAGCTGCT 60  
 25 GCGGTAAACAC CACCACTAAA TGT 83

## (2) INFORMATION FOR SEQ ID NO: 2152:

30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 73 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2152:

GTATTCGTAC ATTTTTCAGC AATTAACCAA GATGGTTACA AATCATTAGA AGAAGGTCAA 60  
 40 GCTGTTGAGT TTA 73

## (2) INFORMATION FOR SEQ ID NO: 2153:

45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2153:

CCCCCCTCCC CCCTCCcnc CCCCCCCCCC CCCCCCCCCC GCCCCCCCCC 50  
 55

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 55 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2154:

TATTTTAGGC TTAGCATTGA TGATGTTGCT CATTTTCAAT AATATAGGAA TTATT

55

(2) INFORMATION FOR SEQ ID NO: 2155:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 68 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2155:

ATGCTTGCTG ATATAATGTA ATAGCGTCGT GATAACGTTG CTGGCTTATA ATATACATT

60

GCGAGATT

68

(2) INFORMATION FOR SEQ ID NO: 2156:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 68 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2156:

TAATCTTTGT CGTCGAAATA CAACTAACT TTTGAGTTTA ATGATGAAGG TACGCATTGT

60

GTATCACT

68

(2) INFORMATION FOR SEQ ID NO: 2157:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2157:

TCATTCATT TCCTCTTTTC TTTTATTTAA AATGTTTCATG GTTGTTTCTC TTAATTCTGT

60



AGATGCTAAA TGGTCAAATT GAATAATTGT TTCTAGACTC ATTCATAAA TTTCGAAAAA 180  
 TAATTCTTCG GGATTACGTT TTGTATTTTC TCCAAATGTT TCATAAAGCA AATCAATTTT 240  
 5 ATCAGCAACT GAAAGTATTT GGCCTTCTAA TGAATCATCT TTACCTTCTT GCAGTCGTTG 300  
 CTTATAAACA TCTCTATATT GTAATGGAAT TTCTTCTTCA ATAAAGGTCT CTACCATTTC 360  
 10 TTCTTCAACT TGCGAAAATA ATTTTnnTAA TTCACTACTC 400

(2) INFORMATION FOR SEQ ID NO: 2158:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 232 base pairs  
 15 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2158:

TATTTTTTTC TTCTAGGCAG TGTTAATACT GCITCAATTT GTTTTTTACT AAATTGATAT 60  
 TTCTCTATGA TTGAATTAAT CAATTGATTG TCCATTTACT TAACCCACAC TTTTCTTAA 120  
 25 ATTTACTCAT TTATTTTAAAC ATATTCTAAA ATACTTCTAT TAAGATATGA TACTTAATGT 180  
 AATTTTCACT TCCAAAACAT TTAAAACGAA TGATTAGGnC ATACTATATT nT 232

30 (2) INFORMATION FOR SEQ ID NO: 2159:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 60 base pairs  
 (B) TYPE: nucleic acid  
 35 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2159:

40 CCGTTTTTCC AAAAACTTGA TCATAAACCC GCTCCTTTTT TCATCATAAC AAAATAAGAA 60

(2) INFORMATION FOR SEQ ID NO: 2160:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 60 base pairs  
 45 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2160:

CGATTTACTG CACGACACAT TGCCACATCC TGGATGGGCA ATCTTTTCTC TTACCCGTCT 60

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2161:

ATTAGTTGAA GTTTTGTAGC AATTGAAAGA TATTCAGGGT CAAATAAAAA CGACAAAAAA 60  
 AGAATATCAA CAGACCAACA AAGAACTTTC TGCTGTAGAT AAAGAAATTA GAAATATAGA 120  
 AAAAGACCTC AATGATACAA AAAAAGCACA AAATGAATAC GAAGAGAAAT TGTATCAAGC 180  
 ATATCGATAT ACCGAAAAAA TGAAACACG TATTGATAGT TTGGCAACGC AAGAGGAAGA 240  
 ATATACTTAT TTTTTCATG GCGTCAAACA TATTTTGAAA GCTAAAAATA AAGAATTAAA 300  
 GGGTATTTAT GGTGCAGTTG CGGAAATTAT TGATGTGCCA TCTAAATTAA CTCAGGCAAT 360  
 TGAAACAGCA TTAGGTGCTT CATTACnACA TGTCATTGnA 400

(2) INFORMATION FOR SEQ ID NO: 2162:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 66 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2162:

GTGCGTACCA TTGTAATCTT CGTAACTGG GTAATTATTT TGTCTTTCTT CATCATAAAG 60  
 TAATAA 66

(2) INFORMATION FOR SEQ ID NO: 2163:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 72 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2163:

AGAATGGTAA CATGGTAATA ATAAATATA AACAGAATAC TAGTTAATAC ACTTTATACT 60  
 AGAAAAAGAT AT 72

(2) INFORMATION FOR SEQ ID NO: 2164:

(A) LENGTH: 325 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2164:

10 CGATAATCTG TTTTTTTAAA TCTGTTGCTG TTAGATTTAG CACCGATTCTG TTAACTTCA 60  
 AATAATTTTT ATTACCTTTG GAAGAAAGTG GAACTATTGT AACTGTTTCT TTTCCTTTAT 120  
 TGTCTTTGTT ATCTAATATT ACACAAAAAT GATTACCAGA AAACCTCACTT CCAATATTAC 180  
 15 TCCCTAGTTT TACATATACC ACTGTTCTCT TACnATATGA TTTATAATAT CTTTnTTTAT 240  
 TGCTTGTAAC ATCGCTATGT ATAGCAATTG GAATAAACT CTAGCCAATG AGGCATGTnT 300  
 ATAACTTTCA TGTTTTTACT GTCGG 325

20

(2) INFORMATION FOR SEQ ID NO: 2165:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 121 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2165:

TAAACCCCTT TTGGGTAAAA AAGTTTGGA AAATTTCCCC GGGGGGAAAG GCCCCAAAA 60  
 AATTGTGCCC CTCnCGGG GAAAATTAAA ATTTCCCCC TTTTAAAAGG GTTTCCTT 120  
 35 T 121

(2) INFORMATION FOR SEQ ID NO: 2166:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 52 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2166:

CGGACAGTTA AATGAACTGT TCAATGAGCC CAGGATGTTG TAAATGGTTC GG 52

50

(2) INFORMATION FOR SEQ ID NO: 2167:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 53 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2167:

ATTACAGTAA AAAATGGATT AACATTACAA GCGTGTCTTG CTAGAGCAGC CAA

53

(2) INFORMATION FOR SEQ ID NO: 2168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2168:

AAAGATTATT TATTTGCACT CATTAAATTGT GATTTAATAC GGTCAGCTTT GTTTGAATGT

60

ATTAAATTAC nTTGAGCAGC TTTGTCTACT AACTTAACTG CTAAGCTTAC TAAT

114

(2) INFORMATION FOR SEQ ID NO: 2169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2169:

AAGGAACCCC CCCCCCTTAA AATTTTTGGT GGTTTTAAAA AATTCCTTTG GATTATTAC

60

CTTTATTCTTCT ATnATTTTCC GTTTGGATT TCTGGATTA AATTTCCCCA TTAAGCCATT

120

TCCGCTTCCC TTATTTTATn ATTTTCCAAA ATTTCCAAAG GTTCCATTTG GGATTTTGGC

180

AATCCTTTTT TATTAAAATG GCCTAAAAAT TTTT

215

(2) INFORMATION FOR SEQ ID NO: 2170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2170:

TATCGTTTTT AGAAATGGAT GTTCTCTCCA AAGATGATGG TATCTAACAT TATCTTATTG

60

GTATCATTAT GCAACnTTA CAAACATTT ACGCAAGATG ATACATTATC CAAC

114

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2171:

ATCACAGATG AGATAACAGA TCCACTGTAA CTTTACAATA AATAAATGGT ATCATAATTA 60  
ACACGTAAAT GGTTTC 76

## (2) INFORMATION FOR SEQ ID NO: 2172:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2172:

ATTATCACAA AATGTTGACA CGCAAAAAGT TGGTCAGTTA TCAATATGGT ATATAAATCT 60  
GAGA 64

## (2) INFORMATION FOR SEQ ID NO: 2173:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2173:

AAAGGCCAAC CAACCAAAGG CCAAAATTAA CCGGCCAATT CCAAGGGGTT AATTAAACCC 60  
G 61

## (2) INFORMATION FOR SEQ ID NO: 2174:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2174:

CACCCCGCAC TCTCCCATCT TTTACCTACT GGCTTCITTTG CATTGCCCTG GCACCTCCGT 120  
 CCTCAGCCTC CCAGGCTGTA TTCATTCATT CCCTTACTGA GCACGCACCA TACACCAAGC 180  
 5 ACCATTCAAG GTGAACCACT CAAATGAAGG CCTGGCTCAT TTTAATGGGG GACAATGAGC 240  
 ATTTTTGTGA CAATTTTCATG GAGTGATGAG TGCTGTGAAG AACTAAACAG GTCAGGTGTA 300  
 10 AGTGGCTCAT GCCTGTAAATC TCAGCACTTT GGGAnGCCGA AGCAAGTGA TCATTTAAGC 360  
 CCAAGAGTCA AGACCAGCCT GGGGnnACAT AGTGAGAnTC 400

(2) INFORMATION FOR SEQ ID NO: 2175:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2175:

ATATCGTTTA AACCATCAAC AAGATTTTAT AGATGCAACT TTTACTGCGC TGAATCAGA 60  
 25 TAGAGCACGT TTAAGAAG TGCCAGTTCA TGTTGAACTT ATAAGTTATA TTTCTAAATC 120  
 AAAATAAACT GCTATCTAAA ACGCAAAGTT GATCAAATA TCGATTTTGT GTTTTTTATT 180  
 30 GAGAAATTAT ATAGGAGTGT CAATCGATGA TTTATTGTGA ACAGAGCGTT TAATATTAAG 240  
 AGACTGGCAT GAAGATGATC TGTTACCTTT TCAAAAAATG AATGCGAATT ATGACGTACG 300  
 TAAATATTTT CCAAGTTTAT TGAGTTAnCG nCGTTCAGAA TTAGATATGA GACCTATGGA 360  
 35 TCGGTTATn AAAGATTATG GCCATTGGGA TTATTGCCnG 400

(2) INFORMATION FOR SEQ ID NO: 2176:

40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 71 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2176:

TAAATCAAGG AAAGACATTT TAAGGTACGA AGGTTGATAA CAAAAACCA ACAGATTTAG 60  
 GGGTATCAGA G 71

50

(2) INFORMATION FOR SEQ ID NO: 2177:

55 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 51 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2177:

GTTGAATTAG GCAGCACGAT TATTGATGCT GAACTGTTAG AGTCAGATAA G

51

10

(2) INFORMATION FOR SEQ ID NO: 2178:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 61 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2178:

20

TTAATTAATG GTATTTACAT ATTCATAACC AAAGGATAAA ATAATTGTGA AATTATTCAC

60

A

61

25

(2) INFORMATION FOR SEQ ID NO: 2179:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2179:

35

CATTTTACCA TGCAGCAAAT AATACAGGTG GTGCCGTTAA CAAACGTGAN

50

(2) INFORMATION FOR SEQ ID NO: 2180:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 73 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2180:

GCCGAACGAA TCAAATACCA TACCTAATTG ACTGCAGGCA TGTCCATATA GTGCAGTTAA

60

50

CTGTCTACAA GGC

73

(2) INFORMATION FOR SEQ ID NO: 2181:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 301 base pairs

55

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2181:

	TACTTTTGGC GATATTCGGT ATCGTTATTA CAGTTATTTT ATATGCAATT AAATTGCCGG	60
10	GTTCTATCTT TATCGGTATG ATCATCACAG CAATCGTTGG TATGTTCACT GGATTGATTC	120
	AAATGCCATC TGGTATTGTG GGTAAGATTC CAAGTATTGA ACCAACGTTT GGTGCTGCAT	180
	TTGAAGCGTT TAAAGACCCA AGTCAATTAT TAACGATACA GTTCTTAATT GTTATTTTAA	240
15	CGTTCTTATT TATTGATTTT TTTGATACAG CTGGAACATT AGAAGCGGTT GCAnCnCAnG	300
	C	301

20

(2) INFORMATION FOR SEQ ID NO: 2182:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 54 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2182:

30	TTGATTTCGCC TTGGCCAGAA TTACTTTTGT TTTGGGCGTC ATTGCAAGTT TCTA	54
----	--	----

(2) INFORMATION FOR SEQ ID NO: 2183:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 118 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2183:

	TTAGTnACAT TGGGACATTT AACTGATCCA CCAGTACTTT TGGCGATATT CCGTATCGTT	60
45	ATTACGTTAT TATTGCATAA TGCGGTCACT ACGAGACACC GCACTGAGTC CGATATCA	118

(2) INFORMATION FOR SEQ ID NO: 2184:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 303 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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55



AGATAGTTAT ATAAAGATTT CATCTTCTGT ATTACATTGA TATTTT TAGG TCCCTGTATA 60  
 TAAAAATCAT ATGCCTCATC AACACATCA CTTTTATTTT TGATTGCAAT TTGATGTAAT 120  
 5 ATCTTTTGAC TAAAAACACG ATTAATCATA TTTCTATTAT CCATAGCTAC GCACCTCCTT 180  
 CAACATACAT TTAATGCTTA TCCTGTTAAT ATTATAAnCh ATTTTAAATG CCTATAGACA 240  
 10 TTATTTCTAT ACACATACGA TTATnAAATT GTATTGAAAC CAAATGATGG TTGCCAAACA 300  
 CAT 303

## (2) INFORMATION FOR SEQ ID NO: 2185:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 110 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear  
 20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2185:

CCGGGGTTTT GGTAAACCC TCCCAAnATT TTTTTTAAGC CCAAACCTTG GAAAAACCCA 60  
 25 GGCCACCCGT TGGAATTTTT AAGCCTTGGA TTAATCCGGT TTGGTTAACC 110

## (2) INFORMATION FOR SEQ ID NO: 2186:

30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 86 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear  
 35

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2186:

CCTATATTGT CACCCAATT CATTACGGCA CCTTTACCGA AAGATTTCTC CATATTTTTA 60  
 40 ATTACTGTAT CTAAAGCTTT TTGACG 86

## (2) INFORMATION FOR SEQ ID NO: 2187:

45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear  
 50

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2187:

TTTGCTAGAA AACATACCAC ATTTGCCAAT TATATTATTT ATTCTGATGT TTATTTTCGG 60  
 55

TATTTAGAGG TGATAAAATT TGTCAACTAT TACAAAGACT AAAATAAAAA TCTTTATTAA 180  
 TTATTTTATT GGTATATTAG CCTTGGCGTT TGCTGCTTAT ATATTATTTA AATAAGGTT 240  
 5 AGAGTGAAAC GTGTTTATGA ACTAGACGTT CTAGTATAGT TACTACAGCT TTAGTCAGAA 300  
 GGTATCATTG ATAAGATCAT ATTAAATCAA AGAGGCATTG ATATACACTA AAAAGAGGCA 360  
 AGATTACCTG CCTCTTTTTTA GTnATTAAAT ATACGTGTTA 400

## (2) INFORMATION FOR SEQ ID NO: 2188:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2188:

TTTTATAAAA TATCAGACAT TTTTGnTCAA CATACTCTC TTTGATGTT TCTAATACTT 60  
 TATCATTAA CATTACACCT TAAAGTTATG ATGTGGCATG TTTTCTTATA TTCATAACAT 120  
 25 CAATTTTATC A 131

## (2) INFORMATION FOR SEQ ID NO: 2189:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2189:

CGTAAATAT TTTGATTTAA AATGGAGGGT ATTAATATGA AAAGGTTTCAT GTAAATCTA 60  
 40 GGGGTATTCC AATATTATAA GGCAC 85

## (2) INFORMATION FOR SEQ ID NO: 2190:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2190:

CCCGAGGAAT ACATGGCATT AAATACACGT TTAATATTTA TAAAGGTGAC TTAATTTTGT 60

ATAATTGTTT ATCAGTGATA AAATATTTGC AATAAGAAGA GAATGACTAA ATAATCTTAA 180  
 TTTTCAGAA AGTAATTGTA ACCTTACTGG TCTTATGGTA ATAn 224

(2) INFORMATION FOR SEQ ID NO: 2191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2191:

AGCTTTTGTA GTTTTCTTAA GCACACCGGC GATTTGATTA TTACATAAAG GATTCCCTTT 60  
 TTTTGTTGTG AATATGAACC CTCTGTCAAC ATAGCTCGAA TTCCATCTTT TCAACATTTT 120  
 GTTTTCCAGT ATTATCTTTT TAAAAATTTC TACGGTTCTA GAATTGATGC TGATACTTCT 180  
 TTTTGAACCT ATAGTCTTTG TAGTGTCTTT GTATCCGAAT CCTTTCTCGT ATTTAATGCG 240  
 GTGAATTGTA CCTGTTATAT TGATAGTnTT GTTTAATAAA TCTATATCTT TTTCTGCAG 300  
 TGCTTGTAGT TCTCCTATGC GCATACCACT TAAAGCCTGT ACTTCTAAGA TGCTGGCAAT 360  
 TAAAATGCCA TTTGCTTTT GTAACCTATT ATCATTTAGT 400

(2) INFORMATION FOR SEQ ID NO: 2192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2192:

GACGACTGAG AGGCCGTTGA ATTTGACGTT GCCATATnTT CAAATTTAAC 50

(2) INFORMATION FOR SEQ ID NO: 2193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2193:

GTTGTTTTCA TATCAAACA CCGTAGAATA AACAATGAAT GGAATTACTT TTGCAATGAT 60

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 56 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2194:

CCAGTCACTG ACTACGTCTT CCTCGGTGCT GGCGGTGGAG CCATTCCCTT ATTACC

56

(2) INFORMATION FOR SEQ ID NO: 2195:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 69 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2195:

GTAGGGAAAG GAAAACTGC TTCCATTGGG AAATGTTAAA CCTTGTTCTT TGGTGATGCC

60

ATTGGATTT

69

(2) INFORMATION FOR SEQ ID NO: 2196:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 55 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2196:

ATATGACACT ATATTTTATA AACATACATT TAATGATTCA TTATACAATT GCCAA

55

(2) INFORMATION FOR SEQ ID NO: 2197:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 71 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2197:

GCCCTAGTTC AATCATATAA CCATCTTTAC GATACGATTG AATCTTTCCC CCCGGACGAT

60

TCGATGCTTC A

71

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 54 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2198:

AGTAGCACAA CAGCCATGCG GAGACAGAGA ATCGTTAGAG ATTAATGGAG ATCA

54

(2) INFORMATION FOR SEQ ID NO: 2199:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2199:

GGCGGTTTTA TATTTATCGT TGCAGTTATG CAAATTGTAC TTGGTAGAAG TATAGATTCT 60  
 CGTGATTCGA AAAAAGTACT TTTAACGGGA TTGGGAATAG TAATCATATC TAGCTTTATT 120  
 TGTGCAGTGA CACATAACTT TATATTATTT GCTATATCAA GGTATTTC AAGCAATTGGT 180  
 TGCAGGAATTA TTCCTCTCGT GACTTTAACT TTATTAGCCA AACTAAGTAC AGATAATGGT 240  
 AGAGCTCAAG CTATGGCGAA CTATCAAATA TTTTATCAT GTGCACCAGC TTTGGCACCA 300  
 ATCTTAGGGA GTACTTTAGG TGGCAAGATG GGGATATATT GGTATTTTAG TTTTGGGCT 360  
 CGTTATATCT ATCGGTATTA TTTTGGGATA nCTnTTAA 400

(2) INFORMATION FOR SEQ ID NO: 2200:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2200:

GGATATGCGA TGGATGACGC ATTGCTATAT CGGCAATTGn GAAGCTGCTG

50

(2) INFORMATION FOR SEQ ID NO: 2201:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2201:

ATCGAATATC ACTACTATCT CTTTtAAAGT ATCTACAATC TCTCCAATCT

50

## (2) INFORMATION FOR SEQ ID NO: 2202:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2202:

TCGACAATCC TAATGCAATT GCTTCATGTG GtTGTGGTAG TTCATATTAG AACTGCAAAA 60

GTTGCAGGTG ATCCTGAAAA TTGCTAATAA AATAAGTTTT TAATGGTTAA CCCAATTTTT 120

GGGATACAAA TTGATATCAA TAACGATTAA GGACATATTT GATTATGTCC TATTTTTGCG 180

TAAAGATATT TTGTTTTATT AAAAAGCTTA TTGAAAATTA AGAATCTGAC TATAAATAGT 240

ATTTTAAATG ATCGTGATAG CGGATACATT TTTAATCGAA ATCAGGCTAC GAAAAAATTA 300

ATTAATTTTT TCACAATCTG ACTGAATCTT GCTTGAAAAT ATAACATAAA AGCTATAGAA 360

TTAGTATTGG ATTAAAAATG TCTTTTTTGT GAACATCACA 400

## (2) INFORMATION FOR SEQ ID NO: 2203:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2203:

GCGTTGTCCT TTTCGTGACA TGAAACAATG TGGAAAACAT AATTAAATnn AGGGAAAGTG 60

TGAATAGTTA AAAAATTAGT ATTGTGTTAT AAAAAATAAT TAATACTGTT AGGATTTTCAT 120

TAACTAACTT AACGTTGGTT CAAAAATAGT TAAAAAGAGG TTAATTCATA GCGCAGTATC 180

TCACTTATAT AATGATAGTA GATTGTTTCG ATTACGTAAT TGAATTAATC ATATAAAAAT 240

ATATTAAGAC AAATTTATAA ATAGATTGGG AGAnTAGTAC TGTGAAATTA AAAACGTTAG 300

CTAAAGCAAC ATTGGCATTG GGCTTATTAA CTACTGGTGT GATTACATCA GAAGGCCAAG 360

CAGTTCAAGC AAAAGAAAAG CAAGAGGGng TACCACCATT 400

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 136 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2204:

10 GTTATTTTGT ATGGTTAGTC TTTAAAATAn ATATAGATAT TAAATATTTA TTTTACGAAT 60  
 TGTTAAGTAA AGAAAAAATA TTAATCAATC CGGGTTACAT TTATGGCAGT AAAGAAAAGA 120  
 15 GTATAAGGCT ATCTTT 136

(2) INFORMATION FOR SEQ ID NO: 2205:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2205:

TTTTATTTTT TCGCAATGAA AAACAATCTT TCTGCATCTT CATTATGTTT ATCTATATT 60  
 AAATCAGTAA ATGTTTCAAC ATGTTTAAAA CCAACTTGAG CTAACCAAGA CAAATATGTC 120  
 30 TTTTCATCAA ATGTTCTCTG AAAATGAGAC TCATCAAATC TTGAATATGT TTCATCTTCA 180  
 TGTCGAATGA AAAATGTCTAT ATCATGATAA ACACCTTAAAG GTAAATCTCC TTGCACAGCA 240  
 TCCCATGCTA AAAAAATGTC CCCTTTATCA TCAATATAAC TTTGATTATT AAACAAAGTC 300  
 35 ATCATTTTTAT AAACAGTATG TACATCAGAA ATAAATACAC CTGAATCAGT CAGATGATGA 360  
 TAAACATTGA TGAATGTTTC AATCACTGCA GTTTCATCTT 400

(2) INFORMATION FOR SEQ ID NO: 2206:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 379 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2206:

50 TTGAATATCA TATAAAAACA TCAGGTTCAA AGTTGACTAC TCTTAATAAT ATAAAAATAA 60  
 GAATTAAAAA CATTAAACGA TACTGCTCTG AGAACTTGCT TTAAACAAA CTTGATACAA 120

GTCAACTCGG AGATATGAAA GGAGCnATTA AATATGCAGT TAAATTTTAC AATTATCCAA 240  
 ATGAATATTT GTTAACTAAT GTCAAAATTC CTAAAAGAAG AnAAACAATA GAGGATATCG 300  
 5 AAAAAGATGA ATCTAAATG GTACCACTAT TTAGAAATGG AACCAAGTCC TACnGATACG 360  
 TGATCATATA CTAATGGAT 379

## (2) INFORMATION FOR SEQ ID NO: 2207:

- 10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 137 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2207:

20 CATCTTGGGA CGTTTTAAAA AGTAACGTAG CGAAGACTAT TGAACAACA ATGAGAACCA 60  
 ATGCTAGAAG GATCAAAAAG TATTTTAAAA ATTTATTCAT GATTGATGCT CCTATATTAA 120  
 ATTTnTGTTA AATCATA 137

## 25 (2) INFORMATION FOR SEQ ID NO: 2208:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 72 base pairs  
 (B) TYPE: nucleic acid  
 30 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2208:

35 GCGCCGCTCT GTTCATTTTA CCTAAATCCA ACGTTTCAGG AATAGATGTT TTCAAACCAC 60  
 TTTGAAATGG AT 72

## 40 (2) INFORMATION FOR SEQ ID NO: 2209:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 52 base pairs  
 (B) TYPE: nucleic acid  
 45 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2209:

50 ATGTAGCAAC TAAAGATGAT AGTGGATAGC GACACGGTCA ATAAACTGCC TA 52

## (2) INFORMATION FOR SEQ ID NO: 2210:



- (A) LENGTH: 206 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2210:

10 TTTTTTATGT TCTTTTTTAA TAAGAGGGAA GTGAAGTTGT ATAAAAATGT ATTAAATATG 60  
 CACTTTTTAT ACAITTAACGA TTCATATATG TCTATTATGT ACCAAATTTA TAATTTGTAT 120  
 AATTTTCGAA CTGGTTAAAT TCGAAAAATA TCACTAATAT ATnTAGATCG ATGTGTAACA 180  
 15 TTACGTTCTA nTAATTTAAT GTTGCA 206

(2) INFORMATION FOR SEQ ID NO: 2211:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 60 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2211:

ACGATGTATT TTGATATCGT TACCAAAGTC TTTTAATAAC TCATTTTCAT CTAAATAAAT 60

(2) INFORMATION FOR SEQ ID NO: 2212:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 331 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

30

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2212:

40 TGATAAGGTT TGTCCCATCG CTATTTGAAA TGATGCATTG TAAAAAACTA TCATTTGTTG 60  
 GTAATATCTT AGTTCGATGA CTTTCTTTCC AATCTTTCCG TGTCATAGAG ACAAGATTTT 120  
 45 TTGTAGCTAT CTTAGTTGCT TCTTGAATGT TCATTTGTTA TTCCTCCTTT TAAGATGTTT 180  
 GTnTTTCTTT AAATGCTAAA ATAATTGATT TCTTTTTATC ATTCGTGAAT ACGAAATTTT 240  
 CGTATTCATT ACCTAAAAAA ATATCATCAT ATTTAACATT AAAAGCACTC ATATACTTAG 300  
 50 AAAGTAAACT AACnTTAATG GntGTAGAGT C 331

(2) INFORMATION FOR SEQ ID NO: 2213:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 61 base pairs

55

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2213:

AGCATAAACC AAAAGATGCG GATATACTTG AACGCGTCAA AGATATACTT AATAAAAAAG 60

10

A 61

(2) INFORMATION FOR SEQ ID NO: 2214:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 56 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2214:

TCTATTTGAG TTTACATTG ATTAATGAA TGACAATTAT ATGAACCTGA CTGGT 56

(2) INFORMATION FOR SEQ ID NO: 2215:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2215:

35 ATACCACTAC TATACAGTTA AATTAATATA CGTTAAACT TTAATCCGAT ACATTGGTTA 60

AAATGATGTT CCTCGCTGGT GGATCGAGAC ATACTTCGCT CTGACTTCTT TAGTCAGTTT 120

TTTTTCAGCT TTTTAGGTGT AATCACTGAC TTTGTTACAT CACGTCAAAT TTACAGTCGC 180

40 TATTATCTTA ACTTATCnAC GCTTATCACA CATCAATTCA GATATTATAT TGCATTGGCG 240

nCTATCACTT TGAACCTGCT GTGACTGGAA CTACTGGCTG TCAnGAGCGA GGGCTGATAA 300

TGAGCATAAA GCAACATATA AGTAATACGG CCGAATATGT AAATTCGGCA GCTTTAGGCA 360

45

ATGCTGCCCCG GGCATGACTA GnACATTCAc AAGAAGCTCA 400

(2) INFORMATION FOR SEQ ID NO: 2216:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 133 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2216:

TTTTTAAAAA AGGGGTTAAC CAAAGTTTTG GAACCCCAAA AAATTCGGA GTTAAAAAAA 60  
 5 CCCCCAAAAA TTAAATTAAC CGGTATTCC GTTCCAGGAG CCAAATTTT ATGGTTCCAA 120  
 TTnCCAAAGT GGG 133

(2) INFORMATION FOR SEQ ID NO: 2217:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 64 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2217:

TACTCGTACC ATTAACCACT CTGATTAAACC ACAATACTAA GGTATTCAAT ACATCACTGA 60  
 CATC 64

(2) INFORMATION FOR SEQ ID NO: 2218:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 82 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2218:

TATTCTATAG AATATGGATA ACGTTTAAACA TGATGTAGAG TATTCATCAT TGTAACACGT 60  
 35 CAATTGATA TGTGAGATTA AC 82

(2) INFORMATION FOR SEQ ID NO: 2219:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 70 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2219:

TTTGACGCAA TGATTAGCT GTAAATATGC AATCTAAAGG AAAGTACCAC TTATGAGATG 60  
 50 TATTAAAACG 70

(2) INFORMATION FOR SEQ ID NO: 2220:

- (A) LENGTH: 66 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2220:

10 AAAAATTACC CCAAAGAATT GAAAATTTGT TGTTCGGTT ACCGGGTTTA AGATTAATCC 60  
GGTTGA 66

(2) INFORMATION FOR SEQ ID NO: 2221:

- 15 (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 54 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2221:

GATCGCAACC AAAATAATGG TCTTCCTGGA TTATTACTTT ACCAGCTGGC ATAC 54

25

(2) INFORMATION FOR SEQ ID NO: 2222:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 50 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2222:

35 GTGTTGCTAC AGCTAaCATT TCATATTTAA CGnGTTGTGG TATTTCTAAA 50

(2) INFORMATION FOR SEQ ID NO: 2223:

- 40 (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 50 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2223:

AATGGGGGnA CCCAGCnTGA GTTATGTCAT CATATCGGTA TGTGATACAT 50

50

(2) INFORMATION FOR SEQ ID NO: 2224:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 54 base pairs

55

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2224:

GTAGATGCGC CCTCATATGG ACAAAGATAA AGTATCAGCA GATTGGACGC TTTA

54

10

(2) INFORMATION FOR SEQ ID NO: 2225:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 63 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

15

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2225:

20

CGAGACTTCA CTTTGACTAA ACGCGTTAAG AATTTAGATT ATGCTTACGA TGAAGAAGAA

60

TTA

63

(2) INFORMATION FOR SEQ ID NO: 2226:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2226:

35

TGGCCATTTT TAATGGGGGG AAACCTTAAA AAGGGGTTTT TAATTTTAAA CCAAG

55

(2) INFORMATION FOR SEQ ID NO: 2227:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 131 base pairs

40

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2227:

TCCATTTGGT TGCCTTCTTT AAATAAACCT TGGATTATGC CTTTCCTCCG GTTAATTAAT

60

GGGACCAGGG GCCAAAAATA CCCCCTTTTA AATATATATT CCCAAAATCC ATAGTTAAAT

120

50

AATCCATTTG C

131

(2) INFORMATION FOR SEQ ID NO: 2228:

55

(A) LENGTH: 350 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2228:

10 CCATCTGTGC TTCGTTAGGC GCTTTCGGCA TCACGGTGAT GGTTCGCGAC AGATCCGCCA 60  
 TCCGGCTGAA TGGGAAGCCC GCGTTA AAA GCGCGTAGA TCCGGCATCG GGATGAAGTG 120  
 GTAATACTTC GAGAAGTCGA TGGTGGAGTC GTCACCAATC ACCACATGAT TCTGCACCGG 180  
 15 CTGGAAGGTA ATACAGTTAT CCACCGAACC GCCCGGCATC GGGTTCATAT ACTCAAAGTC 240  
 GAAGCGCACT GGnTTTGGTC GCGCCCAGTT TCAGCGCCGG AATAGAGACA TCTGTTTTGC 300  
 CATCCAGCAA ACCTTGTAAT ACCGGAnTCC GCAGCAGCAG GCGGTTTCGC 350

20

(2) INFORMATION FOR SEQ ID NO: 2229:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 58 base pairs  
 (B) TYPE: nucleic acid  
 25 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2229:

AACTAAAAAT ACTATATAAA AAAGGTTGTT ATAATTTAAT GGATATAAAT AAAAACGA 58

(2) INFORMATION FOR SEQ ID NO: 2230:

35

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 40 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2230:

45 GGGCGAAAGC TGGACGGAGC CAACGTCGCG TGAGTGGATG GAAGGTTCTT 50

(2) INFORMATION FOR SEQ ID NO: 2231:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 50 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

55

AGCCATACGT GGTAAGCACA TGCTAAATTT GCCAGCCTGA AAATGTTTAG

50

(2) INFORMATION FOR SEQ ID NO: 2232:

- 5 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 132 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2232:

15 TGTATCATTT TGGCAAAATC ATAATCTTTA TCGTCGAATA CAACTACTTT TAAGTTTAAT 60  
 GATGAAGGTA CGCATTGTGT AATCACTTCA TCTAACTTTT TTAAATCAGG TGTCATAGTT 120  
 GAACTTGGnG GT 132

20 (2) INFORMATION FOR SEQ ID NO: 2233:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 78 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2233:

30 GATCTTGAAG CAGTTGAAAC ATATGTATCA GATGCATTAA GACAAGTACA CTTACAATCA 60  
 GACATTTTTG CTGTATCA 78

(2) INFORMATION FOR SEQ ID NO: 2234:

35

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2234:

45 TTTAGGCACA GACGGTAATA AGCTACAATT TTCATAAAAT CATCTCCTTn 50

(2) INFORMATION FOR SEQ ID NO: 2235:

- 50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 54 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2235:

ATCCTGGAAA ATCTGGTAAG ATATCTTGGA AATAACTAAT ACCAATTCCT AAAA

54

(2) INFORMATION FOR SEQ ID NO: 2236:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2236:

GGGTGATGGT CATTGACAAA GTCAACTTGT GATAAGCCAT GGATATTTTT CGTT

54

(2) INFORMATION FOR SEQ ID NO: 2237:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2237:

TTATTTACTT TAAATTTCTC AATCTACAGT GTAATCTTAT TTCTTATTAT

50

(2) INFORMATION FOR SEQ ID NO: 2238:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2238:

CCTTAATGGG TTTTGGGGGG GGGCCCCCCC GGCCCAAAC CTTTGGCCCA ATTGGTTCCT

60

GGGTTAAGGA AAAA

74

(2) INFORMATION FOR SEQ ID NO: 2239:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear



CCACCCATGG CGCTTGACAA AATATGGATG GAACATAACC ACACCGTCCA AGTTCACGTG 60  
TAGCACCGTG T 71

5 (2) INFORMATION FOR SEQ ID NO: 2240:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 64 base pairs  
 (B) TYPE: nucleic acid  
 10 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2240:

CAGCTAGGTA GTTAGGGATT CGACTCGTAA AACGGATTAA TAGGTTTTAT AAGAAGGGGG 60  
TTTG 64

20 (2) INFORMATION FOR SEQ ID NO: 2241:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 58 base pairs  
 (B) TYPE: nucleic acid  
 25 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2241:

30 CTTGACACGT ACATCTAATA CGACAGTCTG TCGGTTTAAA ACCTTTTGGG TCAAAC TG 58

(2) INFORMATION FOR SEQ ID NO: 2242:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 35 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2242:

40 GACTCATCAC CGnTTGTTAA GAnATACAAT TTATTACCCA GCAnTTAACA 50

45 (2) INFORMATION FOR SEQ ID NO: 2243:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 71 base pairs  
 (B) TYPE: nucleic acid  
 50 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

55

AAATTTGGAT TGGTTGGAAA TTTACAGTTA AAATTTAAAG GGTGGATGGA AAAATTTTAG 60  
GAACTTCTAA G 71

5

(2) INFORMATION FOR SEQ ID NO: 2244:

10

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 50 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2244:

GGGGGCCCCCT TGGGGGTTTG GGTTTTGGGG GGCCCCCCTT TTAAAAAantT 50

(2) INFORMATION FOR SEQ ID NO: 2245:

20

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 52 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2245:

30

TTATAATTTT TGAAAATAGA AGAGGGAAGC CTTAAATTAC CAAATGGATT TA 52

(2) INFORMATION FOR SEQ ID NO: 2246:

35

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 55 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2246:

ATTAGTTGAA AAGTACAATA TTCCGCAAGT TACCAATCGA TACAGGTATT ACAAG 55

(2) INFORMATION FOR SEQ ID NO: 2247:

45

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 50 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2247:

55

## (2) INFORMATION FOR SEQ ID NO: 2248:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2248:

GGGAAGGTAA AACTTCCTGC TTTTATTATA AGTATTCATA CTCTATTGCT ATATTAGTAG 60  
 AAACCGTAAA ATCAGTCATT CACATACATT nTGAAACATC TAAATAG 107

## (2) INFORMATION FOR SEQ ID NO: 2249:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2249:

GTTGGATACC TGnAACTAAA TAACTATTCT TTAAAAGTTA AAAACCAACC ACTAGTGGCC 60  
 ATTGGGGATT AAAATTCCAA CCTGGGCCGG TCCATCCCCA TGGTGGGTAA AATGGGGGAG 120  
 GGAAAATCCT TATTAGCCAA AGGATTCCTT ACCTAATAAT AGGGGGAA 168

## (2) INFORMATION FOR SEQ ID NO: 2250:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2250:

TTTAGTTGTG ACATACTGAG AACTGTAGTA CTTAGTGcna TACCAAAGGG 50

## (2) INFORMATION FOR SEQ ID NO: 2251:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

GCAGAACATA CCACGTGTCG CTGATTACCA ATACAGTAGA TCAAGATGGA CTCGATTGC

59

(2) INFORMATION FOR SEQ ID NO: 2252:

5

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 52 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2252:

15

GTTTGTGTTT TAATTTTAAG GGGAAGGGAT TTTTTCACCA AATGGGAATT TT

52

(2) INFORMATION FOR SEQ ID NO: 2253:

20

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 80 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2253:

AGTGTAATTA GAAAGGCAAG TACACCTGTT TAAAGTTTAT CTTCTAAGAT TTGTTTACTT

60

30

TAGAACTATA GCAGTTAATC

80

(2) INFORMATION FOR SEQ ID NO: 2254:

35

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 66 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2254:

GTAAATGACA GAGGAAATAT AACAATGATT AATAATGTGA CAGCATTTAC TGCAAATATC

60

45

TACTAT

66

(2) INFORMATION FOR SEQ ID NO: 2255:

50

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 50 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

55

ACATGTGTTA ACTCTTTGGC AATATATCCT GTTCTTCTT CTAATTCACG

50

(2) INFORMATION FOR SEQ ID NO: 2256:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 69 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

10

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2256:

15

AATCTTTTAT AGGAAAGAAA GAAGAAGATG TTATCAGTTG CGATTATCGG CCCAGGCGCT

60

GTCGGTACA

69

(2) INFORMATION FOR SEQ ID NO: 2257:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 64 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

25

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2257:

30

TAGCGGGAGA TAGAAAAACC ATTCCGCATT AGCTTTGGTC AAGTTGGGAA TGGGTAAAAA

60

AATA

64

(2) INFORMATION FOR SEQ ID NO: 2258:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 106 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

40

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2258:

45

GGTTAAGGTA TGGCGAAATA TCTCCAACAA CACTTCAAAA GTTCAAGAA AATAGAAGTC

60

GACTGAACAA TGTCATTAC ATGTGTGCGT CATGCACACC NTATGT

106

(2) INFORMATION FOR SEQ ID NO: 2259:

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 79 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

55

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2259:

CGGAATAACT GACTATGTAT CATTTGATGT TATTAACATC AATATTTTTG GTTAAATGAT 60  
 5 ATGCTAGAAA TAAAGCATA 79

(2) INFORMATION FOR SEQ ID NO: 2260:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2260:

GCTGGnTGTT AntGGCAGAG CATGTGAGCT GGATAATCAG TTGGAGAGGC 50

(2) INFORMATION FOR SEQ ID NO: 2261:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2261:

nCCATTAATG ACCGAGATTA GTGAGCATGC ACAAATTGTT ATGGTAGGAT 50

(2) INFORMATION FOR SEQ ID NO: 2262:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 51 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2262:

AATGAACCAC ATAATGACAA CTTGAATGAC AATATGAATA TGATGTCAAC A 51

(2) INFORMATION FOR SEQ ID NO: 2263:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 55 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

CATTAGGTGC TTATATAAAT TACTTTGTGG TGGCTCCAAA ACTTCGGGTT AAAAC

55

(2) INFORMATION FOR SEQ ID NO: 2264:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2264:

TTTCnTCCCC CCCCCGGGGT TTTTGGTCC CTTTTTTTTT TTAAATTTC

50

(2) INFORMATION FOR SEQ ID NO: 2265:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2265:

TCATTCATAG AGGTGTAAAG ACATAAGGGG AGCTTAACTG CGAGGACCTA CA

52

(2) INFORMATION FOR SEQ ID NO: 2266:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2266:

AGATGATGCA ATAATGGTGC AGTATAGAAG TACTGAGCAA TGCAAATTTT AGACG

55

(2) INFORMATION FOR SEQ ID NO: 2267:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2267:

GTTTCATCACA TTTATTACAT TCAGCGTTGG AATCAGTACT GGGTTATCAT G

51

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 54 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2268:

CTGTTGACAA CAAATTAAAA ATGACAACAT GTCGTAGTTA TAGTTAATTG ATTG 54

(2) INFORMATION FOR SEQ ID NO: 2269:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 312 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2269:

AACCAAAAAG AAAGCAAGGT CAAGGAAATT TCAGCGnGAC GTATCTTTAG TTTTGAATAA 60  
 GCATATTAAT ATGGTGATAA TATGCAAGAn AACCTGTTTA TTCGATTCAA TGAAATTATA 120  
 TTATTAATAT ACTTAATCAG TATCATTTGC TATTTTTATG ATTTTGTACA AAAAAGTCAT 180  
 AAGATTAGAA GTTTAGGCAT ATATTTATTG GGGATTGTTT GGGTTTTACA AACAACTCTCT 240  
 TTATCTATTT TTATTATACA AACTAGACAT ATTCCATTAG GGnCTATTTC AGATGTATTC 300  
 TATACTTTAA GT 312

(2) INFORMATION FOR SEQ ID NO: 2270:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 58 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2270:

GTTGATGGAT TCTCTTGGTT TGGTGTAGTC ACAATTCTG AACTGGCCCT TGTTTACG 58

(2) INFORMATION FOR SEQ ID NO: 2271:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2271:

CGTTCAGACG CTAAATCAGG CACCAGGTTG TACAATTGTC CTGGTTCTTC

50

(2) INFORMATION FOR SEQ ID NO: 2272:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2272:

CAGGTGTTGG TAAAACATTT GAGATGCTTT CAAATGCCAT TGAATATTT CAAAGTAA

58

(2) INFORMATION FOR SEQ ID NO: 2273:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2273:

TTATAAATTG GTGTAACAAT TTCATACACA TGATCATTCT TTGATTGAGG TAAAAATGAT

60

TCTACTAAAC GTACACGTTT ATGCTTCTTA TATTCTTTCA TCAATAAATA TCTATGATTA

120

GCTAATGATA AATTTAGTAG AAGCTTGTTA TCTCCATAAA CTAAATTCAC GATATTAGGT

180

ATATTGAATT GTTCTTGATA TTTCAAAAAT TGTGTGATCCC ATTCTTCATT TTTAGGTAAA

240

GGTAATACCA TCTCGTTAAT TTTCCAATAT GCTGGTTTAA GAATGACATT TTTATATCTG

300

ATTCGTGGTG AATAACTAAA TGAATCAATA CTCACATCAT TCATAGGTTC AATGCATTTC

360

ACAGATTCCA TTGAAATTTT TCGTAACAAT CGATATnaAT

400

(2) INFORMATION FOR SEQ ID NO: 2274:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2274:

GGGTACAAAT TTGTnGATGA TAGAAAAGTT CGTATCGCTA GAAAGTCTGG

50

- (1) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 65 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2275:

TGATTTACCA GTTGATTACG ACAAAGAAGA ATTTTCAAGA ATTGTTGAAG CATCAAAACG 60  
CATT 65

(2) INFORMATION FOR SEQ ID NO: 2276:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 55 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2276:

ATGGCGTTCC ACCAGCAGTC AATAATCCTG TTGGGATAAA TGCCAATACT GTCGA 55

(2) INFORMATION FOR SEQ ID NO: 2277:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 76 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2277:

TAATAAATCA CGTGCATTTA CGCTCACTAG CTTTCATCTC CTCATTTTTC CTTTCAAAT 60  
TTATTAAGTA TGAATA 76

(2) INFORMATION FOR SEQ ID NO: 2278:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 65 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2278:

GTGGCTTTGT CTGTGTTATT GTAGTTTGT TTCGCTGCGT CCAGCTTTGC TGCTTTTCCC 60

## (2) INFORMATION FOR SEQ ID NO: 2279:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2279:

TTAAGTGCCA AAGTCCTTGG TAGCCAGAAT GAACCACCAA CCTCCATTTT TCCAAAAATG 60  
GTCTTACCT 69

## (2) INFORMATION FOR SEQ ID NO: 2280:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2280:

GGATGGAATT GGGTTAAGAA TAAAAAGGT AATAATTGAG TTTATGATAA TAATAATAAT 60  
ATTGAGA 67

## (2) INFORMATION FOR SEQ ID NO: 2281:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2281:

TTGTTACTTC GGCACGGATA AATCCACGTT CAAAATCAGT ATGAATGATA CCAGCACATT 60  
GAGGTGCAGT CATACC 76

## (2) INFORMATION FOR SEQ ID NO: 2282:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

AACCCAGAAG ACTTATTATT AGAATCTTAA TCCACAACAC AAAATAGTTT ACTATTCCTA 60  
 AAAGCGGGAT TAAATCAATA ACAAACAGCA GTAAGATTAT TTCCTAGTCG AAATATCTTA 120  
 CTGCTGTACT TTATTn 137

## (2) INFORMATION FOR SEQ ID NO: 2283:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 52 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2283:

ACAAAGATT ACTATTTAAC TAATTTATAT GAAGAATAGC TTTCCCTAAT AA 52

## (2) INFORMATION FOR SEQ ID NO: 2284:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 51 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2284:

ACTCCTGCAT ATCACAAC TA GATTAAATAT ACATCAAACA GATATAGTAA A 51

## (2) INFORMATION FOR SEQ ID NO: 2285:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 77 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2285:

CTAACATGTG TGAACGATAT GCAAATTCAA TATCTCATTC ACGCTTTGCA CTTTATTACT 60  
 ACAATCAACG TAACTAT 77

## (2) INFORMATION FOR SEQ ID NO: 2286:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 58 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2286:

5 AAACCTGTAT TTTTAATAAA CAATCGCTTG GACCTATTCA CTGCAGCTCT TCTGGGAC 58

(2) INFORMATION FOR SEQ ID NO: 2287:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 204 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2287:

AATTCATAAA ACCAATAAAT AAGAATTTTA TAGTAAAAGG AAATGGANTA GAGTTGGCAG 60  
ACTTATACAA TATTAAAAAC AAAGAGCTTT TCACGATTAA AAGAGGAATT AATACATCTT 120  
20 TATCTCTTTA TAGTCTAGAA CAGGAATATA ATAACAATTA ACGCCTTAAA ATATCCAGAA 180  
TCATATAATT TTGAAGAATT AATA 204

25 (2) INFORMATION FOR SEQ ID NO: 2288:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2288:

35 GCTCGTAAGG CGTCAACTGT GGCCTTGGGT GCTACATGTA AAGGTTACTT 50

(2) INFORMATION FOR SEQ ID NO: 2289:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 53 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2289:

TCGCTTCGGT GGTAAAAATG TCGTGGAGGT CCCGTTGCAG ATGGTTTTAA ACG 53

50 (2) INFORMATION FOR SEQ ID NO: 2290:

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 68 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2290:

TTGGAGGTCA ATGTTCCGGC TAATCTTCAA TGTTTCCGTA CACAATTGCT GCGGTTGACA 60  
CACATACG 68

(2) INFORMATION FOR SEQ ID NO: 2291:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2291:

TTCGACGAAT TAAACAAAT CCTTTATAT GTTGAAGTGT ATTCGAGATT AAA 53

(2) INFORMATION FOR SEQ ID NO: 2292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2292:

ATCAATTGTC AACATCTAAT ATTCACTACC AATTATATCG CCACATGTTT TTAGCAGTA 60  
ACA 63

(2) INFORMATION FOR SEQ ID NO: 2293:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2293:

CGACTCAGGT CCATCAAGAG AGACACATTT CGACTACAGG TTATTACTTC TTTGA 55

(2) INFORMATION FOR SEQ ID NO: 2294:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2294:

AAATTTTGGT TAATTTTAAA ACCAAAAAAC CTTGGAAGGA AATGGCCCTT TTCCCAATTT 60  
T 61

(2) INFORMATION FOR SEQ ID NO: 2295:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 158 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2295:

AATCTTAAAA CCTATGGCGT CTATTACATT CCCAAAACCT ATTTTCAGnA ATGTTACCAA 60  
TTAAACTTGC CGGGGTATGG ACCAGGTAC CAGGCTAAAA ACTGGAAGAA AGGAAGGAAT 120  
TTTAGAAAAT AATTTATTAA CATGGACCAG GTAACATA 158

(2) INFORMATION FOR SEQ ID NO: 2296:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 68 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2296:

TGTTCCAACG ATGAATGTTT GCATGCTTTG TTGCACTGAA ATTGATGAGT TGCTACTTGC 60  
AATCCTAG 68

(2) INFORMATION FOR SEQ ID NO: 2297:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 72 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2297:

GTAGGGATTT TTTTAAACCG GGATAGCCCA ACCAAAATTT AATTAATTTT GGGTTTTTGG 60  
ATTGAAGGAA TT 72

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2298:

AAAAATTTTA CCAGGTGAAA AATTATTTTG GTAGGATTTA AATnTAATGG TTAAATGGT 60  
 GGTTTATTAC CTAATTTAAA AATGGTTAAA AGGGCCTTTA CCATTTTAA AATTTAATCC 120  
 GCCTTTTGGG AGGGGGATT TAGGGATGGT CCAGTTAGGA CCCCATTACC ACTGGAAACC 180  
 AACTTAAAT TTAGCCAAAT TTCCTGGAAA AAA 213

## (2) INFORMATION FOR SEQ ID NO: 2299:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2299:

TATTTTAAA GGAGGGTAAT AATCTTAATT TAAGTTCATT ATTTTACTT TCATTATAAA 60  
 TATTTAATGT TACTTTCTTA TTTAGATAAC AATAAAAAA TATAATCTCT nAAAACCCAA 120  
 TGAAACAGCT GCTCCAAACA ATTAGTTCTT CTAATTGAA 159

## (2) INFORMATION FOR SEQ ID NO: 2300:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2300:

ACAAGGTCAT TCGGATTGA CTTTGTTTCA ATTGTAAAT TTTGCTCCAT CAATTGTCTA 60  
 ATTCT 65

## (2) INFORMATION FOR SEQ ID NO: 2301:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2301:

5 TTTATTCTTA TTTAAAAACC CANTGAAAGT AntCTTTnCA TTantAAAAA 50

(2) INFORMATION FOR SEQ ID NO: 2302:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 62 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2302:

GAGATATATG CATGAGCTCT ACGACTTCCT TAGGTTTCAT GCGACTATC CTGGCAGGGA 60  
20 TG 62

(2) INFORMATION FOR SEQ ID NO: 2303:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2303:

ACCAATCCCG TTGTTTGGT TTTTAAAAA AAGGAAATTC CAAAAATCCC CCATT 56

(2) INFORMATION FOR SEQ ID NO: 2304:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2304:

45 TTAAAAACCC AACGGGTTTG GTTAAAAATGG CCTGGGCTTT TCCAAAACCTT GGC 53

(2) INFORMATION FOR SEQ ID NO: 2305:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2305:

CGAACAGGTT GCCACTGTAA GATCTGGTGG CATTTAATGG CAATCGTATT TTATTTGGAG

60

5

(2) INFORMATION FOR SEQ ID NO: 2306:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 74 base pairs

(B) TYPE: nucleic acid

10

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2306:

15

CTTTATAATG GCGGCGCACT TGGCATCTCT GCATTCAGTT ACACGCGGTG GCAACACAAA

60

ATTTAGGGAA TTCT

74

20

(2) INFORMATION FOR SEQ ID NO: 2307:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 base pairs

(B) TYPE: nucleic acid

25

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2307:

30

TGTCCATGCA CAGCTTTATT GGAATTTACC TTTTACAGG CAACCGCTAA AGA

53

(2) INFORMATION FOR SEQ ID NO: 2308:

(i) SEQUENCE CHARACTERISTICS:

35

(A) LENGTH: 76 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2308:

TAAATGATTA TGGGAATATC CAAAATTATC GAGATCTAAT ATGAAGTGAC TGCACACATA

60

45

TCAGCTCTGA ATGAAT

76

(2) INFORMATION FOR SEQ ID NO: 2309:

(i) SEQUENCE CHARACTERISTICS:

50

(A) LENGTH: 117 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

55

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2309:

TCCTCAAAAT GTGAGTTAAT AGTCGAGTGG AAGCTGTGAC TTGAGCGACG ATACATCATC 60

5 AACTATCAA TAATGTTTGC ACATCACTTT TACTACTATC ATTTGATGTA TAAATAC 117

## (2) INFORMATION FOR SEQ ID NO: 2310:

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 52 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2310:

AAACTCATAT CGCTTCCGAT AACCAACCCT GCTGCTGTTG GTACAAATTG TC 52

## 20 (2) INFORMATION FOR SEQ ID NO: 2311:

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 56 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2311:

30 AACACTGGAG TCCTAATGTC ATCAAACATC TACCTATAAG ACCTTATATA ATCGTC 56

## (2) INFORMATION FOR SEQ ID NO: 2312:

## (i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 72 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2312:

GATAACATCA TAGGCCATAA CTTCCATTTA GGCCATCAGT TATAGCATGC GGACGACATA 60

45 CTGTGCCATA TG 72

## (2) INFORMATION FOR SEQ ID NO: 2313:

## (i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 52 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2313:

CATCTAATGG GAACGTGTCG ATCCTAGTCA GTATAGTCAT CGGCAGGTAC GA

52

5

(2) INFORMATION FOR SEQ ID NO: 2314:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 64 base pairs

(B) TYPE: nucleic acid

10

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2314:

TAAACTGAAA TTTAATTTTC GGATGGTATT GTTATTAAGA AATAGACATA ATTTGTGCTG

60

GATA

64

20

(2) INFORMATION FOR SEQ ID NO: 2315:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 base pairs

(B) TYPE: nucleic acid

25

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2315:

30

CTAGTTTAAA TTTCTTAAAC TTCTACATCA GTAAAAGGCC GCTCTGGGAC CATACAATC

59

(2) INFORMATION FOR SEQ ID NO: 2316:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 base pairs

(B) TYPE: nucleic acid

35

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2316:

GCATAGTAAC TTAATTGATA GGAGATGAAA ATCCGCAAAG TCATTGGAAG GATT

54

45

(2) INFORMATION FOR SEQ ID NO: 2317:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 150 base pairs

(B) TYPE: nucleic acid

50

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

55

GTATATGCTG GAAAGATAAA GTATGGAAAA TGCATGGCGA ACATTTTGTA AGCAGAATGA 60  
GCTATAAGCG TTGAATGGGT TTGAACGTAA ACAATCGAAC AATGATATGT CAGACATACT 120  
5 TGCTTTAGAG CACATTTAGA GAGCGACATG 150

(2) INFORMATION FOR SEQ ID NO: 2318:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 52 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2318:

AAATCATCGA TGTAAATAA TTTAATGACA AGGATTAATG AAAGACGGAT TG 52

20 (2) INFORMATION FOR SEQ ID NO: 2319:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 52 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2319:

30 TTAAGGAAAC CTTGGCCAAG GTTAAGGAAA ACCGGGGGTT CCAAGGTTTT TA 52

(2) INFORMATION FOR SEQ ID NO: 2320:

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2320:

ATGAAGTTGA TTTAGGATGA AAATTAATCT TGGGATATTT AATACTTTGT 50

45 (2) INFORMATION FOR SEQ ID NO: 2321:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

55

CTAACGCTAA GGGCGACGGA TGGTGGTnAT GTCAAAGAGA CAAATAGGAT

50

## (2) INFORMATION FOR SEQ ID NO: 2322:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2322:

CGTGGTGATT AATTTTTCGT CGCGTTTTGT TTCCTTTCCC CAGTCATGTT TTATCATTGT

60

GGGCATCATT GCACCTGGGT TCCATATTAT GACGTCATTT TTTAnAAT

108

## (2) INFORMATION FOR SEQ ID NO: 2323:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2323:

GTCACCGAAT TTCGATTTAT ATTATCACTC AATTTATTAT CTTGAAGCAC GCGTTAAATC

60

GTCTTTAAAT TGnAACAGTT GCTACTTTAT TGTCTTTACC ATTGATCTGA ATTTGATCCG

120

CTTTAAGTCC ACTATCTTTT ACAACTTGCh CTACCTTTTG TTGAGTAATT GCTTGTTTAG

180

ATTGGAAATC TACGCGTGTA CCACTTGAAA AA

212

## (2) INFORMATION FOR SEQ ID NO: 2324:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2324:

TCATTTGTTT TTAATACGTT GTCAAAATTA CCAACAAATG ACAAATTAAA TTTTGCAATA

60

CATATCAAGG TGTTATTTTT TTCCTATTTT AATTATGTAT AACGCATTAA AAGTGACGTh

120

AATATTCAAA GGA

133

## (2) INFORMATION FOR SEQ ID NO: 2325:

- (A) LENGTH: 216 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2325:

10 ATGAACGACC GTGGACAGAC AATATTTAAA GCATTTAAAA ACAGCGTTCC CAGAAAGACA 60  
 ATATATAACC AATATTAACA AAAGCAATGC ACATTACTTC ACAAATGAAA TCAAAGCAAC 120  
 ACACATATAC AATGCAATAA GCGGGCAACA ACAAACAGAT TTCAACACGC CTGTCATACA 180  
 15 GCAATATCGT TAACAAATGA CACC GCCCT TTAGGC 216

(2) INFORMATION FOR SEQ ID NO: 2326:

(i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 141 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2326:

TGACCATATG ATTGAGGAAG GTTTTATTGA TCCTAAGTAT CGTGCTCTTG CACCGTTATG 60  
 CGACACTAAG GAATCATTAA TTGAATCAAT ATTAAATTTT AAACCTCTGG GTACTCGTTC 120  
 30 ATACGATTAA TCATTCTAAG G 141

(2) INFORMATION FOR SEQ ID NO: 2327:

(i) SEQUENCE CHARACTERISTICS:

35

- (A) LENGTH: 55 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2327:

TGAAACTGCA GCGTGGCCGA GTGGGGGTTG TGCCAGGTGA CCCCAGATGG GCGTG 55

45

(2) INFORMATION FOR SEQ ID NO: 2328:

(i) SEQUENCE CHARACTERISTICS:

50

- (A) LENGTH: 54 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

55

GAAGCCAGCC TAATTGGATA CCACCGGAAG TAACTTTTGA CCAGGGCCGT CGCA

54

(2) INFORMATION FOR SEQ ID NO: 2329:

- 5 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 54 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2329:

15 GTTCCCCGGT CCAGGCCGTT GTCTTGTCGCC GGGGTGTTTG GTCCTTGGTT GTGT

54

(2) INFORMATION FOR SEQ ID NO: 2330:

- 20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 190 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2330:

TATATTATAT ATTTAACTGC TGTGATGTAT TCTGAAAAA TAGTAGTATT GCCTATAATC

60

ATCTATGCCA TTGTGTTTGT AATAATTGGT ATCACTTATA TCTTTATAGG CGACAGCTAT

120

30

GATCAATTAA CAAATTTCAA TGTGATTTTG TATATGGGGA GTTTGTtTTA TGCATGGATG

180

GCTATTAGAA

190

(2) INFORMATION FOR SEQ ID NO: 2331:

35

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 54 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2331:

45 TTTTCACCTC GTGTTTAA TCAATTGAA TCTAACTAA AAGTACCTTT AAGT

54

(2) INFORMATION FOR SEQ ID NO: 2332:

- 50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 246 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

55



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2332:

5 TTCTAAAAAT ATTAACGAAT TATACAACTT TAAGAGTTTT TAGTATGTAA ATATTCTTTT 60  
 CATATTAATA CAATACACCC CTATATATGC TCACTTGTTT GAATTAATAA ACTTTAGCAT 120  
 TCTGCAAATA ATATTTTAAA AATAACTATA CTTTTTATTT ACCTATTGAA AAATAGTGTT 180  
 10 ATCATATTTA TTAAGAAGCT ATTTTATAC TAGTAGGTGT CAGTCATGAA TAACATTTTG 240  
 TTAAAT 246

(2) INFORMATION FOR SEQ ID NO: 2333:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 52 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear  
 20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2333:

25 CCTTCTAACA TCTTTTTTACC ACTCATTGAA ACATGTGATC CTAATAACAT AA 52

(2) INFORMATION FOR SEQ ID NO: 2334:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 60 base pairs  
 30 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2334:

AGAAAAGAGA CTGAAACAAC AAATTCAGGC AACTTTTGAA CAACAGAGAC ATCGATTAAT 60

(2) INFORMATION FOR SEQ ID NO: 2335:

40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 193 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2335:

50 CCTCAATCAG CTCCTAAAGA ACAAATAGC GACTCGATTG ATGAGGAAAC AGTAACGAAA 60  
 AAAGAACGAA AAAGTAAAGT AACACAATTA AAGCCATTAA CACTTGAAGA AAAGCGGAAG 120  
 TTAAGACGTA AGCGACAAAA GCGAATCCAA TACAGTGTTA TTACAATnTT GGTATTGTTG 180

55

## (2) INFORMATION FOR SEQ ID NO: 2336:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 58 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2336:

CCTACAGTCC CAACACTGTC AGTACACTGC CGATACCCAA CCTCTGGCCG GTCCGGCA 58

## (2) INFORMATION FOR SEQ ID NO: 2337:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2337:

ATATTTTThA TTTAATGGTT TTACTACTGC TACAACTATC ATAGGTGGCA 50

## (2) INFORMATION FOR SEQ ID NO: 2338:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 378 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2338:

CTCCTGTAGA TTAAAATCT CCTAAATAAC AAACGAATAA TCGGCCATCT TTATGTATTT 60  
 TGATTGCTGC AGGATTCGCT TTGTGACTTA CAAAAGGTCG TTTGATTTC TCGTTTCAG 120  
 GATTGATTTT GAAAATATTG CCTTCGAATA CATCCAATAA AAAGAGTTGT CCCTGCCGAT 180  
 CAAAGTTCAA TCCTTCTAGT TGCAATCCTT TTTTGGAAAT TTCAAGCCAT GGTTCAGCTG 240  
 TAATTGTTTG TAATTCACCT TCAGATATAA TTGGAACAGC ACTATTGGAC TTCCCGChAT 300  
 AAAATAATGG AGGGnAAAnC TGGTGGGGAC ATCCATGAGC CATTCTTTC CATTCCATTC 360  
 GGTTTTAACT AACCAATT 378

## (2) INFORMATION FOR SEQ ID NO: 2339:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2339:

ATGAAAATAA ACTGTGTCTC CnGATGTATA CGTCCCTTCA AGCAGACTTC

50

10

(2) INFORMATION FOR SEQ ID NO: 2340:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2340:

20

TATCCATATG TGAAAAATGT CATATATGAG TCTAGTTTTG TATAAATGGA GACTCGAAC

59

(2) INFORMATION FOR SEQ ID NO: 2341:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 189 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2341:

ATTGATAAAA TATGATTAAG CGTTGTTGCA AATGACATTT TCTCAAAAAG CGCTTCACTA

60

35

TCAATTGGTA CTTGTGTGTn AATTCAGCC AGTCGCTTCG ATAAATATAG TTCATCTAAA

120

TTGTCATTAA TCTTATTACG TTGCCAGCT GATAATGCAT CAATGTTTTC AACCACATTT

180

TCAACGCTT

189

40

(2) INFORMATION FOR SEQ ID NO: 2342:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 165 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2342:

50

ATCAATTAAA ACAAAGCATA CAACAATTTG TTGATGTTGA ATCTAAATCA ATTTTAGAAC

60

AACAAATGAT TCATCAGCTT CAACAAATGG ATCGTTCTTA TG TAGAGATG ATTACAGAAT

120

55

## (2) INFORMATION FOR SEQ ID NO: 2343:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2343:

CTTAACCCCC CTTTTTCCC AATTTTAATG GGGAAAATT GTAATTAACC TGGGC

55

## (2) INFORMATION FOR SEQ ID NO: 2344:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2344:

GACAAATAAA CATGACCTGG ACAAAGAAGA ACAATAAACA AGCCTGGCAA

50

## (2) INFORMATION FOR SEQ ID NO: 2345:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2345:

GTATTGCGAT GATGCATACG GGTATTGTTT TGATTAAATA ATATTTTATA TTTAATGTTG

60

ATAAATGTTG AATAAACAAT CCGCAAAGnG CACTTGATGA TAGTGCTAAG A

111

## (2) INFORMATION FOR SEQ ID NO: 2346:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2346:

GCAAACAGTT TCCGTGTCCG TTTTCCAATT AAGTTAAGGA ACCCAAAGAG A

51

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 60 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2347:

TCGTAGGTGC CATAACACAC GTTACCTGGG ACTCATATGA AGTATTATGT CGAGACGACC 60

(2) INFORMATION FOR SEQ ID NO: 2348:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 118 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2348:

GTTTTTAATA GGCTCTTTAC GTATCTAAAA ATAATTGCAT TATTGGTGTG CCTTGATGTA 60

ATTGAATTAA AGTACCGTTT GGTGTGAACG TTTCAGGTAT ATCATTITTC AChATAAC 118

(2) INFORMATION FOR SEQ ID NO: 2349:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 176 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2349:

ATGACAGAAA GCAAAATCCC AATGTTGATA TACCGTTTTT GACACCACTT GATTATCATT 60

ATTTTTTCTT TAGCGATGGA TTTTATATTA CGATTTCAT TCTTACTATC GTTGCATTAT 120

TGTCATTCAA ACTGTATCGT TTTTACTTtt ATAGACTTTT CGCAATAGTA ACATGG 176

(2) INFORMATION FOR SEQ ID NO: 2350:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 201 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2350:

CTACGACTGA CATTAACTGT GCAGATGTAC CTGGATTCTA TTTTTTCAAG AACAAATTGT 120  
 AATAATTGAT AGTTATATGG TGCAATGTCA CCTTCATCCA TTGAGCGCTC AATAATTTCA 180  
 5 GCTGChAGAG CGGCnTGACT G 201

## (2) INFORMATION FOR SEQ ID NO: 2351:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2351:

ATCGCTATAA CCTATCAGTG ATAATATTTG ATTGCATGGT GCACCATTTG AnATTTCACT 60  
 20 TAGAATGGTG GTACCTAATT GCTTATTTTT ATATGTCATT TGAAGATTTA AAAATTAAAA 120  
 ACTTTGATAC AGAGTGAAAC CATATTTCAA CAAATTAC 158

## (2) INFORMATION FOR SEQ ID NO: 2352:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2352:

TCGTAATCAA AACATTTTGA ACAGGATTAT AGTAAGGGAA TTTTGGATT TTAAGTTGTG 60  
 TTTGTTTCATT TTTTAATAAG AGTCGAGCTA AGTCTTGCAA CATCATTACT TGCTTGCCAT 120  
 40 CTAAGTGTTC GTCATTAAAT TTTATGAAAC GATCACTCAT GTTTTATCCC TCTTTAAAAG 180  
 TTTAGTTCTA CAGCATTATA TATTGCTTGT TGTTACGTT CATCTTCCAA TTTATCAATA 240  
 ATTGTACGTT TAATTGCACG TTCAACTGGC ATTACAGTGA TTAAATCACA CAAGTCTAAT 300  
 45 AATGCACGGG ATACTAGCGG CTTCTTCAGA AATTTGTCCC TGCTTAGACA TAGTACGTAA 360  
 ATCTTCATTG AACTTnAAT AATTGGTTT GATTGGTTT 400

## (2) INFORMATION FOR SEQ ID NO: 2353:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2353:

ATTAATGGGG TTAAATAACA TTTTGACTGC GAAAGATTTA TTCTTTTCAG GTAAATCATT 60  
 5 GATAGATGTA TATAGTCAAT TTGCTGGATT AGCTGAAATG ATAAATGThT TTGCGAATGC 120  
 ACCATTT 127

## (2) INFORMATION FOR SEQ ID NO: 2354:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 223 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2354:

20 ATCTCGCTGT TTTTATGAAA GAAAAC TACA TTTTCGAGAG AATAAAAAGA TTTTCTGAA 60  
 ATTTAATCTA TCAATTACAT TGATTTACTA ATATAATTAG AAAGTAAATT TTATTTGATC 120  
 25 AAAGTAAATG GGGGAAGTAC TGTGATAGAA AATAAGAAAA CAGTTGAAGA TACATATTCA 180  
 ACAGGCGCAA TTGTTGATTC AATATCATCT TCAGTnCAAA Tn 223

## (2). INFORMATION FOR SEQ ID NO: 2355:

- 30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 35 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2355:

40 ACACTTGTTT AAACACTCAC AATGATAAAG CATATTATCA GTATTGTAGT GTGTGGAAAA 60  
 TGACAGCCAT CTAAGGAGAA AAATGATGAA AAGAATATTG GTAGTATTTT TAATGTTAGC 120  
 AATTATATTG GCAGGTTGTT CTAATAAAGG TGAAAAGTAT CAAAAGATA TTGATAAAGT 180  
 45 GTACAAAGAA CAGAATCAAA TGAATAAAAT TGCCTCGAAA GTACAAAACA CTATTAAAC 240  
 AGACATTAAA CAAGAAGACA GTAATACACA TGTTTATAAA GATGGTAAAG TCATTGTTAT 300  
 TGGTATTCAA TTATATAAAG nTCGTGAAAA AATGTATTTA TTTCGCATAT GAAnTAAAG 360  
 50 GTGGTTAAGG CCAGAGGATT TAATCAGnGG AAAnTAGACC 400

## (2) INFORMATION FOR SEQ ID NO: 2356:

- 55 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 344 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2356:

	AATTTACTTT GTGCCACAAG GTTATCAATG TCTTTTGAAC CACCAAACAT TCTAGCGATT	60
10	AAGTGACCTC CATCATCGTC TGGTAATCTA TCCTCTCCCC CCACAGTTCT TTGTGCATGG	120
	CTATTACGAT CCCCATCTTT TAGAGAGAGA TTGTCTACAT AAACCTCTTT TATGCGACCT	180
	TTATGATCGG TTCGATATAT GTGACCAGTA GGTGTTGTGT ATTCAATATT CGCCTTTAGT	240
15	TTCTTAGGTh CTAAGTCTTG GCATAGTGTT CTCCGAATTC nAACCTTGGT GTTAGTTTGG	300
	TGATTCAACA TACTTTTGAT GGAATTCATT ThCATGGGCT ACTT	344

20

(2) INFORMATION FOR SEQ ID NO: 2357:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 53 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2357:

30	TATGCGCCCC TGCTTGATCT TTCATTTGCG TCCACTCAAT TAGTTGTTTG CGC	53
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(2) INFORMATION FOR SEQ ID NO: 2358:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2358:

	ATTTTTTCAC CTTCTGAAAT TGATAAATCT AGGTTATCGA ATATAGTCTT ATCGGCATAA	60
45	GATTTATTIA AATGTTCAAT TTTATATGCT TCCATACCCA TCTTCCTTCT TCTGTTGAAA	120
	TCTCTACGTA CTAAATCAG TTCTATACAT TATACACCTT TTTGAAATCA AAAGAAATCG	180
	ATACCGTTAA GTGTCATAAT TTAATATATT GTTGCTTCAA CTATAAATAA AACTTGTTAA	240
50	GGCTTTGATG ACTATGCTAA TGATCTTTAT AATATACCTT TTTATCAACA CATATAATGT	300
	AAAACATAAT ATAnAAGAAC ATAATAAAAA CCCGGATTGA TATTTTATCA ATCCGAGTTC	360
55	GTGTTTAGAT ATTATTTTTT AGAGTTTGCT TTAGGTCCTG	400



- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 154 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2359:

TTAATGTCGC CATT TTTTGT TAGGTAGACG TATAAATCTG GACCTTTTGA TGATTGTAG 60  
 TTAGTAAGCA TTAATTTACC ATTTTAAATC TCAGCTTTAC CTTCAACAGT TTCACCGTTT 120  
 TTAGAAGTGA nTGACCTGT TAGGTGTTTT GTTT 154

(2) INFORMATION FOR SEQ ID NO: 2360:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 57 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2360:

ATATGTCTTG TGATTTTTC A GGTGTAAGTT AGTATGCAAG TGATTATGAT TGATAGT 57

(2) INFORMATION FOR SEQ ID NO: 2361:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 58 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2361:

GGCATCAAAT TAGTAGCGAC TCACACGTGA TGCATCCTGT GTTTTGGATC TCATTCT 58

(2) INFORMATION FOR SEQ ID NO: 2362:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2362:

TGTTATTATC GnAGAGGCTT TTCGCTTTGG AATAAGGTAT TACGTGAATG 50

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2363:

CTCTTCTGGT CCCTGACATA CATAGGAGAA ATAGCnCCAT GTACAACGTG

50

(2) INFORMATION FOR SEQ ID NO: 2364:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2364:

ATTGCCAATG TCGTTAGTTC GTGAGGCTGT TGGTGAAAGT TGTGTTTGAA

50

(2) INFORMATION FOR SEQ ID NO: 2365:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 111 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2365:

CCATGATTTA AATCATTGAT TAATGGTGCT TGTCTACAT CTGTGTAAAA TTCATACAAT

60

TCTTTAGCAT CGTCGAATAG TTCATCACGA CGTTGGnTAA ATTCTTCTTC T

111

(2) INFORMATION FOR SEQ ID NO: 2366:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 139 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2366:

TAATGCTGAG CGTGTTACTT TAGTTGGATC AACGATACCT TCTTCTAACA TATTAACCCA

60

CTCnTTTGTA GCAGCGTTAA AACCAACACC CGGCTCTGCG TTTTCAAAC GTTCTACAAT

120

## (2) INFORMATION FOR SEQ ID NO: 2367:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2367:

CCTGATTGCA AAGTACAGCA AGCACTACAG ACGCCTAAnC ACTnACACTA

## (2) INFORMATION FOR SEQ ID NO: 2368:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2368:

AAAATGGTAT TGCAATTAGT AATGTTACAA CAAGTGTGT AATAGCTGCA TAAAT

## (2) INFORMATION FOR SEQ ID NO: 2369:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2369:

TATAGGATGA AAATCCTGCC AAAAGATTAA GGGGTGGCCT AATGAACCAT G

## (2) INFORMATION FOR SEQ ID NO: 2370:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2370:

TTGCTCGAGG TGGTAAATAC GCAAAGTTTA TTTGGTTGTG CTAAGAGAGA AA

## (2) INFORMATION FOR SEQ ID NO: 2371:

(A) LENGTH: 66 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2371:

10 TAATTTGAAT AAGGTGGAAG TGATAACAG TGCTTTGCGA ATCTAGAGTC ATTAATCAAA 60  
 ACCCTA 66

(2) INFORMATION FOR SEQ ID NO: 2372:

15

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 65 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2372:

25 AGACAGGTAC TGTCCTACGG TATGGAGCAG AAGCGGGAAA GCTGCCCAGA GCCAACTGTA 60  
 GACAA 65

(2) INFORMATION FOR SEQ ID NO: 2373:

30

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2373:

40 TTGCAGTGAC GGCTTATAAT CATTCCAAGC GAACAATTAG ACATTCCATA TAAATATAC 60  
 AGATGGCTTT CAGTAGAGTA GTGGATTCGG ATTCACGAAC TATACTGGAA GCTTTTATT 120  
 ATAAATGAAG AGAAGTTATA TTTTATAGCAT GTATAGTTGA ATACTGGGTT AAAATACCAT 180  
 45 ATTAATAATG AAGTAAAGGT ATGAGTGATT ATGAAAGTGT TTTGAATGAA ATATATTTAA 240  
 TTGGTGATGC TTTTAATTGA AAAGATTAAC AGGATTCAAC TTGGTAAATT GTATTAAATG 300  
 TGAGAAAATA AAAGTATATT CATTGAGAGA TATATGAGTC AATGATCGTT TTAACAAGA 360  
 50 TAAGTGTATT TTAATATGTA AAAGTTATGT AATAAATATT 400

(2) INFORMATION FOR SEQ ID NO: 2374:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 70 base pairs

55

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2374:

CCTATCATGC CTCTCTCTCA CTGAATCCTT TAGATCCCCT TCCCTCCCTC TCCCCCTCT 60  
TTTCCCCCTCC 70

10

(2) INFORMATION FOR SEQ ID NO: 2375:

15

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 50 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2375:

CCAAGTCAGA GCAGCAGTTC AGTTCGTCAG CnGTTcAGTT CAGAGCnGTC 50

25

(2) INFORMATION FOR SEQ ID NO: 2376:

30

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 50 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2376:

GTTGGTGAAG CTGTTGCCGA nGGAGAAGCG GGTATGGATC CTGACGGTGn 50

(2) INFORMATION FOR SEQ ID NO: 2377:

40

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 59 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2377:

AATTGCAGGA CAGGTCAAAG GCAAATGCAC GTATTCAGGT CATGCTCATG TGCATGTTG 59

50

(2) INFORMATION FOR SEQ ID NO: 2378:

55

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 229 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2378:

5 TTTATCATCG TATAAATCTA TATCTAATTG ATTAAACTTC GGGTGCTTAA CTAACCTCTCT 60  
 CAATACACTT ACACCAGCAG TTCCCATGCC TATTATTGCT ACACGCATAT ATCATCCATC 120  
 CTTTTGTAAT TCAAAATATT ATATTTAAAC TATTACCTAT AATTATAGCA ATTTGGTATT 180  
 10 TCCAATAAAA TTTATnAAGG TAAGCnATTA TTTCACTTTC ACAACCATT 229

## (2) INFORMATION FOR SEQ ID NO: 2379:

## (i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 116 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2379:

AGTTTTTTGT TTGACGTATT TAATTTACTA TTTGCTTGAT TGATATTTTT AGACATTAAA 60  
 25 TAGTGTCTC CTAATCAATT TATTCTTCTT TATnTCAGCA TTATTCGCAC TGACAT 116

## (2) INFORMATION FOR SEQ ID NO: 2380:

## (i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 136 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2380:

CAAATCTTAG CGGATGATTG GCATGTATAT TCTGCTGGTA TCGAAnCACC CGGTGTTAAT 60  
 40 CCCAAAGCGA TAGAAGCTAT GAACAGAAGT CGGCGTTGAT ATGTCGAATC GTACGTCAGA 120  
 TTTAATCGAT AATAAT 136

## (2) INFORMATION FOR SEQ ID NO: 2381:

## (i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2381:

TTAATTGATA GCTTTTATCT GTAGGAAAAG CTATTTTAAA GATTCTAGT GTATCTATAA 120  
 CTTTTTTGGG ACGATATTGA ATATTACAAT CTTTAAATGC CTTTTTAATA AAATTCAAAT 180  
 5 CAAAATCTAC ATTATGAGCT ACAAATAATGC AATCTTTTAT CTTATCGTAG ATTTCTGTG 240  
 CAACTTGATT AAAATATGGC GCTTGTTGTA GCATATTTTC TTCAATGGAT GTTAACGCTT 300  
 GAATGAACGG CGGAATCTCT AAATTTGTTT TAATCATAGA ATGATATGTA TCAATAATTT 360  
 10 GGTTATTGCG CACAAACGTT ATACCAATTT GAATGATATC 400

## (2) INFORMATION FOR SEQ ID NO: 2382:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2382:

TATTTTGTTA ATAAAGTTAA TATATGTTTG TTGTACAGAT AGTTCAGGAT ACA 53

## (2) INFORMATION FOR SEQ ID NO: 2383:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2383:

CCCGAGCTTG CCCTCCTTCC CCCCTCTTCG CCTCCAGACG AAGTGCCCTT CTGTCCTTG 59

## (2) INFORMATION FOR SEQ ID NO: 2384:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2384:

AGCCAACATC CCGATGGTA CTTGCATTAA TGCATAACCT AGAGAGAAGA ATGATGCCAA 60

TAAACCAAAT TGTGGTTTTG TCATCCCTAA ATCATCCATC ATTTGCTTAG 110

## (2) INFORMATION FOR SEQ ID NO: 2385:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2385:

10

TGAAAGTTCT TTTAnGCATC AATTTTAAnA CTACGAGCGG ACnCTAATAT

50

(2) INFORMATION FOR SEQ ID NO: 2386:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 245 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2386:

GGCAATTTAT TGACACAATG CTTGAGCnAT TGATAGCAGG ACAAGAAAGA ATACTTGATG

60

25

AGTTAATACC AAAAATGGAT GCGACTGAAA AATTAACGCT TTATTTAACT AGTCATTATA

120

AACAGATAGA TTATGAATTT TTGTATCTCC TTTCATGGA TAAATTGTTT GGAAATAAAA

180

GAAATAGATT AACATTAATT GATTTAGAAA ACATATTGGG AGTAGGAAGA GTAAAAATTA

240

30

GTnGT

245

(2) INFORMATION FOR SEQ ID NO: 2387:

(i) SEQUENCE CHARACTERISTICS:

35

- (A) LENGTH: 140 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2387:

CACAAAATTC GAAATCGTCA TCGGTGATAT GTTTAATACT TGGGAAAATA TAAAACGCGC

60

45

CTTCAGGTTG AGCGGTAATC TCAAAACCTA ATTTAGTTAA TTCAGATACT AAATAATTC

120

TTCGTTChAC ATAAGCTTCG

140

(2) INFORMATION FOR SEQ ID NO: 2388:

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

55



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2388:

ATATAACATT GTAGGGCCTA ATAATTTATT TTATGTCTCA GACTCATACA ATGGTTATTT 60  
5 AACTTATTTA CCACAAATTG AGCACTAAGA CTCACTATTA TCGATTCTTC TATTGAACAn 120

(2) INFORMATION FOR SEQ ID NO: 2389:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 85 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2389:

TCTAAATCCA GCATGATCTA CATCAAAGCT GAATTCACCT TTTTCATCGA CTGCAAATC 60  
20 AGGGAATTCT TGACCTTCAC CTAGT 85

(2) INFORMATION FOR SEQ ID NO: 2390:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 61 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2390:

GGTGTTTATA AAGCAGGGGC TGAGCCTCGG TCAGGACTGG ATACACAGGC AGTACGGGTG 60  
35 A 61

(2) INFORMATION FOR SEQ ID NO: 2391:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 51 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2391:

TAAAGTAACC ACTTTAGATG ACATTTTGA AGTTATGGGC CGAATGCAAA C 51

50 (2) INFORMATION FOR SEQ ID NO: 2392:

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2392:

5 GGTCCGANTC CCGGGTCGAC CCACGCGTCC GCATCAACCT AGnAGAAGCn 50

(2) INFORMATION FOR SEQ ID NO: 2393:

10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 55 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2393:

ATTTCCAAAC GAATTGAAAA ACGGACGTAA ATTCTTAACT AAAGGCGATA AATGT 55

20 (2) INFORMATION FOR SEQ ID NO: 2394:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 120 base pairs  
 (B) TYPE: nucleic acid  
 25 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2394:

ATAGGTTGCT ACTATTTATA TCGACTCATT TTCACCTACA AATATGACAT TGTCTCTAGA 60  
 ACACnAAAAT TAATTTGCGT CATATCTGCT ACAGTTTTGA GTGTGTTATC AAGTGTATTT 120

35 (2) INFORMATION FOR SEQ ID NO: 2395:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 261 base pairs  
 (B) TYPE: nucleic acid  
 40 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2395:

TGGACCATAG TAAAGCATT ACGTCGGTTT ATTATTTTCT AAGGAAGTAT GTTTATATAA 60  
 ATCTATGCTC ATTTGTTTTT TAGCGTCTGT TTGACCTATT ATTTTAGAAC CAGCCATCTG 120  
 50 CTCTTTATAA AAATTTATTA CATCATCTTT TTTTAATGTT GTATATTCAT AGTTTATTTT 180  
 TATTATnTCA GAATCGTGAA AACTATTTAG TGATTGANAT ACTCTTTTGG GAGGATTCTG 240  
 AATATAGATT TTCTTAATAT T 261

55

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2396:

GTTTTGAATA TAGGGGCTTT TATCACTCTC CGAAGTCTnT TCTAAGTTAG ATTTGGAAAA 60  
 TAACACTTTT TTAGTTTCAT TCAAGCGAGT CGAGTGACTC CAGA 104

## (2) INFORMATION FOR SEQ ID NO: 2397:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2397:

GATTATCGAT CACAGTATGA TTTACGTAGC AATTTCTGGT ACATATACGC CTAT 54

## (2) INFORMATION FOR SEQ ID NO: 2398:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2398:

GCTTCACCTT GAACTAGCAA ATAAGGATAA AACAAGCATT CTTTACATGT TTCTTTTAAA 60  
 TACGTTTGAT ATTTTAATAA TACTTTTTTCG ATTTTACTCA TATAAGTTTG AAGTTCTAAT 120  
 TTTTCATTCT CACTTATTTT GTATATATTA CATTCAATTAT GTTCTGTCAG AAAAATATAA 180  
 GGGTCAATAT TAATTTTCGTC TATCAATTCA TAAATTTTAC TTAAGTATTT nTnCT 235

## (2) INFORMATION FOR SEQ ID NO: 2399:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

TTTGATGCAC TTATTTGTGT AATGACATCT TTACAGTCTT TTCCTTCCTC CATCATTTTA 60  
 ATAATTCCAT TTAGTTGCCC TTGTATTCTA TTAATACGAT TAATCATTTT n 111

(2) INFORMATION FOR SEQ ID NO: 2400:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 54 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2400:

AAATGCTGGC TGAGTTTGG GCCACCCGCA AAGGCACTGG ACCGGTGCGA AACC 54

(2) INFORMATION FOR SEQ ID NO: 2401:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 205 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2401:

AACCACTCAT CACTACTAAA ATGATACTTA AAAACAAAGT CTTAATACAC TTTTTCATAA 60  
 TATCAACTTC TTTCTATATT TAATACATTA ATTATACATC TTTnTnAAAT AAAAATATGT 120  
 GTAAATTTT AAAACTTATT TAATTGATGT TTTAATAATG TATTATAGAA ATTATTGACA 180  
 TATGATTAAA AACCCTTAGG ATAGT 205

(2) INFORMATION FOR SEQ ID NO: 2402:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 140 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2402:

AGATAATCAT AGAGAAAGTC CACAGTCGGT AGAGGTGGTA GCTGAAAACA ACATACTATT 60  
 AATTATGAAG TGCTTTGTAA CTTGTCGAGA CGTTTGCCGC GAATCTATCA TGATGGTGAT 120  
 CAACGTTTTG TnACAAATGA 140

(2) INFORMATION FOR SEQ ID NO: 2403:

- (A) LENGTH: 58 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2403:

10 ATTAAACCAC TCCTCCAATG ATAAGATTGA AAGGCAAGAT GACCTTCCAA TCTTATTT 58

(2) INFORMATION FOR SEQ ID NO: 2404:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 61 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2404:

CAGCTTCTAC AATACGGCGT GCTATAGCAA GCATTAATGT AAATCCTAAT TCTGCAGTTG 60

25

T 61

(2) INFORMATION FOR SEQ ID NO: 2405:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 217 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2405:

AATAATCATT TTAATACGGT CTTCAAGGAAT TGAAGTGTCT ACAGGTACAT ATCCACATCC 60

TGCTTTAATG GGCACCAATC ATCCCAACAA TCATATATGG TGACATGTGA CCGANTAAAA 120

40

TCATCGGGTT TCTTACTACC TTGTAATCGA TGTGGCTAAT TTACTAGACT CATCCATTAA 180

CTGTTGATAA GTTAATTCCA TCAGTTGTGT GTCTAAC 217

45

(2) INFORMATION FOR SEQ ID NO: 2406:

(i) SEQUENCE CHARACTERISTICS:

50

- (A) LENGTH: 228 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2406:

55

GTAGTATCCA ACGTATTTTCG GATTGCATCG AGTTGATTTT TATTATTTTC TTCAATGCTA 120  
TCAAGCGCAN CTGTATTACG TCTTACTTTA GGTTTTATTT GCTCTATTGC CTTGATTGTT 180  
5 TGATnTCTAA CATCAGTAAC AGCAGCATCT TGATTTGTAT TGTCTATT 228

## (2) INFORMATION FOR SEQ ID NO: 2407:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2407:

CCTTTCGTCT CGCGCGTTTC GGTGATGACG GTGAAAACCT CTGACACATG CAGCTCCCGG 60  
20 AGACGGTCAC AGCTTGTCTG TAAAGCGGAT GCCGGGnAGC AGACAGCGAT 110

## (2) INFORMATION FOR SEQ ID NO: 2408:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2408:

GGAGACCCCA AAAATTTTGT CGTTGAAGAT GCCTTTTTTTT AAGCGTTATT TGGCTATATC 60  
35 AGTTTCTAAC TGT 73

## (2) INFORMATION FOR SEQ ID NO: 2409:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2409:

AAATCATTAG AGAGGAATAG TTCCCTTTGT TACGCCAAAG ATTCGATATT GAC 53

## (2) INFORMATION FOR SEQ ID NO: 2410:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2410:

CCATATGATT GTATAGGATC CATGACGTCT CCACTGACCC CTGACTCTAG TATC

54

## (2) INFORMATION FOR SEQ ID NO: 2411:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2411:

GTTCTCTTC AATTGTTATA TGTATATCAC AAAAATTATT TCATTATTTT ACCATTATTA 60

TTTTACAAAT ATTATCCCAA GAATACAATT CAAGAAATGA TTAACCTTTAC TTTAGAATTG 120

TACCTTATTA CATTATTTAT GAAAGTACTC TCTCAATTAT AACNAAAAAG AAGGTGTTCA 180

ATACATnCAT ATTTAGTCTT ATAT 204

## (2) INFORMATION FOR SEQ ID NO: 2412:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2412:

CAGTGGCGCA GAAACATAAC GCTCAGGGAA GCACAGCACC TCATTATGCC AAAGCT 56

## (2) INFORMATION FOR SEQ ID NO: 2413:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2413:

TCGCTGGCGG GTCCGCGCG CCTAGCGTGC TCATGTGCGG TGTTCTAGGT GTTGGGGTTG 60

CAGTCA 66

## (2) INFORMATION FOR SEQ ID NO: 2414:

- (A) LENGTH: 65 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2414:

GGATAGAAAT GGAATCCAC CCATCGGTGG GGGTACCAGG CTCTTCATAT GGCCTTGTGG 60  
 ACTTC 65

## (2) INFORMATION FOR SEQ ID NO: 2415:

15

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2415:

TTAAATAGAT AGAATAGAAT TAAAGAGACG ATGATAGGTG CTGCTATCGT CTTAAAAACG 60  
 ATGATAAAAG GATCAAAAAC ATATGATACT TTTTCGAAAA TAAAAATAAC AATACCCAAC 120  
 AATACTAGCG CTATTAATGA GAAGACTAAA TCATTCCCAC CAACAAACTT CATATACCGT 180  
 GATTCGGTAA ATTTTnnAAA ATTCTTTCTT ATATTCTTTT CATTTTCATT CAATTATAGA 240  
 TTCACCACCA CTTAAAATAT TCATAAG 267

35

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2416:

TTAAACAAT GAATATAGTA GTTCATTAT CCTCACTTTT AATCGTTTAT 50

45

## (2) INFORMATION FOR SEQ ID NO: 2417:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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TTTGCTGGGA GTTGCAATTA GAAAATATAC ACATTTACTT GACATTCAAC TTGATAAAAA 60  
 ATTAGTTATT GCCATATGTT GCATCACATT TATAGGGATT TTAATATTTT ATGTACGCCT 120  
 5 AATTAAAAAA TCATCTTTAA ATATTTATAA TACTAAAAAT AAAAGGTCAA AAATnTT 177

(2) INFORMATION FOR SEQ ID NO: 2418:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2418:

AAAATGAAGC GGTGCGAAAA TATAATGACG TGAAAGCATT TTATACTCAT GGACATTTAT 60  
 20 ATCAAGTCAA TCGAACAAGA GATTTATTAG CTGAAAAAGG ACTTGAATTA GGTGTTTGT 120  
 TTGCATTTTA TGGACATACA CATGTGGCAA AATATGAGTA TATTAATGGT GTTCATGTTA 180  
 TTAATCCTGG AAGTATATCT CAATCTAGAA GTTCAATGGA AGAAACATAT GCTGAAGTTA 240  
 25 TTATTGATGA TCAAACCTTA CATGGCACCA TCAATTTCAA AAATCGACAT CACGAAACAA 300  
 TCAATCATACT TACTTTTTAA ATAGAAATAG CTATGGCTTT TTTTAGTTTA TAGACTGATT 360  
 TAACTAGGAG GTCGTGTCAT CCAATGTTTG TTAAAAAGTA 400

(2) INFORMATION FOR SEQ ID NO: 2419:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 53 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2419:

AGGGTGCCGA GTTAACCAAG AAAGGCCGTT GGTGCCCCG GGTATTTTCC CCC 53

(2) INFORMATION FOR SEQ ID NO: 2420:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 58 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2420:

(2) INFORMATION FOR SEQ ID NO: 2421:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2421:

ACCAGAAGAC AATAAGTGTA ATGATGCCTG TTCTAATACA GAATCTTTAC TTTTATTGCG 60  
 CTTTCAAGT CGTTGTTCCA CTTTCTTAAT TTCATTGTC ATGTTTAACT TTGCCAGTT 120  
 AATCACCTTT GGTATTATCT TTTTCTTTAT AG 152

(2) INFORMATION FOR SEQ ID NO: 2422:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2422:

GTACGTTTT ATTAGTTGTT ATATTTCCAT CTTGATAATT TTTTAAATCT TTAAATCAG 60  
 CATACTGACT AAAAAATTTA AAATTTTCAA TTTTGTGTT AAGTTTTTGT CTTCTACATT 120  
 ATCCAAAAGA ACAATCTTAT TATTTTTTAG TTCAACACGA TATTTTTTCT CATTATGATT 180  
 TTTGCTAATA TCATCATAAA CTTTATTTAC AAAATAATAA CCTGTTGCCT TTTTGGTATT 240  
 TCTATTAAGA TATAACACCA TGCCTTCATC ATCTAATACT CCTGGTTTGT TACTTTTTGA 300  
 AAAACCh 307

(2) INFORMATION FOR SEQ ID NO: 2423:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2423:

ATTGTGTTGT ATTTTAGACA AGACCTTCAA TTTTGGAGAT TTCACGATTT ACCACC 56

(2) INFORMATION FOR SEQ ID NO: 2424:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2424:

10 AGTCCTTTGG ATCGTCAAGA TTTCACACAT TTACanTTAT TanCTCGTGA

50

(2) INFORMATION FOR SEQ ID NO: 2425:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 248 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2425:

ATGTAATATT ACAATTCAAT TAGnAAAGAA CTTTATCTTT AATTGCTTTT CGATTTTCATT

60

25

CATGTCATCT TCTGAAATTA TTATCGTTCC AGTAGGATCA GAATCAITTA TTTTGCTTAT

120

ACGTCTTTTG CTTATTGTTG TAATTGCTGA TATATTAACG TATGTATCTT TCCCTTTGTG

180

CTTGGAATAA ACACCTATCA CTCTATACAG TTCATTAGCT TTTTGanTTA AGTTAGACAA

240

30

AAGCTTTT

248

(2) INFORMATION FOR SEQ ID NO: 2426:

(i) SEQUENCE CHARACTERISTICS:

35

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2426:

CCTTATTATA TGACAGGTTG CCTAAACAAG TGCCTAGAGA AAAAAGTAGC CCC

53

(2) INFORMATION FOR SEQ ID NO: 2427:

45

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 173 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2427:

55

TATCCACTAA AATGATTGTC GCGTATTGTA ATATTAAATCG TTCTACTTTT TATGATTATT 120

ACAGGGAGCA ATTTGATTTA TTGGATACCA TCAACTCnAA GCATAGGTGG AGG 173

(2) INFORMATION FOR SEQ ID NO: 2428:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2428:

TACTTATGTT TATGTCGCAA TAATTAATGT TCGANTTAGT GGAATTGAAC 50

(2) INFORMATION FOR SEQ ID NO: 2429:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 68 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2429:

AGTCATCATA TTATCAATAA TACGCCGCGT TAAATCTGAT AAATTCATAT AGTCTGTATC 60

TAACTCTG 68

(2) INFORMATION FOR SEQ ID NO: 2430:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 374 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2430:

TGAATTGAAA ACGGTCGGTG AAGCGCTAAA AGGTAGACGT GAAAGGTTAG GAATGACTTT 60

AACAGAATTA GAGCAACGTA CTGGAATTAA ACGTGAAATG CTAGTGCATA TTGAAAATAA 120

TGAATTCGAT CAACTACCGA ATAAAAATTA CAGCGAAGGA TTTATTAGAA AATATGCAAG 180

CGTAGTAAAT ATTGAACCTA ACCAATTAAT TCAAGCTCAT CAAGATGAAA TTCCATCGAA 240

CCAAGCCGAA TGGGACGAAG TAATTACAGT TTTCTATAAT AATAAAGACT TAGATTATAA 300

GAGTAAATCC AAAGAGCCAA TACnATTATT AGTAATCATG GGNATTACAG TTTTAATAAC 360

## (2) INFORMATION FOR SEQ ID NO: 2431:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2431:

TGACTTCGTC CAAGTACAAC TGCAGTCAGT ACCTACGAAA TCAAGATCAG CATGGAT 57

## (2) INFORMATION FOR SEQ ID NO: 2432:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2432:

ATTCTTAATC GCATCATAAT TAATTAACGG ACGCATAACA AATCCGATAA TACTATTATC 60  
TTTCCAAGTC ACTGACACTC CAAATTGATT TGCTTCnTCT ATCCATATTT GCTCAATAGT 120  
ACCATCATTT TGAGTACACA CTTTAAATTC ATGTACATCA GACTGCCTTG TATAAGATTT 180  
GAAAAGTTTC CTAAACTGCC AATAACTGnA CTCTCGCTTC AAATT 225

## (2) INFORMATION FOR SEQ ID NO: 2433:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2433:

CGGCCTGACG TTACATTTCT TCAACTTCAC GTCAAAATTG CTTGCAATA ACCAGGA 57

## (2) INFORMATION FOR SEQ ID NO: 2434:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

TTAAACGTGT CTTTAATGTG GAAGTTGAAA TATTAGTCCG TAAAAAATG AAACTTAAAA 60  
 AAAAATAATA TTTATATTTG TCGTACAAAG ATGAAAGCGA nAGA 104

(2) INFORMATION FOR SEQ ID NO: 2435:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 51 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2435:

TTTGCTAATC GTTTCACGGA TTGTGGGGAT GGGTAAAGAC TTTGCTAGTG G 51

(2) INFORMATION FOR SEQ ID NO: 2436:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 140 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2436:

AAAnTTAATT TTTGGGGGGC CCTTTTTTAA CCGGAAAATC CAATCGGGGC TTTTAAGGAA 60  
 TGGTTTTGGT TAACAGGCTT TGGAATTGG TTTGGCAAAA CAATCCTTGG TTTGGGGTTT 120  
 CGGTCCGGAG GGTCTAATT 140

(2) INFORMATION FOR SEQ ID NO: 2437:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2437:

GAAGCGGAAC CACCGTTGTT TTTCTTTTCA GGTCCAATTG AATAAATGTT ATGAATAGAA 60  
 TGGATAAAAA TATAATTATT TAAGTGTTAA AGTAAACCAA ATCATGATTT AAGATTATAA 120  
 GAAAGAAAAA TTGACTAATG TTAAAACCAA CAATCATATG GGTTGTAACG TTTATACAAT 180  
 CATCGTAAAA CTCAATATGC TTAATTTATT CAAAATGTTC GTCAATAAGT ACAATGAAAA 240  
 GGAGATTGAT TTTTGAATAA AAAATATCTT ATGATTGTAA TTATAATTTT AATATGATTC 300

AAGATACGAT TTTGAGACCA TGTGAAGGGA TTAAATATAG

400

(2) INFORMATION FOR SEQ ID NO: 2438:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 59 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2438:

TCTGTTTTGA AAGTTGCAGT TTGGACAGCA CCCGATGATT AGGTGAGTCT TTTGGTTTA

59

(2) INFORMATION FOR SEQ ID NO: 2439:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2439:

TTGGTnAAAC CGTTACAGTT GCAAGTTTTG AAGTGAGTTA TTTTTGGTT

50

(2) INFORMATION FOR SEQ ID NO: 2440:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2440:

ATTAAAAATA AATTAAAGT TCCAGAACCA GTTAACCAGA ATATTACGA

50

(2) INFORMATION FOR SEQ ID NO: 2441:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 54 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2441:

TGCTGTTTTG GCGGTTTTTC TCCGTTTGGT TGAGTATGTG GTGTACCTTT TGTC

54

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2442:

5 GTTGTTGGGT GTGTGGTTT GGGTGTGTG GGTGTTGGGT CTGGGTTTCGT TGGTGG 56

## (2) INFORMATION FOR SEQ ID NO: 2443:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2443:

20 GAGACAACT AGTCGTCCAG AACGGAATTT AAGTAATCAT AATAATTACG GAAGTGCACT 60  
 25 TTTGTTTTTG ATTTATCATT GATGGAAATT AGAACAAATT ATCGAATGAT ATTAAAATTA 120  
 CATAACATCA TGTGAATGT GAAATTAGGA TTGAACATTA CCTGTTTATT TGAAAAACCT 180  
 30 TCAGTTTTTA AATCACTAGT ATCACAAATA AAGCGACTTA AATTCGATTC GTTAATAATA 240  
 GATAATGCAA ATTTAAGTAG CCCT 264

## (2) INFORMATION FOR SEQ ID NO: 2444:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2444:

35 CCGTCTTTAG TACGTACGTT GTTTCGCGGG CTGCGGGTGC TTCTGGGGT TGGTCATTG 60  
 45 TATTGGG 67

## (2) INFORMATION FOR SEQ ID NO: 2445:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2445:

AGCTGCATTT CTCGTGCAGG CTATCAGCAT CGATATCTGT ACCATTTAGT GATCATGC

58

5 (2) INFORMATION FOR SEQ ID NO: 2446:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2446:

15

AACCAAAACA AACATTTGTT CGTTAAATA TTGACACAGA ACATAAGTTC TGA

53

(2) INFORMATION FOR SEQ ID NO: 2447:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

20

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2447:

CACAAATTAC ACCCATTGTT AntACTAATA CTnCCnTTT CATTTGTTTA

50

30 (2) INFORMATION FOR SEQ ID NO: 2448:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 75 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2448:

40

GCACAAACCA AACGCACCTT AACTGCTTTA AATGGCTGGA CGGGGGGTCA ACTGGCCTTA

60

ATGACACTTG AATCG

75

45 (2) INFORMATION FOR SEQ ID NO: 2449:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

50

55

GCAGCCTTCA AGTGTGTTGCT ATTTGCTTTG GTGTCACAAG CCATTATCTA CGGTCCCGCA 60  
 ATTTAGCCCG C 71

(2) INFORMATION FOR SEQ ID NO: 2450:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 351 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2450:

TGGCGTGAGG AAAAATATCA TGTATTGTTA CACAGTCAAC AGTCTTACCA AATGATAAGG 60  
 AATGCTTTAA AAACGGATTT ATCACTTCAT CAAGTTCAAC AAATGATTGA TGTGCTTTG 120  
 TTAATTGAAC CGGTATAGG AAGTGATGT AATGCTTTTG ATCATATGTG GGGATATTTA 180  
 AAAAAATGTG CGAATGAAGA AGGAAAGACA ACAATCAAAA CTACTTAAAA GCTGATTTTA 240  
 TTTAATGGnA AAAATCGACA CCCCACTTT ATTAGATTTT TTAGCAGAAC TTGCCTAATA 300  
 AATATGGAnG TCAATATTTA CTACAAAGCC GnGTTTTTAA ACCCCAAAAA G 351

(2) INFORMATION FOR SEQ ID NO: 2451:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 54 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2451:

GTGTACCGCC TCGGCTGGCG TTCGCGGTGG GTGGTGCGGT CGGTGCGTGT CTGG 54

(2) INFORMATION FOR SEQ ID NO: 2452:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2452:

TGCCATTCCA ATGTTACCAT CGTCTTGTA CTACTATATA CTGCGGCTAT 50

(2) INFORMATION FOR SEQ ID NO: 2453:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2453:

10 AGACGTGTTT CCACGGTATG GGATAAATGA AGCACCGACT GATAAATCAA TATAGCCTCG 60  
 TGTTTTTAGT TTACCCGAAC TATCCCTTGA TAATGATTGT GACATCTGCG GATAATATTT 120  
 CATTTTCTTA GATATCGTCG AAATATCACC GATTACTTGA AGTCCATCTG TCGTAAACAA 180  
 15 TTCAATTCTG CTTTGTGTTGT TTTTACTTGG GCGGTATGTC ACTTCGGCAA TATATCGTCT 240  
 AACTTCAGGT GTCATTTTCAG ATAACGCCTT AATCATATCA TCTTCTTTTG TACCTTTGAA 300  
 ACCATCCATG ACAGGTGCAT CATTAAATTT GACATCATTT GAACCTTTAA GCAATTTACC 360  
 20 ATTTTCTAAT AAAGGTAAAT ATTTACCTTT ATATTTCACT 400

## (2) INFORMATION FOR SEQ ID NO: 2454:

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 156 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2454:

AGAAAGAAAT ACCATTTGGA GATAGAGACT CGTGTATTTT CTTAGCGATG GGAGATTTTT 60  
 35 ATAATAAAGA AGATAGnAAG AAAATTATCA AAGGTTATGA AAATAATTAT GGTAGAGGTA 120  
 TTAATATTCC TCGAGCACAT AGTATATATT TATATG 156

## (2) INFORMATION FOR SEQ ID NO: 2455:

## (i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 77 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2455:

ACTTAGGTGA TATGAAATGT GGTCCGCGAC GATCGTCAGT AACAAAATAA CAGGCAGTCA 60  
 50 TTGGATTATG TTTAACG 77

## (2) INFORMATION FOR SEQ ID NO: 2456:

55

- (A) LENGTH: 65 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2456:

10 AGTGAAATCG CTAAAGAAAA AGATGGAACC TCGGTATCTA ATACACAAC TCTTGAACGT 60  
TTTTA 65

(2) INFORMATION FOR SEQ ID NO: 2457:

15

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 54 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2457:

25 TATCAATAAT TGCCACTTGC AATGACTGAT TAATTTGAGG TGCACATAAG CCAG 54

(2) INFORMATION FOR SEQ ID NO: 2458:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 166 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

30

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2458:

AATTTTATTT CGAGATTCTT CAATATAGAT GTTCTTCAT TAATTTGATT CTCTAACTCT 60  
TGCTTACTAC CTAATAGTTT ATCTAATTCA GCTTTAGCTT TTTCATTTTC TTTAATTATA 120  
TTAATTTTCAT TATTTATGTT CGTnATCGTA TTATTTAGTT CGATAA 166

40

(2) INFORMATION FOR SEQ ID NO: 2459:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 66 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

45

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2459:

55 CCAATGATTA AGCAATACAA TCGTCACTAA AATTACACCG ATAATCTGAA TCATCGTCAT 60

## (2) INFORMATION FOR SEQ ID NO: 2460:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2460:

AAATCAAAAA AATGTATAAT GAAAAGAAAA AGAAATTTGG AAAAAATTGG GAAGACGCTC 60

AAAAAGCTGG AAAAGCTGTA GGTGAAGATT TGAGTGThAA TGG 103

## (2) INFORMATION FOR SEQ ID NO: 2461:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2461:

TTTATATCAG AATAGAATAG TAACTAAGG CATTTGGAGA ACTTATTCCA TG 52

## (2) INFORMATION FOR SEQ ID NO: 2462:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2462:

CAGCAGCGAA TTTTGGACGT CCAGTGTAGA ATGGATGTGA ATCAGATGAA ATATCTAAAC 60

GAATAACTGG GTATTCTTTT CCATCTTCCC ACTCCATCAT TTCTGAAGAn GTT 113

## (2) INFORMATION FOR SEQ ID NO: 2463:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2463:

CTAACATAAT TGTTAACACT AAAATATTTA CTA CTTT TAG AACTGTGCGA TTAAATACAA 120  
 TTGTCAGTAT TGT TATGACT AGGCTAACGA TACATAAAAT AAAGAAACCG TTAAAGACTA 180  
 5 AAATTAAGCG ATCGATTCTT TGTGTAAAT CATTGATATT ACCCAAATTA ATAnTTAATT 240  
 GGATGCATTT nCCAA 255

## (2) INFORMATION FOR SEQ ID NO: 2464:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 58 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2464:

20 TATGCGACAA TTCGAAACAT TTTATATGCA AAAGGTTATA CAACAGAGAA TGTTGATT 58

## (2) INFORMATION FOR SEQ ID NO: 2465:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 65 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2465:

30 TGAATTTTCAT TACCACATAT CGGACATTGA TCTCCAATAT TTACAGCAGA TTTAATTTC A 60  
 35 CTTAT 65

## (2) INFORMATION FOR SEQ ID NO: 2466:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 51 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2466:

45 CGTGACCTTC AAAGACCGAA CGAGAGAGTT GAAGAGCATT TGCGAAGGCC A 51

## (2) INFORMATION FOR SEQ ID NO: 2467:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 55 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2467:

AGTTTGTTAA GTTTGTAGTTT ACTAAGTTT CCATTAGATA TTATTAATGA AAAAC

55

(2) INFORMATION FOR SEQ ID NO: 2468:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2468:

TTGTTGGTAA GGCACCTTCTT AAATATCAAC AACGCGATGA TATTTTCATT GGTACAAAAG

60

TAGGCAATCG TTAAAC

76

(2) INFORMATION FOR SEQ ID NO: 2469:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2469:

CTTCTATAAT AAAACCATCT GCAATTAAGT CTTCAATAGA CGATGGATTT CTATTATGTA

60

TCAATGCATA C

71

(2) INFORMATION FOR SEQ ID NO: 2470:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2470:

CTTCGTCATT GTATTCGAGC GCCTGTATAG CTTGCTCAAA TGATGCATAA AT

52

(2) INFORMATION FOR SEQ ID NO: 2471:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2471:

AGAGGTTATG TTGATGTGCT TTATTTTCAT CAATGTCATT AACACAATCA TATTTCTTCT 60  
 5 GTTAATGCAC TGTATTATAT TCAAACGCGC TATCGACAAT TAATTTGn 108

## (2) INFORMATION FOR SEQ ID NO: 2472:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2472:

GTCCCCAGTT GATATAGGAT CACAGTTTAA TATACTTGGT GAGATAGTAA TACTATTATT 60  
 20 AATTCAAATA GGTGGTCTGG GTATCGTGAC CGTAACCCTA TTGACACTAG TATTTTTTAAA 120  
 TAGAAAGATA TCAATGAAAA ATAGATTCTT GATTATGGTT ACATGGAATA TTGACGAACC 180  
 TGGTGGTGTT ATTAAGCTAA TTAAACACTT GGCTATTTAT AGTTTAGTCA CTGAATTAAT 240  
 25 TGGTATGATT TGTTTGTGTT TATCTTTTAT ACCAAAATTT GGTATAGGCA AAGGTTTATT 300  
 TTTAAGCTTA TTCACATCAG TATCAGCTTT TAATAATGCT GGGATTTGCC CTTTTTAAAGA 360  
 30 ATAACCTAAT AGATTATTCT AGTGATCCAA TTGTCATTAT 400

## (2) INFORMATION FOR SEQ ID NO: 2473:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2473:

CTTCAAATAC TAAATCAGCG TTGCTAAACA TACCGTATAC ATTTGATGGC GTTGATAACG 60  
 CGTCCTGCGC TTCTGTTAAT AACTTTTCAG TTTCAGCATC TAATATATGA GGACGTTTTT 120  
 45 CATTAAATCAA CTTCAAATCA AATGCGA 147

## (2) INFORMATION FOR SEQ ID NO: 2474:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2474:

5 CTTTAGGTGC TTGTGGTAAT TCTAATTCAC AAGATCAAGG TAACAAAACCT GAACAAAAAA 60  
CA 62

(2) INFORMATION FOR SEQ ID NO: 2475:

10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2475:

15 CCTTTAAAAT CATCTAGAAT ATCTCTTGAG AAAAATTCGA AATCTACAGT 50

20 (2) INFORMATION FOR SEQ ID NO: 2476:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 113 base pairs  
(B) TYPE: nucleic acid  
25 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2476:

30 ATAGTGGTTA GTCAATGTAA TTAAATGAGA ATAGAATGGT GATTTCATCT TAGCTTGATA 60  
ATTAGCAGAA TCTTTAAAGA AAATTTTGTC TTCAAGCCT AAGTTTACAA CGT 113

35 (2) INFORMATION FOR SEQ ID NO: 2477:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 51 base pairs  
(B) TYPE: nucleic acid  
40 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2477:

45 CGTAACTAAC TCAATTTACT GAAAAAATCG CTGCGATGC AATAGCATTT G 51

(2) INFORMATION FOR SEQ ID NO: 2478:

50 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 60 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2478:

TAGTTGCCGC TACGTTTATA CTCGTATTAA TGAAAAAAC TAGCAAGAA TCTAAAAAG 60

(2) INFORMATION FOR SEQ ID NO: 2479:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2479:

TCGGACATGA TGGTAAACC GTATTGGGTA TTCGCACTGA CACCTTAAGG GA 52

(2) INFORMATION FOR SEQ ID NO: 2480:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2480:

TTCCTAATTA AGGATTAAAA AGGGTTTCCT AATTAGATTA AAATTCCGGG ACCTGGATGG 60

AAAAAAGTTT TTAACTTTTC CATCTGGTCC CGTTTTTTGA TTTTCGATAT AAAAAAGCG 120

CAATTATCTC TAT 133

(2) INFORMATION FOR SEQ ID NO: 2481:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2481:

AAATGTTTTG GAAGAACGTA AGAATAATCA ATCTGAAACA AATGCACGAT ATGAAGAAGA 60

ACAAGAAAAT TTAATGGAGC TTTTAGAAAA TATATCAAAT GAGATTCTG AAGCTCAAGA 120

TACTTATAAG TCTCTGAAAA GTAAACAAAA AGAACTCAAT GCTGTCATTC GTGAACTTGA 180

AGAACAAC TA TATGTTTCAG ACGAAGCACA TGATGAAAAA TTGGAAGAAA TTAAAAACGA 240

TACTATAGAA GAGAATGAGG CTAAAAAATC CAGACAGGTT CTCGTTAGTT GGAGTTTTGA 360

GCCATTGAAA GTATTcnggg GGCCAATTAA AACCGCCAAA 400

(2) INFORMATION FOR SEQ ID NO: 2482:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2482:

AAGGTGCATA GTCAACAACA TTTACAGCAT CATTTGATTC TGAAC TAACC GAAACATTAT 60

ACTTACCG 68

(2) INFORMATION FOR SEQ ID NO: 2483:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2483:

ATGAGCCnAC ACAGTGGTGA GGTAAATCAAC GGTACAGTGG TTAGTGTGAT 50

(2) INFORMATION FOR SEQ ID NO: 2484:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2484:

CGGAACTCGT CGAATAACTT TTTAGATTCT TCGTTAGCTT TTACATTAGC GAATGCTTCT 60

nTGATTGCTT TGTATTCTTC GCTTTCTCTT AAAGCTTGTT CTAATTGATT TGCATAATCA 120

TATAAATTTA CTGCCATGGT TATAGCACTC CTTGGTnGTG ATGTTTATTA AAACGTTTCA 180

TATTACTTTA CCACATCTCG CTTTTTTAGA CAA 213

(2) INFORMATION FOR SEQ ID NO: 2485:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 376 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2485:

GACCAAAATT ATCTTTAGCA CTTATAGGTA TCTTTTAAAT ACTTTGTGAG TTTTCTATG 60  
GCATTCCTTT TTTAGGTGCA ACGTTTATTT TAAGTTTGG ATGGCAGCCT TTA CTCTTTA 120  
ATGCATTACT TTATCTAATT CTTACTATTA TATTATTAGT GAATAGACAA AATGCGATTA 180  
GACCTATAGC GATTATTCCA ATATTTGGTA TAGTAGTAG TTTT TAGCT ATTATCCCCT 240  
TCTTAGGAAT TTTGATTCAT TGGATTTTAT TTTTCCTAAT GATTCCATT GTCCTAGTTG 300  
GATTATCAGC GCCAACCTAT ATACCCAATA AAAATGCTCG TGCnTTTTA CACACAATAC 360  
AAAGATGGAC CTAGAG 376

20

(2) INFORMATION FOR SEQ ID NO: 2486:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 51 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2486:

TTGACCTTGA CGGAAACTTT TTTCCAAGTT CTAAAGTGG GCCAAATCT T 51

(2) INFORMATION FOR SEQ ID NO: 2487:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 103 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2487:

GAATTTTGGC ATACACATAC ACTTTAAAAG ATATTATTGA AATTACAGGT GTA ACTAAAA 60  
GAACTTTACA TTATTACGAT GAAATAGGAT TATTAGTTCC AGn 103

(2) INFORMATION FOR SEQ ID NO: 2488:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 106 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2488:

5 AATTACATTA GCACCAATCC ACACATCATT TTTAATTGTT GTACGGCTAG GTTGGTCATT 60  
AAAGTCTATA AACGTTTnCT TTAAGTTAAA TGGATTATTA TTTAGA 106

(2) INFORMATION FOR SEQ ID NO: 2489:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 61 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2489:

20 TGAATTTGCT TGAGTCGTGC TGCTGATAAC AATAAAATTG CACATGGATA AAGAATGACG 60  
C 61

(2) INFORMATION FOR SEQ ID NO: 2490:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2490:

GCTCGTATGA TACAAATTCA TAATCTGAAA CTTCTGTCGT TTGTCGAACA TGTGGTAACC 60  
35 AATTCTTCAA GATGCTGTAT ATTTCTGCGT AATTTTCGTC ATTCCTGAAT AACCTCAACT 120  
TTAAATGTC ACCTTGTTG ATATAACGCA TTAAAAATA TTGATCTATA TCTCCCTTAT 180  
CTTTAAGATG TTTTACAAAT GGATACAAAT TGTCGATGAT AAATGTATCT TGCGATGGCT 240  
40 TATCGATATG AATATGTAAT GCAAACCACT CTTTGTCTATA TTCAATATCT GTATTTTAT 300  
ATTTTGGAAT TTCGATTTCG GGTCCCTCGAT AAGATGATTT TTTATAAATT GGTGTAACAA 360  
TTTCATACAC ATGATCATT CTTGATTGAG GGAAAAATGA 400

45 (2) INFORMATION FOR SEQ ID NO: 2491:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 57 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

GACTGTTTTA TCGCAACTAT TTACACCTAT ATTATCGTTA GTAGGACATC TCGTCGG

57

(2) INFORMATION FOR SEQ ID NO: 2492:

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2492:

15

CATTGAACCTT GCTTTTGACG TACACCAGTA ATCAATGCCA TAATACGATC CGG

53

(2) INFORMATION FOR SEQ ID NO: 2493:

(i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2493:

AATACAACCTA ACATACACTT ACCCATGTCC GAAGTCCTTG TTGAGGAATG

50

(2) INFORMATION FOR SEQ ID NO: 2494:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2494:

40

GCTGTTTAGC TTGCTCAAAT GATGCATAAA TATCTGATGC AACTATCATA TCAGCTAGTT

60

CATCA

65

(2) INFORMATION FOR SEQ ID NO: 2495:

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2495:

55

ATTAAGCTTT CTAAATCATT GATGTTAGGA GCTAATGTGC TCGATAAGCA GAGTAAAGAA 120  
 GAATTGCTTA AACAAAGCTAA ACATATAACA GGTTTAGAAA ATCCTAATAG TCCTACACAG 180  
 5 TTATnGGCTT GGTAAAGGA TGAACAAGGA TTAGATATAC CTAATTTACA AAAGAAAACG 240  
 GTTCAGGAGT ACTTAAAAGA AGCAACAGGA AAAGCTAnAA AAATGCTAGA AATTAGATnG 300  
 CAAATGTCTA AAACCAAGTGT GA 322  
 10

(2) INFORMATION FOR SEQ ID NO: 2496:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 59 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- 15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2496:

ATCAGTGTTA ATTCGCACGG AATTTCTTC CATTAACTA ATCCGATCAT ATAATGGAT 59

(2) INFORMATION FOR SEQ ID NO: 2497:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 126 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- 25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2497:

CTAATTAAGC CAAAGGGGA AGGGTCCACC AACCCTTGGT TTCCCCCAT TGCCCGGAAA 60

CCACCAGnAA GTTTAAAGCT TCCCTTTAAG CCGTCCGATG GGTAGTCCGA ACTTTACCGT 120

TCCCGC 126

(2) INFORMATION FOR SEQ ID NO: 2498:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 58 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- 45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2498:

CACTTTGCGC CAGTTTTTCAG TTGAGTGGCA TAGAGTCTGC TCATCAGTTC CTTGCTCC 58

(2) INFORMATION FOR SEQ ID NO: 2499:

(A) LENGTH: 90 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2499:

10 TCATGATGCA GACGCAACAG CATTGGTTA TGAATATGGA CAAATACCAC AGATGCCGGT 60  
 AGCATTTCAC TCAAGTAAAC CTTTAATAGA 90

(2) INFORMATION FOR SEQ ID NO: 2500:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 292 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2500:

25 TGCTCAAAGT CGTGTAGACA GCCAACTAAT GCATTTTCAA GATCAGTGAC ATCTCCGACA 60  
 CCAAAGAAAT CACCGAATAT TTTTGCATGT TCGATTTTAC CTCGTTTAAC ATCAAACCTA 120  
 ATTTGTACAA ATCCTTTTTC AAATTTTTC TCGCGTTCAA AGTTATATTT AGGGTTTCTA 180  
 30 CCATAATTCC ATTCCCAAGT TCTATATTTG TCGTTACTTA ACTTTTCAAT ATTTTCCCAA 240  
 TCTTCATCCG TTAATTGATA TTCTTCACT TCAGTTTCGC CAAAGATAGT TT 292

(2) INFORMATION FOR SEQ ID NO: 2501:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 58 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2501:

45 GGTGTGTGTA GAGGTCGAGA GTTGGGGGGG GAGTAACGTG GAAGTTGCCC GGACAGCA 58

(2) INFORMATION FOR SEQ ID NO: 2502:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear



ATACGGGAGG TATCAGCACG TACGTGCAGT CGGTAATGGA TCnAAATACG

50

## (2) INFORMATION FOR SEQ ID NO: 2503:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2503:

ATCCCCACTC TTTTTTAAAT GATTTAACCA TATTTTATTT TTAAAATAAA TATCCATCAA 60

AGTGTATCAA TAAATTTATC ACATGTCAGA AAGTATGCTT CATCTGAATA CACCAATACT 120

CTCATGAAAC TTATTAAAAA TTAATCTCTC AACGTAAAAA ACCATTCAAA TTCATGAATG 180

GTTTGGAAGA ATGATTCATT GTTACGCTAT TTAATCACTA CATCTTAATT ATTGTTGCTC 240

TAAACGATTA CGCTTACCAT TTAAGAAAGC ATAAACGAGA CCTACAAAAA TACCGCCACC 300

GACAAAGTTA CCTAAGAAAG CAAAACGAT ATTTTTTAAA ACGTGTAACC ATGAAACTGC 360

ATCAAGGGTA AAGAATACCA TACCTGCATA TAGACCTGCA 400

## (2) INFORMATION FOR SEQ ID NO: 2504:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 355 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2504:

ATTATCTATG AATAAAATTT ATAATAACA TATATTGAGA AATTCTCTAA TACCTATTAT 60

TACATTTTTA GGTGCTGATA TTGTAAGTAT TTTAGGTGGA GCCGTGATTA CGGAGACTAT 120

CTTTTCATAT AACGGTATCG GTAAATTATT TTTAGAATCG GTAATAGGCC AAGACTATCC 180

ATTAATGATG GCATTAACTG TATTTTCTC ATTTTATAGT TTAATGGGTA ATTTGATTC 240

TGATATTACT TATGGATTTA TAGATCCAAG AATTAGAAGT AACTAGGGGG GATTAGAATG 300

CAAAATAAGT CAAAATCGCC TTTnAAAATT GCATTTTCTA AATTnATTCA TAnTA 355

## (2) INFORMATION FOR SEQ ID NO: 2505:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 254 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2505:

5 CCGTTAGTTC CATACCATAT TTTTCTCTAT AAAATAATTT AACATCTAAT TGCCTTTCTA 60  
 ATTTTTC AAT AGGGGTAGAT ACAGTTGACT GTGAATAGTT AAGTAACTCT GATGCTTTAG 120  
 TAAGGTTCTT TGTTTCACTA GTTACTAAAA ATGATTTTAA AATGTTTAAG TTCAAAGTAG 180  
 10 TACCTCCTTT AGGGTTCCTT TTTATCGAAT CCTGAATTCT AAGAATTCTG ATTTAATAAT 240  
 AATATATnAn ATAT 254

## (2) INFORMATION FOR SEQ ID NO: 2506:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 268 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2506:

AACTCCACCG TGTAGTTGCG CTTTCATCGCC TTGAGGATGC GATTGGCGCC GTGCTGCGCG 60  
 25 GCACGTGCAG ATAGTGCAG CACTTGGGCA GATCGCGCAC CGCCTCCAGC AGGTCGTCGG 120  
 TCATATCCTT GGGATAGTTC GTTACGAnTT GGATCCGGTC GATGCCGTCG ACATCCGAGA 180  
 TGCGGCACAG CAGGTCGGAC AGTCGCGTTG nCCGCTGGCA GTGTCGTAGT GGTAATGTTT 240  
 30 CACGGTTTTG ACCTAGCAGC GTTCACCT 268

## (2) INFORMATION FOR SEQ ID NO: 2507:

35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 66 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2507:

AAAAGTGGCT AATATCATCA GCAGAATGTA TAACATAATC GAATTGCAAC CAGCGATTAT 60  
 45 ACCTTT 66

## (2) INFORMATION FOR SEQ ID NO: 2508:

50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 53 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2508:

ACCTCCGCTT CAAATGTCAT TGATAGACAT TTAAAGCGGA GGCATGTACA TGT

53

(2) INFORMATION FOR SEQ ID NO: 2509:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2509:

ACCCTATGAn AGATGAAGTn ATTAACCAAA AACCACGTGT TGTAATATTA

50

(2) INFORMATION FOR SEQ ID NO: 2510:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2510:

TTAACCTATT ATATTAATTT TAGTATCAAT TCTTTCTCCA GTTCTGCGT CATTTTT

57

(2) INFORMATION FOR SEQ ID NO: 2511:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2511:

ACGTGTTTCAT AACCCATAAA GGCGAATATG GTAACACCGA ACATCATGAC A

51

(2) INFORMATION FOR SEQ ID NO: 2512:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

GTAAAGCGGT CCGCGCTTAA AGCGCTTGCT AACTTCGAAC AATGAATCTG CGGAACATCT 60  
TGC GAATCCA CGAGATGATC TCATATGACG GGCAGCGAGG T 101

5

(2) INFORMATION FOR SEQ ID NO: 2513:

10

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 67 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2513:

GGGTAATGTA ATAGTATTCA TCTACATCAT CTTGATCATC GTAATGCTGA TTGTACCCTT 60  
CTAAATC 67

20

(2) INFORMATION FOR SEQ ID NO: 2514:

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- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2514:

CCCGTCGTTT TCGTGTGTTTT CGCGGCGTGT CTCCTGTTCTG CGCCTCTACT 50

(2) INFORMATION FOR SEQ ID NO: 2515:

35

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 275 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2515:

45

AAGAAAATAT CTCTTGAATA CTGATCGATT GCCATCGAAA AACACTGTTA AATCAAGTTG 60  
CCCAGTCCAT TGTGTGTCAT CCATTATGAT AATCCTTTGA GTAAAGTGTC GCGTTCAATC 120  
CAATCGATAA CTTTCATCAA ACCTTCGTCG GTTTTTAAGT TAGTAAAAGT AAATGGACGT 180  
TTACCACGAA ATACTTTAGT ATCTTCAGCC ATTTGTTCTA ATGATGCACC TACATANGGA 240  
GCTAAATCAG TnTTGTTAAT TACAAAGACA ATCTG 275

50

(2) INFORMATION FOR SEQ ID NO: 2516:

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- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2516:

10 CTGCACCACC AATAACGTAA ATACTGTATA TACTAGTAAT CGCTAATACA CCGATATTA 59

(2) INFORMATION FOR SEQ ID NO: 2517:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2517:

TCTGCTACTA CGTATACGAT AGAATGGATT TCTTTTGTAA CCTAAACGTG TTAAACGAAT 60

TTTAACTGCC ATTTATAAAA TCTCCTTTAA GTCATGTTTT AATTTTATT TTCTACAG 119

25

(2) INFORMATION FOR SEQ ID NO: 2518:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2518:

ATTCCTTTT AAGTTTTTAA AAATCCAAAA TCCTTGTGGT AGGGCCATGA AAGGGTTGGG 60

(2) INFORMATION FOR SEQ ID NO: 2519:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2519:

ATAGAAGTGA AGCACGTAGA TTGAAACGAT GGTAAATAA CGAGAGACAT TTAGAAAACA 60

50

ATAAAAATGA GGAATAATCA ATGATACATG GAATTGGTGT AGATTTAATC GAAATCGATC 120

GAATACAAGC GTTATATAGT AAGCAACCAA AATTGGTTGA GCGGATTTTA ACTAAAAATG 180

55

GGTTTGCTAC AAAAGAAGCG TCAGTAAAGC ATTAGGCCCC GGCCTnnGGA AACA

294

## (2) INFORMATION FOR SEQ ID NO: 2520:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2520:

TTTTAGGCCG AAGAnTAGT AATTTCCGGT CCTTTAAGGG GCGGGTGGTT AACCATGGCA 60  
 ATTAATCCCA GGGATGACCT TACCTAATAA CCACCTAATA ATTACCCGGA CCAAAGGTGG 120  
 AAATAATCCC TCCGGTCCTT CCCGG 145

## (2) INFORMATION FOR SEQ ID NO: 2521:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2521:

TTTtagTCAC CAAAATTCTC GCATTTAACT GATACGAATG TGCAATAACT AAAAATCGAT 60  
 CTAATAATTG CGTTGAAAAA TTTGGCTCGA CAGCACTCAT TACAATTACn AGTGTATCTA 120  
 TATTACTTAC AGGTGGTCTT TTCAACTCAT TTTCCCGCTC AAACACTTG 169

## (2) INFORMATION FOR SEQ ID NO: 2522:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2522:

ATCCAGCCTT TCAACAAATA AATCTGAAAT TCGATGTTCT AAAATTTCTG CTTCTTGATG 60  
 TACTTCTTCC CAATTATATT TCAATATT 88

## (2) INFORMATION FOR SEQ ID NO: 2523:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2523:

CAGTAACATC AATCTGTCCT GTAAGCTTGT GGTACTCCGA TACAACCATA AGTCAACGCA 60  
CCACCAAAAA CGCCTTGGAG CCGTTCTACT TATTAGTCCA AGTTTAGACA TTGAAATACC 120  
AACAACCTTG CAnTCCATAG TATCTGAAAA TG TAGACATT GCCTGCAATA AATTTAACnC 180  
ATCATTTTTA TTATGTGGCA TTA CTGCTAA TTTAACGTAT TCTGGGTT 228

15 (2) INFORMATION FOR SEQ ID NO: 2524:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 119 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2524:

25 CTCATCCATA GCGCTGGTAT TAGTATAGGT GTCAAACCAT TAGCGTATAT CATATCTTCT 60  
GGATGTnCTC ACATATTCAT AGATGCACAT TTTACTTCTC TCGTACCTTA GTACTGGGA 119

(2) INFORMATION FOR SEQ ID NO: 2525:

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(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 357 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2525:

40 TACCAATATT AAATTTGAAC ATTATAGTTT GACCATCATA ATCTATCTTC TCTATTTTCAT 60  
TATAACTAAT ACTTCTATAA TAA AATTGGC CATTTCATATC TACATTCATA ATTAATCTTT 120  
CATTGTGTTG TATAAATGCC CCTTCAAATT CATTCTCACC TTGAACTTGA TACTCAATTA 180  
45 TTCCTAGCAC TGACGGACCC TTTTTTTCAG TTGGAAATAA ATCATTGGA TTCACATTAT 240  
CTAAAATCAT AATATCCCTC CCACTTAAAA CTATAAATA TTCTTCATAG GTATATGAAA 300  
TACAAGTGAT TAACTATTnA TnATnAAGCT TAACTGTAT TCCCTTTTCA AGATAAT 357

50

(2) INFORMATION FOR SEQ ID NO: 2526:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 261 base pairs

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- (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2526:

CACGCGTCCG GCCACCTGGA CATGGCCGAC CTAGAAGCCA AGCTGCAnGA GGCCCAGAAG 60  
 10 CATCGGCTGC GCCTGGGTGG CCACTGATGG GGCCTTTTCC ATGGATGGCG ACATCGCACC 120  
 CCTGCAGGAG ATCTGCTGCC TCGCCTCTAG ATATGGTGCC CTGGTCTTCA TGGATGAATG 180  
 CCATGCCACT GGCTTCCTGG GGCCCACAGn ACGGGGCACA GATGAGCTGC TGGGTGTGAT 240  
 15 GGACCAGGTC ACCATCATCA A 261

(2) INFORMATION FOR SEQ ID NO: 2527:

- (i) SEQUENCE CHARACTERISTICS:  
 20 (A) LENGTH: 108 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2527:

CTnTAGAGGA TATGAGTTCC TCATCATAAG AATTTCTGGA TCCTTAATAG ATCTCTTGCT 60  
 30 ATATATAATG TAATAGAAAC ATCTTTTAAG GATCCAGAAA TTCTTAGA 108

(2) INFORMATION FOR SEQ ID NO: 2528:

- (i) SEQUENCE CHARACTERISTICS:  
 35 (A) LENGTH: 109 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2528:

TTTTAAATA CTTGGTAGAA GTTGGAAATGG ATTAATCATT AATTATCTCT CAAGATGTAA 60  
 45 TGA CTGTTCA GCACACTTTT CCGATATGAA AAGAGATTG AAnACAATA 109

(2) INFORMATION FOR SEQ ID NO: 2529:

- (i) SEQUENCE CHARACTERISTICS:  
 50 (A) LENGTH: 150 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

55



GATTAAATTT GTTATACCTG GCTTGTGTC ACGATCAAAT TTAATAATAC CATCTGAATC 60  
 AGTTACTGCG CTTTTAATTT TTTTAGCTGC AACATTCCGC TCGTCTAATA ATGAAATnGA 120  
 5 GTTTTTAGCA TTATCATCAC TCTTACTCAT 150

## (2) INFORMATION FOR SEQ ID NO: 2530:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2530:

TTCTTTTGG CCAGTGGCAG GAAGTACGGT CTTATTGGT GTTATGTAA GAAGGTATTC 60  
 20 CCATTATTT ATCGTTAAAT ATGnATATAG TATAGTAATT TTAATTTGTT GCATCATAAT 120  
 ACTAGGT 127

## (2) INFORMATION FOR SEQ ID NO: 2531:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2531:

CACATAATGA TTCGAATTAT TGTTTAAATT AAACCTTTTT CACATATGTA TAAATTTTAn 60  
 35 AGAGCGCATG CGTGAATATT TTCATTTGAT TCAAAGGCAA AAGATAGCCT TATACTCTTT 120  
 TC 122

## (2) INFORMATION FOR SEQ ID NO: 2532:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2532:

AAATAATAGA GCAATTGGCA CATGTAAGAA TGCAAATTGA CTATGGCATC CAGTATTTTG 60  
 50 GTCACAAATG GGTGTATAT GAGCATGTTG AAAAATAAGT CTTATGnTAA ACACTTAGTA 120

## (2) INFORMATION FOR SEQ ID NO: 2533:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2533:

GAGAGCGGCC GCGTGTAAAG AGAGCGGCGT TCGTTCGCGT GACGCGAGTG TGGTTCGCGA 60  
 GAAGnGGACC AGAGTTCCCG ATCGAGGCTG TTCGGGTAAA T 101

## (2) INFORMATION FOR SEQ ID NO: 2534:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2534:

TTGCTCATTA AAGATTATCC CAATCAATAT CATCTATATT TGTGTACCA CTATTATCTT 60  
 TTTCTCTTTC TCTTACTTTG TnCATTTGTAC CAGTAGATTC AAGATATATT GT 112

## (2) INFORMATION FOR SEQ ID NO: 2535:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2535:

ATAACGAATC CAAAAATATA GAGAATGACA GTGAAACTTA AATAGGACTC T 51

## (2) INFORMATION FOR SEQ ID NO: 2536:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2536:

## (2) INFORMATION FOR SEQ ID NO: 2537:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2537:

GGATGTACCA CCAGCATAAT AAACAAC TTC AAATGGATTG ATAAAGAAGA nACCAGCAGA 60  
GATAGGTAAT TCATTACCAT GTTCTTCTTG TAGACGTTTA CTTTCTTCAA TCTTTTGCTC 120  
ATTTGCATCA AGTTGTTGTT GTAAGTTATC TCGCTTGT 158

## (2) INFORMATION FOR SEQ ID NO: 2538:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2538:

TATATTCATT AAATCCACAA AGCGGTCCCG TATAACATG GGTTCATT 50

## (2) INFORMATION FOR SEQ ID NO: 2539:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2539:

AAAGTATACA TATCACTCAA CTAATCAATA ATCATACCTA CTTCAACAA ATTCTTTAAC 60  
ATGCAGTGTT ATCCCTTGAT AATATGGATA TTTnGTTAAT CTA 103

## (2) INFORMATION FOR SEQ ID NO: 2540:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

CAATCAATTT GTCTATCTGT TGAGTGGCAA CCTCTAATAA GCCTTTTATA TTGTCA

56

(2) INFORMATION FOR SEQ ID NO: 2541:

5

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 126 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2541:

15

TGGAAATAAC GAAAGTATTA TTAATTTAAA GCATCTTTCT CCCAATACTT TAATGAGTGA 60  
 TATTGTTTAT ATACCGTATA AAACACCTAT TTTGAGGAA GCAGACGCA AGGGAAACCA 120  
 TATTTA 126

20

(2) INFORMATION FOR SEQ ID NO: 2542:

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- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 201 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2542:

ATCAGTTTCT TCAAAAATAA CTGAAGTATC TGATGCTGAA AATTGGAATA GTTGATGGGT 60  
 CGGGnTATTG ATTTTATCT GATGTAAAAA TCCATAAGTG CCATAAGATG TATATAGTTT 120  
 CTTCATATGA AAGGTCCCC TTATGThTTT ATTTATTATA CGATGATAAA CTAGTCATTA 180  
 CCACTATTAA TAATTGATTA A 201

35

(2) INFORMATION FOR SEQ ID NO: 2543:

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- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 65 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2543:

GAACTTTATT ACAGGAATAG ATAAGCACAG TCGTGTTACA CAGACGCTAA ATGCGCGTTC 60  
 GTATG 65

50

(2) INFORMATION FOR SEQ ID NO: 2544:

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(A) LENGTH: 102 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2544:

10 AGCTATTAAT GGCCTATAA TTGATACAAT AGTTATGATT AATAAAAAAA TAACCGATAA 60  
 CATTGCAATT TTATnATGAA TAAATTTAGG AAATGCAATT TT 102

(2) INFORMATION FOR SEQ ID NO: 2545:

15

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2545:

25 AATCTACATC CAGCATGATC nACATCaAG CnGGATTCAC CCTTACTTCA 50

(2) INFORMATION FOR SEQ ID NO: 2546:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 100 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2546:

35 AACCATTCAA CACACGACAC TAAAGTGCAG TACAATCCTA CAAAACGATT GTTTTTATCG 60  
 GGTGGTCTAA CCATTGAATA AATAATGAAT AATGGTAaA 100

40

(2) INFORMATION FOR SEQ ID NO: 2547:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 156 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2547:

50 ATTGAAAATC TTTTATCATT TCATACGTGT GCATAATTAA AAAGGTGAAA CCTCTTATTT 60  
 TGAGATTTCA CCTTTTTTAT TGTTAATTTA AATTTAATTT TAATGATTAT TTTGTTTCAC 120

55

## (2) INFORMATION FOR SEQ ID NO: 2548:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2548:

AAAGTGAAAA TTGGAGGTGT AATTTTGACT AGAACTTATA ATATTATTGG TATCCTTTCT 60  
 TGTCTTATAT CTTTATTAT TATGGCGTTA CCAATnATTT GGTACACAGC TTCAGCATT 120  
 TGGTTCTTCC CAGGTGCAAT CA 142

## (2) INFORMATION FOR SEQ ID NO: 2549:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2549:

CCCAACCCTA CnAACGACAT TACACAATCA GTAACAGATC GGTATTAAGA CTGGATATCG 60  
 TGGCATCTGT TGAGTTAATA TCAACAGTCG TCCAGAACTC G 101

## (2) INFORMATION FOR SEQ ID NO: 2550:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2550:

TGTAACCATG ATTTAGATGA CTAAACGTGC TTGCCAACAT GCTTCATCCA ATGCCGAATC 60  
 CTTTAGCTAC AT 72

## (2) INFORMATION FOR SEQ ID NO: 2551:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2551:

CAGTAAGAGG ACAAGGCTAT AAGGTGGAGA ATCATGTTTA AAACACTCTA TGCTAGAATT 60  
 5 GCGATTTATT CCATTACGGT TATTTTATTT AGTGCATTAA TAAGTTTTGT ATTAACAAAT 120  
 GTTIACTATC ATTATAATTT AAAAGCATCT AATGACGCGA AAATCATGAA GACGCTTAAA 180  
 GAAGCAAGAC AATATGAACA ATCAGCTAAA CCAACGCACA TTCAACAATA TTTCCAnACA 240  
 10 TTTAGGGTCA AATGGAATTA CCAAATAATG ACCATGGATC CATAAAGGTC nTnAGACCTT 300  
 TTT 303

## (2) INFORMATION FOR SEQ ID NO: 2552:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2552:

TTTACTTTAG CCTTTATTGC ATTTGTAATT TATAGAACTG CGAACAGGTG ACTACTGTnA 60  
 25 ATTTATGTGA TTAAAGTTTC AATGATATTT GATTTATTAG ACCATTGCAA AAGCGCAAGG 120  
 TTCTCATGTG CTGCTACAGT TTGCGGTCTT 150

## (2) INFORMATION FOR SEQ ID NO: 2553:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2553:

GCACTCGTCA ATAAAGATGA AGCAGCATTT AATCAATATA CGGCAGAATA CAAAAATT 58

## (2) INFORMATION FOR SEQ ID NO: 2554:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2554:

AAAATCGTTG AATAATCAAT CATAGCAGTA AGCTATGTDA TATATTTTTTA AAAATTGA 118

(2) INFORMATION FOR SEQ ID NO: 2555:

- 5 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 102 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2555:

15 ACAACTTCAA AGAAATCATG TCACAAAAAA AGTATTTGAT TTTAATCATA nGTGGCGACA 60  
 ATCCGCATAC CAAAGCACAA CCTTTAGTCA ACCAATTCAG AT 102

(2) INFORMATION FOR SEQ ID NO: 2556:

- 20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 242 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2556:

AGATGCATTA GCAGCATTAG ACGTTAAACC AGTTGGTATT GCTGATGATG GTAAGAAAAA 60  
 30 ACGTATCATT AAACCAGTTA GAGAAAAAAT TGGGGATTAT ACTTCTGTAG GTACACGTAA 120  
 ACAGCCAAAC TTAGAAGAAA TTAGTAAATT AAAACCGGAT TTAATTATCG CTGATAGCAG 180  
 TAGACATAnA GGTATTAATA AAGAATTAAn CAAAATTGCA CCAACATTAT CATTAAAGAG 240  
 35 TT 242

(2) INFORMATION FOR SEQ ID NO: 2557:

- 40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 248 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2557:

TGCACTCATA ATCATCGGAA TATGTATAGA ATCAACTATC ACTTTGCCGT GTTTATCTGT 60  
 50 GTTAAATGTG TAACCATAAC AGTGTGTCCC ATTTGGATTA TGAATCTCAG AATAATCATC 120  
 AAAAATATCC TGAATTTnCA AATTAATTTT ATTATAGCGG nAGCAATGTC TATAAAATTT 180

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TATTTCAA

248

## (2) INFORMATION FOR SEQ ID NO: 2558:

- 5 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2558:

TTTGGGTCGT GATTGAAAAA ATCTAAGGCT AATAAACCAT GTTGTTCTGC GCTTAATAAT 60  
 15 TGTTTGAGTA TACGGTTAAT AATTAACCTCT GTATCATGAG GGTGACGCG AAAGTCAGAG 120  
 CGCATATAAG TCATATAATT CTCGAAGATT TCTCTATCAG TATTGCTTAA TCTTAATGAT 180  
 20 TTAACATTAT TTTCTTTTGT TAATTGCGCA GTACTTTTCA TTGTTACTTA AGCGCTCCTT 240  
 TAAAATGTT TAATTCCAAA TTAAATGGA AATGATTTTA TAGTATTAAT AAGGTCAATC 300  
 ATATCATATT AAACGCATAA ATATAACGAT TAATATTGGA GAGGAAAATG AGGACACTTA 360  
 25 ATAAAGATGA ACATAATTAT ATCAAGCAAA TAGCTAATAT 400

## (2) INFORMATION FOR SEQ ID NO: 2559:

- 30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 333 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2559:

AAGGGAAATT TAAAAGTATC ATTTGATTAT ATAGATTGGA TTAAATTAGG TTTTGGCCCA 60  
 TCAGGAAAGG AAAACTACTA TATGTACAAA AAATTTGGTA TTTTACCAGA TATGGAATAT 120  
 40 GAAATGGAAG AAATTGAGC AGTAGAGAAG TATGTTAAAG AGCAAGAGTA GCAGACATGT 180  
 TATAAAGAC TGTGCAAAAT CACCCTCGTT TTACATTTGA TTCAAAGAAG AAGGTAAAAG 240  
 45 ATAAGANTAT TTGCAACTTA AAAAGTCAAT TAGCTTATCG GTATCCATAC ATCATGGATA 300  
 AATGAGTnCA ACTAATTAAC AAATCACGAT ATA 333

## (2) INFORMATION FOR SEQ ID NO: 2560:

- 50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 87 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2560:

5 GTAAGACATT CACATTTATC ATTTCAACCAC AATGGGTTTA CCAACCATGG TTAAACGAAT 60

CCA AAACTTT GATGCTCGTA TGTCTCA 87

(2) INFORMATION FOR SEQ ID NO: 2561:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2561:

TTGCATTTTG ACGTAAATGA TTAACAAAT CGTGATTATC TCTTAATTTT CTAACCGCCT 60

20 TTTCAATTTT TAACGGCGTA ACTTCCTTTA GAACAATGCC AAATTTATAT TTnTCAT 117

(2) INFORMATION FOR SEQ ID NO: 2562:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2562:

AAGTCAAACA AAATAAGCAA ACAGACTGGT CAGAAGATAA GTTGAATAAT ATAGCTTTGA 60

(2) INFORMATION FOR SEQ ID NO: 2563:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2563:

45 AAGTGTATT ATTGTGATCA TAAAGTGAAG TATTACCTTT TTTATTCGTA ACCCGATTCC 60

ATGCGCCTTC AACATAAACT 80

(2) INFORMATION FOR SEQ ID NO: 2564:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2564:

AGACATGGGC TTATCAGATA AAGTAAAAGC ATTACCTAAA GGGGGAGGCG GTAAGTCATT 60

10

ACCG 64

(2) INFORMATION FOR SEQ ID NO: 2565:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 66 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2565:

GTTTGTTTAT AGTACCCTGG ATTTTCTTTA TTTCCATCAT GTGAAACTGT GTCAGTGAAC 60

GCTGAT 66

25

(2) INFORMATION FOR SEQ ID NO: 2566:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 75 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2566:

TTAATTATTT GTGACGTATT ACACGCATTA CTTTAGAAAG TGATTCCCAA AGCGAATTAT 60

CTTTACGATA AACTA 75

40

(2) INFORMATION FOR SEQ ID NO: 2567:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2567:

50

ATATTATTAT ATTGCTTTTT TTCAGTTTGC CGTTGTTACT TTCATAACTT 50

(2) INFORMATION FOR SEQ ID NO: 2568:

55

(A) LENGTH: 223 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2568:

10 TTTTAGGATT TGTAGTAGGT GAGCGACGTA TnnGGATGC AATCCAGAGA ACAATAAATA 60  
 TTGAGAGAGA GCAATTCATA ACGCAGTTGA AATACATGTG TTACGAATTG CTTTTATGTT 120  
 AGTTTTTATC ACACAAGTTT TTTGATGCAA CCCCGTGATA GCGAAACTCA TATGTAGATA 180  
 15 ATACAGCTTT TTCAGCATCA TCTACATGAA TTCCAAAACA TCA 223

(2) INFORMATION FOR SEQ ID NO: 2569:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 58 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2569:

AATAATGCCA TACAGTGAAG ACCATGCGCA TCAATCGATG TCTAGTGTGT ACTACGTC 58

(2) INFORMATION FOR SEQ ID NO: 2570:

30

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 250 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2570:

40 CGTTTCATTA GTTTTAAATG ATCCCCAATA CTTTTGTAC CTTACCAAC TATCGTTCCA 60  
 AACTATCTA CAGCTTTTTC TGTGGTATTT TTAACAGCG TCTATTTAAT GTCATTATCCA 120  
 ATTAGTTTTA TCTCTAATC CAAATTTATT AGTATGAAAA GTCCAATTTT TAAGAATTGT 180  
 45 CTAAACAGAT TCCGCAACAA AACCAGCTAn AAACCGTCCA TACTATTGGA ATnAAAACGC 240  
 CAATGTTATA 250

(2) INFORMATION FOR SEQ ID NO: 2571:

50

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 174 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

55

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2571:

AGCTCCTTTC TTTCTAGTTA ATATCATThA ATCTTGTTTT TCAGTGTCAA AATTACCTGT 60  
 5 AAAACAACA TTTTATCTT TAAAATAGG GATTACACTT TCCACTTCTA TTTTATTAAAT 120  
 CTCAGATATT TTCATATGAA TTTTTTGAAA TCCTGAATCG AAAAGTTTAG TTGG 174

## (2) INFORMATION FOR SEQ ID NO: 2572:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2572:

CATGCGGTAG GTATTTCTAA TCTATGGACA AATGGCGGAT TTATGCCAAA TGGTATTGTT 60  
 20 GGTTCCTTCT TTGCATTATC AATTGTAATT GGTTCATACC AAGGTGTGGA ACTGATAGGT 120  
 ATTACGGCAG GTGAAACTAA AGATCCTCAG AAAAATATCG TTAAAGCAGT GAATGGTGT 180  
 25 ATCTGGAGAA TTTTAATTTT CTATTTAGGC GCTATTTTTG TTATTGTTTC AGTGTATCCT 240  
 TGGAATCAAT TAGGAGACAT TGGAAGTCCG TTTGTTGCAA CATTTGCTAA AATCGGTATT 300  
 ACATTTGCAG CTGGATTAAT TAACTTTGTT GTAA-TAACTG CAGCAATGTC AGGATGnAAC 360  
 30 TCAGGGnATT TGCAGTGCGA GTCGTAATGA 390

## (2) INFORMATION FOR SEQ ID NO: 2573:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2573:

TAGAGTACAG AACATACGCA AGGAACTCGG AGTTTACTCA CGGGACTTnT 50

## (2) INFORMATION FOR SEQ ID NO: 2574:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2574:

TACAATTACA AACGCATCGT GAGATGTTTT AAGCATCAAT GAGAATCTAA CTCTCCAAG 59

(2) INFORMATION FOR SEQ ID NO: 2575:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2575:

GACACAACGT ATGACGCATG AAGAGTTGCG TGTGACAAT CAAGATGATC ATAGCCAAGT 60

TAGTCTAAAT GGTACACAA AGGGGTCTGA GAAAGATCAA GAAGCATTCA CTAATAATAA 120

GGATGAGGAA GCAGTTGCTG CTAAAAATCC TGAATCAGAA GAATATAAAG TGAATGAAAA 180

AATAAAAAAA GAACATAAAA ACTTTATTTT TGGTGAAGGT GTTTCAnGCG GTAAATATT 240

AGCGGCATTA TTATTCGGTA TGTATTATGC GATTTTAAAC CAAACATTAT TAAATGTTGn 300

TTTACCAAAA ATTAATACGG AATTTAATAT TTCTGCGTCA AnAGGGCAAG GTTGATGACG 360

GGATTCATGT TAGTAAACGG TATTTTAATA CCAATTACGG 400

(2) INFORMATION FOR SEQ ID NO: 2576:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2576:

TTTAAATCGT ACCTTAAATT TGAAAGTAAT AAGACACACC AATTACCTTC TAACTCTATC 60

GATAGTTTCA AACAGAAAT CGnTAGTACA TTCAGTTATT TAGAACGCGT TGATTACCAG 120

CT 122

(2) INFORMATION FOR SEQ ID NO: 2577:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

CACATTGAGG TGCAGTCATA CCTTGTTTAA ATGTCCAAGC ACGTACTTCT T

51

## (2) INFORMATION FOR SEQ ID NO: 2578:

- 5 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2578:

15 AATTATGACT ACAGGTCTGA CTCCTTCTTG TTCAGATCCC TGTACTGGTG ATAAATCTGC 60  
 TAAATAAACA TCTCCTCGTC TAATCATTCA TTCGTTGAAT TAGAAGATAA ATATGTTTCG 120  
 TTGCAATCGC ATGCTTCACA CTCTATCGGA AAAGCTTCGT TCGCTAGGGA GAGATTTAAA 180  
 20 TCAGCCATTT GTGAATATCC TTCTTTTAAA GATTGTTCTA AGCTATGACT TCTATTTTGA 240  
 CTAAAAGATA ACATATGAGA ACCTCCAATT GATTCCAAAA GTTATTAAAT GACCTTTAAT 300  
 TACTCTAATG ATAACAAATT TTATATGCAC TGACCATATT ATTTTAACAA TTCATTTGTT 360  
 25 ACAAAACGGT GGATCACCCA TCATGGATAG AGTCGCGGGn 400

## (2) INFORMATION FOR SEQ ID NO: 2579:

- 30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 112 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2579:

ATAAAAACCT AATTGACTCA TAATCTTCTA ACGGTATATC ATCCACAATC ACAGTATGAT 60  
 40 TAGGATTATC GTTAGATACA TCTnTCACTG CCTATCTAA CCCCTCATCA CC 112

## (2) INFORMATION FOR SEQ ID NO: 2580:

- 45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 231 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2580:

CATGAnThTA ACGGATTCAT TCCATATATC AATTGCGTTT GTTATTTTAA TAATGCTATT 60

55

ACTACAACCTT CGATTTAAGC TATATTTATA AAAAAATGCG CCTACTCATA ACATTCTTTG 180  
GCTATTTAAC TTTAATAAGC TAGGGCCAAG TTTGTCATAA GATAAGCGCA C 231

(2) INFORMATION FOR SEQ ID NO: 2581:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 60 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2581:

ACTTCGTAAA ATTTATCTTG AGTGGTTGTT TCTATATTAA GATTCATTTC ATTACACTCC 60

(2) INFORMATION FOR SEQ ID NO: 2582:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 284 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2582:

GTCAAATGCT GAGTTCTAAT AATGATGTTG GCCACCATGC ATACAAAAAT GCTAAAAGAG 60

AATTACGCAA GATTTTAGAT AGCTATCTCG AAAATGGTAA ATTAAATAT TACGATATTA 120

TCGTTACAAG CAATTTAGCT ACTAAACATC CGTTTTTCGA GTATGCACGT TCATTTGATT 180

TTATCATTGT TTCAGATATC GGTTTAATAA ACGTTGATGT AAAAAGCTGG GGTGAAAAAA 240

CATTTTATCA CTTTGATGTA CCTGATGAGC ATGATACAGA nAnA 284

(2) INFORMATION FOR SEQ ID NO: 2583:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 56 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2583:

GAGTCAGTCG AAGTTTGTCTG TTCCACCCGT AGAAGTGTA AACCGCATTG TGAATG 56

(2) INFORMATION FOR SEQ ID NO: 2584:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 67 base pairs



(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2584:

TCGACTAATG TAATGTAGGC ATTGGACGTC AAATGTAATG TGGGGCAATC CGACGAGATG 60

10

ATGGTGC 67

(2) INFORMATION FOR SEQ ID NO: 2585:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 52 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2585:

CGTAACCGCC CCTTGTCGCG GCCCTCCAAG CCTTTTAAGG GGACCCCCCG GA 52

(2) INFORMATION FOR SEQ ID NO: 2586:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 238 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2586:

35 ATTAGCAACA ATGTCAGATA ATCGATACCA ACTAATTAGG CGAGAAGCGG TTTCTCATGG 60

TCTTAGTGGC CTAGAAATTG ATGTATTGA TTTGCATTCA AATAAGTCTA GACATATTAG 120

CTCGTTATCA GGTGGAGAAA CTTTCCAATC GTCGCTTGCA nTAGCTTTAG GGTTAAGCGA 180

40

AATTGTACAG CAGCAATCAG GAGGTATTTC ACTAnAATCA ATATTATTG ATGAAGGA 238

(2) INFORMATION FOR SEQ ID NO: 2587:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2587:

ACTGGAAAAA ACCGChAACA CGACATTGTC AAAACGACGG CCAGTGCCAA 50

55

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 102 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2588:

GnGCAATTAT ACCACTATAT TTATTTCTTA TACTCCATTG GATTATAGT TGTATTAATA 60  
 CATTGACTCA AAAACTAATT AATCAAATAT GTTTTTTAGA TT 102

(2) INFORMATION FOR SEQ ID NO: 2589:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2589:

GCATAATATC GGATATGCGn GTGTGTCACT CnCATAGTCG nTGGATTGCG 50

(2) INFORMATION FOR SEQ ID NO: 2590:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2590:

TTAnAAAATTG CCTnTCCAAT TnTAAGAATC CTTTTTCCAA GGTAACAAAAA 50

(2) INFORMATION FOR SEQ ID NO: 2591:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 200 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2591:

CTTCATCCCT TACTTTTAAT TGTCACGTCA AATAATATTT GTCTTTAACT AGTAATAACT 60  
 CCAAATATAT TAGTTTGTG GTGCTAGCTA TAAACACAAA TGAnTCATAA CACTATATTT 120

TGATTTTnAA TTATTATAT

200

(2) INFORMATION FOR SEQ ID NO: 2592:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 74 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2592:

TGCATTAATC ATCTTGGATA CTCCTTCTAC CAAAGTAATG ATTGCACTAC CATGACGACG 60  
 ACCAGCAATA GTAT 74

(2) INFORMATION FOR SEQ ID NO: 2593:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 244 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2593:

CACCTGCTCA CCTCTATTTT CAAACAATTA TGATTGAATT GAATCATTCT AATTTTTGTA 60  
 AAGTTACTTG TTTAATTTAT TATATTTATT AACTCTATGA TAACAAAAAT ACTGTTTGTG 120  
 TATAACAATA AATTGAGATA CTCAATAATT TGATAATGTG AAATTGATAC TTTTCAAAAT 180  
 AGTTGAATAT GACAATTAAT GATTAGTTTT GcNATGGTGC TATAAnCAAT ATTTAGCAGT 240  
 TATC 244

(2) INFORMATION FOR SEQ ID NO: 2594:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 201 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2594:

ATATGGTATG GAACTAACGG AAGAAGGCTT AGCATACGTT AAATATGCTA AAGTGATTTT 60  
 AGATAGTAAT AGCGAATACG AGAGAGAnAT AAAAGGACTT TACAATAAGA AGGTAAATAT 120  
 AAGTATTAAC ATGCAAGAnA GTCAGTATTT GTATCGCTAC TATAATAAGA TTAGTGAATG 180

## (2) INFORMATION FOR SEQ ID NO: 2595:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2595:

AAAAAGTATT AAAAATTGCA ATTCTTAAAC TGTTATTCAT ATTAATATTT CTAGCAAATA 60  
 ACATTGTAAA ATAAAGAAAA ATAATTADAG TATTGCACTT TATTGAAATT TATATTACGA 120  
 TAGTAATGCA GAAATTTATA TATGCAAAAT ATTATA 156

## (2) INFORMATION FOR SEQ ID NO: 2596:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2596:

TGATCCGCAA ATCGCTGAAC ACGTTCTTCT ATTGGAATCC CTCCATTCAC TTTTAGCTAG 60  
 AC 62

## (2) INFORMATION FOR SEQ ID NO: 2597:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2597:

TTACCTTTAG nTTTAAAC CTGACCCTCC AACCAGCCTA ATTGGTTAAA TGGGGATCCA 60  
 TTTATATAAT CCCAGGCCTA ACCTTCCAAG GACCAACCTA AGGGATTAAT CCCCCCAATG 120  
 GCCAAAGTGG GATGGGTAAT 140

## (2) INFORMATION FOR SEQ ID NO: 2598:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2598:

ATTAATTGGG GAGTTAAATT AAAAAAAGG GGTTCCTTCC AACCGGanCC ATTCCCATT 60  
TGGATTAAAA ATTCCCGCCT TTGAAAAAAT TGTGTGCCGA ACCGCCCTTA AG 112

(2) INFORMATION FOR SEQ ID NO: 2599:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 63 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2599:

ATACCGCCCC CAGTTCAATA AGAAGCCCTG GATCAGACCT GACCCTGGTA TGGGGGGAAT 60  
CCC 63

(2) INFORMATION FOR SEQ ID NO: 2600:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 53 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2600:

ATACTATGGA ATGCCTTAAT GGTGGATAAT TTCACCAAAT TAATTTTAAA AAC 53

(2) INFORMATION FOR SEQ ID NO: 2601:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 73 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2601:

AACTAAAGGT TCTAAAGATA CAGTAAAAAT TGAAAATAAC TATAAAATGC GTGGCGAGAA 60  
AAAAGATGGT AGT 73

(2) INFORMATION FOR SEQ ID NO: 2602:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 108 base pairs

- (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2602:

CGGTTGCCAG CCAAACTTG GCAnCCAAGG CAATTATAGC AAGGCACCCA CCTAAATTG 60  
CGGACCACCC GGAATGCGGC CACCAAAGTT GGTGGGAGGC CATTTTAA 108

(2) INFORMATION FOR SEQ ID NO: 2603:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 59 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2603:

AAGCTTATAA CTATTTGTGT TTGTGATCGA GATAGGTTTG CCTGTAAAAA TGGCCATCA 59

(2) INFORMATION FOR SEQ ID NO: 2604:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2604:

ACGTCCAAAG GGCCGTTTCG CCCAGAnGTG CTGGCAAGGT TCCACAACGn 50

(2) INFORMATION FOR SEQ ID NO: 2605:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 107 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2605:

GTCCAATGTC ACATTAAATTG ATTGGTATAA GCGATCACAA GGnCATAGTG AATATTTTGC 60  
ACCAGACGGT GTACATTTAG AGTACAAAGG AGTCCTAGCT TTAAAAG 107

(2) INFORMATION FOR SEQ ID NO: 2606:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 54 base pairs

55

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2606:

GTTTAAAGCA ATTTGGAAGG ACATTGGTTA AAGGATGGGA GTGGCAAAAT CTGG

54

10

(2) INFORMATION FOR SEQ ID NO: 2607:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 366 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2607:

20

GTTTTAGCTG AAGTTAATGA TGAAGATATC GGAGCTATGG TAATTAAACT AGTTAAACTT	60
ATTTTCATGC TTGATTATGT TTTATTTTCAT TCAATTCAAA AAAGCTATAC AACACATATG	120
AATGAGCTTA AAAATTGTTT CGATTACATA GCTGAATTAG ATAATCATTA TGCATTAGCA	180
ATGTATCGTA GAACGCTAGA ATGTTATACT GAACCACAAA TTGATGATTC AAATGATGGC	240
ATAGTATTCT CTGAGTTAAC ACATCCACTC ATAGCAGATG GCAGTAGCCA ATGATTTCn	300
ACTATCACAn AATATACTGT TAACTGGGGT CGAATGCTTC GGGnTAAATC AACATTTTAT	360
GGAAAT	366

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(2) INFORMATION FOR SEQ ID NO: 2608:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 142 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2608:

45

TTCTTAGACG TCAGGTGGCA CTTTTCGGGG AAATGTGCGC GGAACCCCTA TTTGTTTATT	60
TTTCTAAATA CATTCAAATA TGTATCCGCT CATGAGACAA TAACCCTGTA TAAATGCTTC	120
AATAATATTn GAAAAAGGAA GA	142

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(2) INFORMATION FOR SEQ ID NO: 2609:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2609:

GGGTCGTCAA TTGA<sup>g</sup>GGCAG GTAGAGCATT AAGTCAGAAT TGTAGTAAAT

50

(2) INFORMATION FOR SEQ ID NO: 2610:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2610:

ATTGGGTGAT GAATTTTGAC GGTATTGTCA AGTCCAGTGG CTA<sup>a</sup>CTTCCG G

51

(2) INFORMATION FOR SEQ ID NO: 2611:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 93 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2611:

ACAAACTTCG GACTGCCAAT TACATTTACC TTGGGGGGTC AGAAACAATG GGTGCATAAA

60

GGCCCGTGTT TCGAAACGGG AAAAAGCCCA GCA

93

(2) INFORMATION FOR SEQ ID NO: 2612:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2612:

ATGATGTTTT TCGGCTAATT TTTATACTGA ATTTAGTTTA ATTA<sup>a</sup>CTTAT GATATTTT

58

(2) INFORMATION FOR SEQ ID NO: 2613:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2613:

TTCTCACCAT TAACTATGCA TACTCACTTT ACACATAAAT TTGCTTAACA TGCAGAACGG 60  
 5 AAATAAATCA TTACCACATA TAGATCCCAT CATATATTTA nA 102

## (2) INFORMATION FOR SEQ ID NO: 2614:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2614:

TGAACTACAA GACGCTTATA TCATTGACGC ACATTCTCTG CAGTGAAAGA AACACTTGCG 60  
 20 TA 62

## (2) INFORMATION FOR SEQ ID NO: 2615:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2615:

TGGAGCATTT CACATACATT GGCAACCTCA TGGAGCTTAT CATTCTACCT TGGGGnACAG 60  
 35 ATATAACAAC ACTAACGCAA CATGGATGGT GTCGTTGATA ACTTTCAATC TATAGAATTA 120

## (2) INFORMATION FOR SEQ ID NO: 2616:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2616:

CTGTAGTAAA TTGCCAGAAT CCGTATCAAT ACCAGTCTGT GACTGCGTTG GCC 53

## (2) INFORMATION FOR SEQ ID NO: 2617:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2617:

ACATATGATA TGAGTATATT AACGTTTAAA TTATGGATAC TCTAAAGACA GGCGATTTTG 60  
5 ANAAATCAGC AAAAAGTTAT ATGATGTAAG TGGGACAGAC ATACTAGATG TAACACATTA 120  
ACCAAGTG 128

(2) INFORMATION FOR SEQ ID NO: 2618:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 59 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2618:

20 CCTAACCGTG TGTGTATGTA TACCTACAAA AAAATTTACA TTGTGACACT GCGTACGTG 59

(2) INFORMATION FOR SEQ ID NO: 2619:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 54 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2619:

30 GCCCATGGTC AATCAGACAC ACGGATTGAA CGTTAACAAT TTATGACTTT AACA 54

(2) INFORMATION FOR SEQ ID NO: 2620:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 53 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2620:

45 ATCATTTGTA CATTGAGTAG CCGTAAATG GTCAGACGAT CAATGCGAAC TGA 53

(2) INFORMATION FOR SEQ ID NO: 2621:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 53 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2621:

CTAAGTGTCTG CCCGAATAAC CGTCAATCCA CGGAGCACAT AGGATCTCCC ATG

53

(2) INFORMATION FOR SEQ ID NO: 2622:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2622:

TGGGACCGAT AATCATTCGC ATGAACACCT TCCACCGTCT CTTACTCACT ACCTACGGC

59

(2) INFORMATION FOR SEQ ID NO: 2623:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2623:

ATTAAATTGT TATTTTCGTCA TTAGGTGACA ACTTGTATGT AGATATTTTA ACATATTTTA

60

TGCT

64

(2) INFORMATION FOR SEQ ID NO: 2624:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2624:

CCGTCCCAGA ATATCATATG ACAAATGTGA AGAGACTTGA ATGATCATAC ACGTG

55

(2) INFORMATION FOR SEQ ID NO: 2625:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2625:

GTGGTCACCA GGTACGGGGG ATACAGGGGG TTAATCCCAC CTTGGATAAG TGGAAAACGG 60  
ATTTC 66

(2) INFORMATION FOR SEQ ID NO: 2626:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 62 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2626:

CCACCAATGG GTGGGGGATG GAATAACCT TAATGCGGTG GTACCGGGT AATGGTAGCC 60  
CC 62

(2) INFORMATION FOR SEQ ID NO: 2627:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 54 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2627:

CATGTTTTTT CATTCCTTGA TGACGACACT AGAGGTTCCC GTGTTCATTA TTAA 54

(2) INFORMATION FOR SEQ ID NO: 2628:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 56 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2628:

TTGGCCAATG GGCATACAC CCTCTCAATT CGATACATAA CTCAAGGCTC AGTCAT 56

(2) INFORMATION FOR SEQ ID NO: 2629:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2629:

TGTCGCTAGG TAACCGTGCA TCGTTCACAG GTACnTATGA TTTCACChGA

50

5 (2) INFORMATION FOR SEQ ID NO: 2630:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2630:

15

GAAGGnCCCA AACCAGGCGT TAAAGGCCGA TTGGGTTTAA ACCAAAGGTT

50

(2) INFORMATION FOR SEQ ID NO: 2631:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2631:

CGCGAGTGTA TCCGTCGATA TGTCGAGAGG AAAGATTGAA GTGTGGAAGA GTGTTGAGTA

60

30

ACCCT

65

(2) INFORMATION FOR SEQ ID NO: 2632:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2632:

TGAAAGAACT TTAGCTAGAC GTTCGTAAAG GTCTTTTGAC ATAAAGCTAG AGA

53

45 (2) INFORMATION FOR SEQ ID NO: 2633:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

50

55

AAAAGCCAAA AGGAATTAAT TAACCCCGGG GTTTAATTTT TAATGGGAAT TTG

53

(2) INFORMATION FOR SEQ ID NO: 2634:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 68 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2634:

GGTGTTCACA TTCTGAAGGT TTAGAGAGTT AAGATTATAT ATATATAAGT TTTGGGGTGA  
 TAGATATG

60

68

(2) INFORMATION FOR SEQ ID NO: 2635:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 80 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2635:

CCAATTTTAC TTGGTGCTGC CATTTTCGGTC TCTCGTGAC TTGTGATTGA GGTGCCATTG  
 TTCCCGTAGA TGGTTTCACAT

60

80

(2) INFORMATION FOR SEQ ID NO: 2636:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 144 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2636:

CTTACACCCA ACTTATTGAC TTATAATCTA TTAAAGTGCC ATTTTACAAT CTGAATCCCT  
 TAATATAGCA ATAATTACAA CTTCCGACAA ATGACTTGTT TTATGTGCGT GATTCATCAA  
 TGAACATCGT AATGCGACnT AATA

60

120

144

(2) INFORMATION FOR SEQ ID NO: 2637:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 104 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2637:

5 TAATTCGGCA ACTAATATCA AGATCATGAT CAAATACTAC TGCCATTTTC TTATACCTCT 60  
 TAATGTGAAA TCACTGnCAA CACATAACAT CTTAAACTT TGAC 104

(2) INFORMATION FOR SEQ ID NO: 2638:

10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 151 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2638:

20 CATTTCATCCG TTTTTTTGGT TCATGTACAT ACCATTGTTT TGTACACAGC GAAGTCAGTT 60  
 AACCTTATAT CCTGTATAA CAGTTGAAAT CGGCAATATT AAACAGTACT TTCCCAATTG 120  
 CTTTCTTCCT CAATTGTGCG ACGGACTGTA n 151

25 (2) INFORMATION FOR SEQ ID NO: 2639:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 51 base pairs  
 (B) TYPE: nucleic acid  
 30 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2639:

35 AAGATCAACT GAAATTCATG TGTTGCCCTT TATTAAGATC ACATGGAAAT A 51

(2) INFORMATION FOR SEQ ID NO: 2640:

40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 52 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2640:

TTAGCTAGTT GGTAGGACGG CTACCAGGCA CGTCATAGCG CCTGGAGGGG TC 52

50 (2) INFORMATION FOR SEQ ID NO: 2641:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 53 base pairs

55

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2641:

CAGGCTTAAA CCTGAGTTAG TGCCATTCAT AATTGCAATC CCAAGCGACG GAA

53

10

(2) INFORMATION FOR SEQ ID NO: 2642:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 345 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2642:

20

ATGTTTGTCA TCTGGAGCnA TAGAACAGGG TTCATCATGA GTCATCAACT TACCTTCGCC

60

GACAGTGAAT TCAGCAGTAA GCGCCGTCAG ACCAGAAAAG AGATTTTCTT GTCCCGCATG

120

GAGCAGATTC TGCCATGGCA AAACATGGTG GAAGTCATCG AGCCGTTTTA CCCCAGGCT

180

25

GGTAATGGCC GCGGACCTTA TCCGCTGGAA ACCATGnCTA CGCATTCACT GCATGCAGCA

240

TTGGTACAAC CTGAGCGATG GCGCGATGGA AGATGCTCTG TACGAAATCG CCTCCATGCG

300

TCTGTTTGCC CGGTTATCCC TGGATAAGCG CCTTGCCGGn CCGCA

345

30

(2) INFORMATION FOR SEQ ID NO: 2643:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 75 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2643:

40

CTTATACGGA TGTATAGGTC GGTCCAAACA TTTGATTTTA GTGGAGAGCA GCCTTTCACA

60

AATTATGTTC AATGT

75

45

(2) INFORMATION FOR SEQ ID NO: 2644:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

50

55



TACCGGTAA TTAACCAGGG CCCCAGTAA AAAATCCCCG GTATCCCCA TTCCAAC

57

(2) INFORMATION FOR SEQ ID NO: 2645:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 66 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2645:

AAAGCAATTC GCCGATAAG AGTAGAGACG AATTGCTTTT AAGGTTAAAA CAAAGTGAGT  
 TCAATT

60

66

(2) INFORMATION FOR SEQ ID NO: 2646:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 63 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2646:

CAGTATAACT TGTGACCTAT TTAGAGGGGC ACGTTGGTA CAATGAGTCT GAAACCGTAT  
 CAA

60

63

(2) INFORMATION FOR SEQ ID NO: 2647:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 208 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2647:

TAGAACATGG ACCGGTATTT TACATCCTGT ACGCCTAATC TGTTGTAAGT ATCTTTAGTG  
 AACCGTTGCT CTGGAATAAC CGCGATTCTG GGCAAACAGT GTGTAAACCG ACTnTATGGG  
 GATGTGTGAG TAATCATTGT GnACTGTTGA TTCTGTTCTG GAATCCCATT TCACAACAGC  
 ATCTTGGAAG TGCTGTCATT TTAGATGC

60

120

180

208

(2) INFORMATION FOR SEQ ID NO: 2648:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 150 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2648:

10

TTTTAACCTA AAGAATACTA AACTAAAAAG AGAATGATTC TGTACCGCTT TCCTTTTTCA 60  
CTCAATAACT TTATATTTAG TTATCCTTAT AATTGTAATT TATGTTAGTT GGTAATnTT 120  
TACATATATG TATTTGATAT GCTTGTAAT 150

(2) INFORMATION FOR SEQ ID NO: 2649:

15

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 138 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2649:

25

AGTTTAACTG ACATCGAGTG GTACACAATA GCAATGGTTG TGTGTAAAGT CCTGGTGACA 60  
ACATATGAGA GTACATTTG TAGTGATTAT CTTGTACTGA GAGAATTGAC ATCTATGnAG 120  
TTTATCACGT GCAAATAT 138

(2) INFORMATION FOR SEQ ID NO: 2650:

30

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 52 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2650:

40

TCACAATTGC AAATTCTGG CACGCACTCA TCTGCGATTT CACAAGCTAC AT 52

(2) INFORMATION FOR SEQ ID NO: 2651:

45

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 65 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2651:

GAGTCAAATT AAAATGCCTA TTGGCCATTG TGATGTATAA TCACTTAGTT CACATATACT 60

55

## (2) INFORMATION FOR SEQ ID NO: 2652:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 67 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2652:

GGGCGGTAAT TGTCAACATC ACAAATTGCT ACGTTGAAAC ATCGAGGATT CAAGCTGGAC 60  
AGCAGAG 67

## (2) INFORMATION FOR SEQ ID NO: 2653:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 52 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2653:

ACACATCTTA TATGTCTTAC TGATTTAAGG AAAGAATCAG TGGATCAAAC TG 52

## (2) INFORMATION FOR SEQ ID NO: 2654:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 261 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2654:

CAAGCTGTAA ACCAAGAATT CCAGCATTAA ATATCTCTCn TGGTATCGGT TGAGATAAAT 60  
ATTCCGTGTG CTCATTAAAT GTAGTAATCT TTATTGTAGT TCCTCAACCT ATGACACGAA 120  
TATTGCACAA TATTAGTATA GACAAATATT TCCTTTATAA TCTCATTCAA TTTTCTCCTT 180  
TAATTATGTA TCATACATTG TATATTCTCA TATAGACGTT TTGnCATATT CATAGCTTCA 240  
ATATTAGTGC ATTTATGTAT T 261

## (2) INFORMATION FOR SEQ ID NO: 2655:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 60 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2655:

AATCCTATTA GCACTTATAA TGATCATGAA AAGATGTCAT CGAGAATCAC CTAGTACACG 60

5

(2) INFORMATION FOR SEQ ID NO: 2656:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2656:

CGCCGAAAAC AATAAATTCT CGGAACATAG AATTTATCAC ATACCACGCT TGGATTATCA 60

CAATGGACTG AGTCG 75

20

(2) INFORMATION FOR SEQ ID NO: 2657:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2657:

TATTAAATAT GCGGTTGCAT ATATCTACGG CATGATTTAA CCGTGAACCA TGAATCATTT 60

TAATCGGGCA CCGGTAAAAT GTCATTGAT CCGCATAAC CACTATATAT CTAATAGCAA 120

35

GCGTCCAGGA TTCTGTGTTT TATAAATTTA AACTAACTGA AACGTGTGTA TCAGTTCACT 180

CCGnTCGATT ACCACACTTC AA 202

40

(2) INFORMATION FOR SEQ ID NO: 2658:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2658:

CGTACATGTG CATCATGTAT CTACGTCAAT AAGATGATGG GGTCACATGA TTGGACCATT 60

50

(2) INFORMATION FOR SEQ ID NO: 2659:

55

- (A) LENGTH: 207 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2659:

10 CTAATCATGT CATGTCTACA ATTATTTGGA GTATTGCTGA CGAAATGCGT TGTACAACTT 60  
 TTTCAATTCTA GCACCTTGCG GGGGCCCAACA AAGAATTGG TCCATTCTCA nCATCAGTGG 120  
 GGGGCGCGAA TAATTTGAA ATTATTCTGC CACTCCCACT TCATCGATTA AGTTGTAACT 180  
 15 CTACATTACA TTTGTCTTAA ACCATTG 207

(2) INFORMATION FOR SEQ ID NO: 2660:

(i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 54 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2660:

TTAATTATGT ATAATACTTA ACAAGATCAC CTGATAGATG TCTAAATATT ATCT 54

30

(2) INFORMATION FOR SEQ ID NO: 2661:

(i) SEQUENCE CHARACTERISTICS:

35

- (A) LENGTH: 130 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2661:

40

ATTAACAAAAA AATGGGGTAA TTTCCGCCAA ATCCCGTTTC CCCCTTGCCA AGGCCAAATT 60

TAACCACCCT TGCCAAATna TTAAGCCAAA TTTTCCGATA TTTGTTTCCG TAATGTTTCT 120

45

TTAATTAATA 130

(2) INFORMATION FOR SEQ ID NO: 2662:

(i) SEQUENCE CHARACTERISTICS:

50

- (A) LENGTH: 104 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

55

AAAGTAAAC CAGTCTATTC AAAAAGGTGA AAAATGGTGA CGCAGCGTAA ATAantGGTC 60  
TCTGGTAGGG TAAATCGCGT TGTGGGTTTG TCACATCAGG AACT 104

(2) INFORMATION FOR SEQ ID NO: 2663:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2663:

AAAAAGAATA AAAGGACTCG AAAAActCAA AACTTATTnt AGATAGTCAT CGTGACAAGA 60  
AACAAACATT TAACTAGACT AAGAAAAATG CTTcGATTAA AAGGCAGACT CATCA 115

(2) INFORMATION FOR SEQ ID NO: 2664:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2664:

GCATGCGCCA CGGTGTCTCA GCAGAGTGAC TGCCACCTTG TGTGCGCAGA GTCTGCGCCT 60  
AGTACAGTCA GGGTGAAACA CnCTATACGC ATTAGGTACA GTACTTCCTG TCTCCGACTT 120  
GAGTAGAACG TGACATATCT ATCAGCATTC ACTCGAAAAA GGGA 164

(2) INFORMATION FOR SEQ ID NO: 2665:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2665:

AATTACGCAA TntCCCTGTC TTantGAAAG GAATTGACCT GTTAATTCGT 50

(2) INFORMATION FOR SEQ ID NO: 2666:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2666:

5     ACAATTCAAT AGAATTTACC CGTAACAGCG TTGCACTGCA CTCAAGACGG CTGACGTATA     60  
       GCAC     64

(2) INFORMATION FOR SEQ ID NO: 2667:

10     (i) SEQUENCE CHARACTERISTICS:  
       (A) LENGTH: 56 base pairs  
       (B) TYPE: nucleic acid  
       (C) STRANDEDNESS: double  
       (D) TOPOLOGY: linear

15     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2667:

       GTAGAACCAG CGACGGCGCG GCGGCTGAGC AACATCTGAC TACCTATCGG CCGCGC     56

20     (2) INFORMATION FOR SEQ ID NO: 2668:

       (i) SEQUENCE CHARACTERISTICS:  
           (A) LENGTH: 50 base pairs  
           (B) TYPE: nucleic acid  
25           (C) STRANDEDNESS: double  
           (D) TOPOLOGY: linear

30     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2668:

       GGATCGATTG ACTACATGAC GTGGnGACGC AATTATACGG ATAGTCCACT     50

(2) INFORMATION FOR SEQ ID NO: 2669:

35     (i) SEQUENCE CHARACTERISTICS:  
       (A) LENGTH: 58 base pairs  
       (B) TYPE: nucleic acid  
       (C) STRANDEDNESS: double  
40         (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2669:

45     GCAAGATCGA ATTACAATCA CGACGATCAA CGCACGTAAT CATCTCTGAT CACAGTAA     58

(2) INFORMATION FOR SEQ ID NO: 2670:

50     (i) SEQUENCE CHARACTERISTICS:  
       (A) LENGTH: 124 base pairs  
       (B) TYPE: nucleic acid  
       (C) STRANDEDNESS: double  
       (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2670:

ATACCAGCCA GACTTCGATC AACAGTGTTC AACTGCATTG CCCAGTAAGT TGGATAGCTC 60  
 GCACATAGTG CTACAAGTTA ACATATACan CGAGTTTGTA TCTCAAGCTT GAAGCTTGAC 120  
 TACC 124

(2) INFORMATION FOR SEQ ID NO: 2671:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 54 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2671:

CGCTTACTGC ATAAAAGCCC CTAACACCGG GGCCTACGC TCGTTGCGCG GCTT 54

(2) INFORMATION FOR SEQ ID NO: 2672:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 51 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2672:

TCAGCGATTT AACACTAATT CTTCTAGCTA TTCTCTGTAT TTGGACGACG A. 51

(2) INFORMATION FOR SEQ ID NO: 2673:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 57 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2673:

GATAAGTTGT ACCATATTTTC GATGCAATTC AATGGACAAT GAGGTCACCT GGCTTGT 57

(2) INFORMATION FOR SEQ ID NO: 2674:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 76 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2674:

5 TCCTTTGGCC AATTTTTCCTA AGTTTAAACC CAAACGGCCC GGGTTGGGTC CCCAATTCCA 60  
ATCCAAAATA ATTTTA 76

(2) INFORMATION FOR SEQ ID NO: 2675:

10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 56 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2675:

20 TCCGGGAACC TTACCCAGTG GCCCTACCCT ATGGGTTAAC CCAACCAAGTG GGGCCA 56

(2) INFORMATION FOR SEQ ID NO: 2676:

25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 67 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2676:

TGCGGGTCT CGTGCCGCCG TCTGCGGTGG TTGTTGTCC GGTGGTGTGT CGGAGTCTTT 60  
GCCAGCT 67

35 (2) INFORMATION FOR SEQ ID NO: 2677:

40 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 55 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2677:

GGACAGAGGC CTTGACCCCC CCACAATCCT GATTCACCGT AAGTTGCTCT CCCCC 55

(2) INFORMATION FOR SEQ ID NO: 2678:

50 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 65 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2678:

AAATTGGGGC TTCCATCCCC ATTCCAAATT ATTAAAACCG TTTAGGGGCC TTATTGGCAC 60  
 CATGG 65

(2) INFORMATION FOR SEQ ID NO: 2679:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 176 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2679:

ATTTTGGGAT TAAACCCTTA ATTAAAATTG GCCGGGAAAA GGAAAAGGCC GGTGGGAAA 60  
 AGGCCAAGGA AAAGACCTTG GGAACATTA AAAACCTTGG GCCAAGGCCT TCCAAAAACC 120  
 GGTGGTTTTT TATTTTGGGA ACCAAATTGG GGGGCCGGGA TTGGGCCAAA ACCTTG 176

(2) INFORMATION FOR SEQ ID NO: 2680:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2680:

GCCCCAAGA ATTCAAATAA CCnTTTCGGAC CCGGTAATGG CCACnTAATT 50

(2) INFORMATION FOR SEQ ID NO: 2681:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2681:

TGTGCATTTA TTGCATAACC TATATATGTG TGACCGATAT TTAGTGCGCA CTTCAATGGT 60  
 GCG 63

(2) INFORMATION FOR SEQ ID NO: 2682:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2682:

TTATCCAAGC TTCCGGATAG TTTCAAGAGA AACCAATGAA ATCCGTTATG GGACCAATGG 60

10

GT 62

(2) INFORMATION FOR SEQ ID NO: 2683:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 70 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2683:

AACAGCATTC AAGTGAGTTA CTGGGGTTTA TGCACCATCA TTGGATATCT GCACAAGGAA 60

25

TTTCAACGTG 70

(2) INFORMATION FOR SEQ ID NO: 2684:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 68 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2684:

CTTAAATTC CCCAGTTTCC TTCCTTTTAA ACCCCATGGA ATTATCCCGG CCAAAAATGG 60

40

ACCATTAT 68

(2) INFORMATION FOR SEQ ID NO: 2685:

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 58 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2685:

TTTTAACAAA ACACCTAGAT ATGTTGCTG ATCAGAGATG CCTGGTGACC GGTGATCC 58

(2) INFORMATION FOR SEQ ID NO: 2686:

55

- (A) LENGTH: 87 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2686:

10 ATCCATCCTT ATAGGCATTC ATCCTTTAAC ACCAACGATT TACATTATGG ATATAACGAC 60  
TTGAGGGGGA ACGTGGGGTC CATCCTA 87

(2) INFORMATION FOR SEQ ID NO: 2687:

15

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 50 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2687:

25 ATGGCTGGGC GCTTTACGTG GCCACATTAG GATTATGGCA CTGAAGCGTA 50

(2) INFORMATION FOR SEQ ID NO: 2688:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 50 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

30

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2688:

AACGGTCGTA GGCAAGGGAC TCCCCCnGG nGCTAnATGA ACTGGTCGTA 50

(2) INFORMATION FOR SEQ ID NO: 2689:

40

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 60 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2689:

50 GCTAGCATCC ATGGCTCCTA TGCCGAAGCT GAGTAGACTT AGGTGACGGG TCGGTGACAA 60

(2) INFORMATION FOR SEQ ID NO: 2690:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 146 base pairs

55

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2690:

ACTTAAAAAA GGAAGATTAG AAAATTCATA AAAAAATTTT GCTGGGGATT CTTGATCCCA 60  
TGGGCCCATn TCTGGATTTA GGTATTGGG TTGGCCAGCC AGGTTAGCGG GGCCCCCATT 120  
CTTCCAGGCT CGGTTTCTCC CAGGAC 146

(2) INFORMATION FOR SEQ ID NO: 2691:

15

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 53 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2691:

ATTGGTGTCT AGATCATTTA ATACTAAACA TACAACACGA CTAATTCAT TCA 53

25

(2) INFORMATION FOR SEQ ID NO: 2692:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 113 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2692:

TATTGAATTC AAACATATGTA CTATTTCTTA AATAATACAA TAAAAACGAC TACCATACTG 60  
GCCAGAAATA TATTTTATTT GTTACACATT AATTTCAATC CTCCATAATT TGC 113

40

(2) INFORMATION FOR SEQ ID NO: 2693:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 54 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

45

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2693:

GACTTATGTC CGTGTTCGCG TGAAGGCACG TCACGTAAAC TACCCGGTAC AGCT 54

(2) INFORMATION FOR SEQ ID NO: 2694:

55

(A) LENGTH: 204 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2694:

10 CTTCAGCATG AAGAAGTCGC GTGATATACA TCATATCGAT ATATACCGAT TATATCATCA 60  
 GAACATTCTC CTGGTATCAT TAGATAGATG ATAATTTGAC ACAGTCCACA ATTTGTnACA 120  
 ACGCCGAGAC TCAATGGCAT CCTGTACnTG ATCTATGCCG GAAAACACTA GTCTATATGC 180  
 15 CCGCAGACGT CCACTATATG CATC 204

(2) INFORMATION FOR SEQ ID NO: 2695:

(i) SEQUENCE CHARACTERISTICS:  
 20 (A) LENGTH: 112 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2695:

ATAACTCTAA TTTGAATTAT CTCTCACTAT TAAACGCGA GCTGTGTAAT AACGAACGCT 60  
 30 GACATAATCT TGTATTGTCG CATCATTCGC TGGTATTATC ATANTGCCGT TA 112

(2) INFORMATION FOR SEQ ID NO: 2696:

(i) SEQUENCE CHARACTERISTICS:  
 35 (A) LENGTH: 148 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2696:

TGGCAAAATT AGATGTCTGA ATAGTTTTAT TTACAAGTAC AAACCTTGTA CCATTTTAAC 60  
 GTAAACACAA TTTACTTATT GAAAAGAAAA TAAATGTATT CATGAAnACA CACTTTCCAT 120  
 45 AGCACTCATC TATAGTACTC AAATTCAG 148

(2) INFORMATION FOR SEQ ID NO: 2697:

(i) SEQUENCE CHARACTERISTICS:  
 50 (A) LENGTH: 101 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

55

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2697:

CCTATAATGC TAAACTTCAT ATATCTCTTT GGCAACTATC TCCCTTCTAT TACCAAAGTT 60  
 5 ACGATAGCAA TACAATAAAG CAAGCATGTC ATGCTTACTT C 101

## (2) INFORMATION FOR SEQ ID NO: 2698:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2698:

TTGATAACAT TTGAAAAGCT GCTCCGATAT CAGCAACCAT TTCATCGACC ACAATATACG 60  
 20 ACATAGTCAC AAAACTGATT AGAAGACACC AATTGCTGAT TATCAAATCA CAAATTTAAG 120  
 ATGAGATTCA A 131

## (2) INFORMATION FOR SEQ ID NO: 2699:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2699:

GATAGCGGTT GTTAATCAAA CGATGGTACA TGCTTACATG ATGCGCCATG TTTGATAACA 60  
 35 GCTCTCTATG ATTACGATGG AAGAATGGTT TATTTCTATCT CAATTATTCC TATTAAATGn 120  
 AACATGCCCT AGCAAACGGA TACAACACAA TCACAACATC ACTTTGAAAT TGTTAAACCT 180  
 40 GAGAACCACA TACGCGnAAC AC 202

## (2) INFORMATION FOR SEQ ID NO: 2700:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2700:

TTCGAATTTA ACAACGTAT CACGCCATAA AGGTTGTATA TGTGTTTGT AAATTC 56

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2701:

TATTGCGGGC TTATTAGTAC ACGATCTATA TGATGGTCAA ACTTATGTCT TTCATATTCA 60  
AGTGTGACAT TGTGCGGTGA TTATATTTAC GCGTCGTTAT CTACGAACGC CACATTAAGA 120  
TTCGAAACTG ACAATCAACT CATAACGCCA TGGTCCTAGA AAn 163

## (2) INFORMATION FOR SEQ ID NO: 2702:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2702:

TAnACAATCG TAATCGAGTC AATGATGTGA ATTGCCCCAG TGAGCGCTAA GAATGCGACA 60  
TTCCACACGA TAAGGCAGTG CGCATGCGCA CTGACCTAAT AACACTGAGG ATGAGTACTA 120

## (2) INFORMATION FOR SEQ ID NO: 2703:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2703:

CTGCTTGATT AGGATCGTAT TTATATGAAG ACTGTGTTCC ATAATGATGT GCGTTTTGGC 60  
TGAAGTCCCT TAAATGTACn TGTGTATAAA TGCTATAATT TAG 103

## (2) INFORMATION FOR SEQ ID NO: 2704:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear



TCTATAACGC CTCTCATCGT TTGGTCACAT ATTACCATTAT TTCATTTTAT GTTCTCGATA 60  
 ATTGTATGCG NTGTTTCTCA CTGTCATCAC ATTGATACAA CTCATTGTCA CTTTATACGA 120  
 5 TTCACACACC TCGATACGAG TGATGATATA TGACAAAGCT 160

## (2) INFORMATION FOR SEQ ID NO: 2705:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2705:

TTATTGTTTA AGATGGTTAA ATGTCATCAT ATAACAATA ATTTTGTAGCA ATTCGATATG 60  
 20 CCTATAACCT ATAAATTTC ACGTCAACAGA AAGTGACAGG CATACGGATG TGTGAA 116

## (2) INFORMATION FOR SEQ ID NO: 2706:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2706:

TTACACCTGC AGTGTATGGA CTATGGCTAG ATACAATAAT TTTAGTCATC AACTACATC 60  
 35 ATACAAACTT ACGACTTACA CATATCTGCT TCTAATCTT CTAAGTATT AAAGCTCGAC 120  
 ATCGGAAGCT ATTCTAAATT ATTATCATAT ATCTAACTAA CTGACCTAAT ATATACTACC 180  
 ATAAATAACC CGCCTCAAGG TTCGCATCCG CATATAATGC TTAGAAGTC 229

## (2) INFORMATION FOR SEQ ID NO: 2707:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2707:

TCCATATCAA TCCTGAAAGT ACACATATAT CGTACACCAT ATGGTACAAT TTCCTATAT 60  
 50 ACACATCAGG CATCTTTCAA GACACATGTT AGGCGCTGGT CGGTGTATCT CAGAAATGCA 120

## (2) INFORMATION FOR SEQ ID NO: 2708:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2708:

GGAACTTTTC TGATTAAGTG TTCACACGCC AACCATACA TGTATTCATG CACACAATTG 60  
 TTGCTAAACT CACTAACAAC ATACGACCAT TTTACTTTCA ATACATATGA TCCGTATAAC 120  
 TCGAATTChC TGCTTATAAA TGACCATTTT GACGTCACA ATGTTAAACG ATTGGAAATT 180  
 TTAAAGTTAG CATGTCCACA TCCGAGCAGT AACTATGCCG TACCATTGTG ATA 233

## (2) INFORMATION FOR SEQ ID NO: 2709:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2709:

TTGTACCTAC CAACGAGGAT ACAATGGATG TCACACGAAA ATTGGGATAT AGATGTCCCA 60  
 GT 62

## (2) INFORMATION FOR SEQ ID NO: 2710:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2710:

CTTTAAAAAG GATAAATGAT TGAGAAAAA ACCCATTCGA AAATCATGCT GCTCATGCTG 60  
 TAGACTTATC GTTTGGACAC TCGCGTAAGA GCGAGCAGTG AAAT 104

## (2) INFORMATION FOR SEQ ID NO: 2711:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2711:

GTCCAGAATA TTAATCTGAC ACAACCATTT TAGCnGGTGG ATTAAATATA TACGACCTCA 60  
 5 CCGCAAGAAT CTCTATTTAA CTTAACCTAT CATGAATAAA CTGGCGCTTG TGATATCATA 120  
 TGAAGATTAG CGAAAGATAG C 141

## (2) INFORMATION FOR SEQ ID NO: 2712:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2712:

20 TGGTATTGAA TAGCAAAATT TTGACACTAT TTGCATACTC AATGATACAT CATATCGTTA 60  
 TATGGATTTT TATGGTCATT AATGGTAAGA ATTTGATACG GAATATTGGC AGGTTTGGAA 120  
 ATCAATAAT ATGAGAAATT GTATTAACnA TTAGTCAAGT TAACGCTCAT AAATAGACTC 180  
 25 ATCnCGCGCT ATAACGCTTA CC 202

## (2) INFORMATION FOR SEQ ID NO: 2713:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 30 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2713:

TTGAACTGTC TAAGACTTGG ACGCTAAATG AATGCGTTGA TACAAACGGT GAATCC 56

## (2) INFORMATION FOR SEQ ID NO: 2714:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 45 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2714:

50 CATGACCGAC ATCAGGTGCA AACTCCCTCA TTAATCTGGG AAAACTGTAT CCCGGTAGCT 60

## (2) INFORMATION FOR SEQ ID NO: 2715:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2715:

CCTATAACTA CTCAATATTG CAATTACACA TCCTCACTTT TGTCAATTGT TTGACAATCh 60  
 AATACACGTT ATGCACAACCT CCATTTTAAC GGAATGGAGA GCACATATGG ACAGTAAATT 120  
 AAAT 124

## (2) INFORMATION FOR SEQ ID NO: 2716:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2716:

GGAATATGTA CTATTATCAT TTGATGTTAT TACTCATATT TTTTGTAATG AATGCTATCA 60  
 CCTACAAAAA ATTTACTTGA AACAGTAATA ATAATTAATT ACCACAAACC ATGATAAATT 120  
 TAATAaCTAA TCTAAAATAT CGCATGTTCA nAGCCACAAG ATATAACGCG TTCGCTAGAT 180  
 GGAAGTAGAT AGTATAAGGC GCCGTGGAGC CTGGCCT 217

## (2) INFORMATION FOR SEQ ID NO: 2717:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2717:

ATGACATACG CGCATATACA TGCTATCCCG AACTAATATT GATGCGTATT ATGTAATTGG 60  
 AGCGAACACT CA 72

## (2) INFORMATION FOR SEQ ID NO: 2718:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2718:

CATATCATCA CTATATCCAT TGCCTAATAG TGATGATATT GATTGGCATA ATGGTATATG 60  
GCAGATACGA TAACATAACn AACACCTCGG ATAATTGCTA TTAGCTGCGA AGTTATCGTG 120  
CCTGATTTAA CGATGTAGA 139

(2) INFORMATION FOR SEQ ID NO: 2719:

15

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 79 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2719:

CTCTATCATA TCTAGCCATA TGCATGAGAT TATCGTTTAT CTCGACACGC TCTTAAAAGG 60  
CGACACCGGC ATATGATGT 79

(2) INFORMATION FOR SEQ ID NO: 2720:

30

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 53 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2720:

CAATCACAAT TGAAATTACA CAAATACAGC CCATTGCATG ACACAGACCA ATC 53

40

(2) INFORMATION FOR SEQ ID NO: 2721:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 66 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2721:

CGCCCGAGGC TACCATTTTA CCATAAAGAC CGGTCTAAAT CCTTCCGGTT TCCATGGGGC 60  
ATTG 66

55

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2722:

TTCCTCGCCG AAAATGACCC AGAGCGCTGC CGGCACCTGT CCTACGAGTT GCATGATAAA 60  
GAAGACAGTC ATAAGTGCGG CGACGATATC ATGCCCGCG CCCACCGGAA GGAGCTGACT 120  
GGGTTGAAGG CTCTCAAGGG CATCGGTCGA CGCTCTCCCT TATGCGACT 169

## (2) INFORMATION FOR SEQ ID NO: 2723:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2723:

CCGGGCCAAG CTGGTGATCA CCGATGTGGA GCGCCAACAT CGCATCGAGG AAAT 54

## (2) INFORMATION FOR SEQ ID NO: 2724:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2724:

ATCGGTGATC ACCAGCTTGG CCCGGGACAA CTGCAGAGCG TGCAGCAGGA ATTG 54

## (2) INFORMATION FOR SEQ ID NO: 2725:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2725:

AAAACCATTG TCCACCTTTA GAAAGCTTTT GTTTTGGGAA TACCTAAACC GTGGTTAATG 60

(2) INFORMATION FOR SEQ ID NO: 2726:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2726:

TTTAGGCCCT GTAACnGnTT GCCGnTTGn CCGTGTGTAT ATCGGGGGAA

(2) INFORMATION FOR SEQ ID NO: 2727:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 56 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2727:

GGATCATTAAC ACGTGTATCA CCATCCAGTT TGCAAGACGG ATAAACTGCT GCAACG

(2) INFORMATION FOR SEQ ID NO: 2728:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 70 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2728:

ACCCATGGAG AATTAAATTT AAAAACCGTA TTCCGGGTGG ATGCTGGGTG GGTAAGTTGG  
 CCATACTGGG

(2) INFORMATION FOR SEQ ID NO: 2729:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 54 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2729:

ACCACCTTCC CCAATAAGCT GGCCTAAAGC CCCATAATGG GCCATGGTGC GGCC

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 74 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2730:

TGTTTGGGGA CCTTAAATGG TTCCAAATTC CAACCACCCA CCAAAGAAT TCCAGTTTCC 60  
AATTAAGCCA GCCA 74

(2) INFORMATION FOR SEQ ID NO: 2731:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 66 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2731:

AAGTTGGGGA TTAAGGCCAG TTATGGAAAG GATGGATGGT CCATTGGGC TTATTAGAAG 60  
AGCATT 66

(2) INFORMATION FOR SEQ ID NO: 2732:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 50 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2732:

TTTGnAAAAG CCnGTAAGAG TATTGATTT TGTTGGAGGC CAAACCAGAA 50

(2) INFORMATION FOR SEQ ID NO: 2733:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 102 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2733:

AGTACCAGCG GACAATTCGG ACCCAACTTG GCAATTTGnG GTTTTGGACC AGGAAATAAA 60



## (2) INFORMATION FOR SEQ ID NO: 2734:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2734:

CCAGGCTGGC AGTTTTTCTA AAATGGTGGT AGGAAAATTA nCCAAACCAT TTAGGATGGC 60  
ATGGTCTTCC ACGGATGGCG GCCGTTAACC CCAAAAAGG CCATTCCATT T 111

## (2) INFORMATION FOR SEQ ID NO: 2735:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2735:

CGTATGGGAT GGCCATTCTG ATGACACACA ACGGTTAGGT TAGCAACGTT GTCAAA 56

## (2) INFORMATION FOR SEQ ID NO: 2736:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2736:

CAATCCGGGT GTGCGGGCGT GTGTACAAGA CCCGGGACGA TTACCGACAT 50

## (2) INFORMATION FOR SEQ ID NO: 2737:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2737:

TAAATTTTAT TGTGGAGAAA GTTAGGTATC GTGGTACTGA GGATTGTGTT 50

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 53 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2738:

TAAATTTAAA CCCGTCCCGG TTTCCCAAAT TTGGAATTTT TTGGAACCCC TGT

53

(2) INFORMATION FOR SEQ ID NO: 2739:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 85 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2739:

ATACCCACCT TGGATTCTTA ATACCCCAAA AAGGCCGGGG CAACTTGGCT TAAAAAACTG

60

GCTTGTTTAA ATTGGATTTC CGGCT

85

(2) INFORMATION FOR SEQ ID NO: 2740:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 70 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2740:

GGAAAGTTTA GTAGTTTAGA GTCGAAAAAT TAGTTTTCTA GTGTAACGAA TCCGGACCCA

60

AATTTTTTTC

70

(2) INFORMATION FOR SEQ ID NO: 2741:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 53 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2741:

CGCGCCAATT TACCTGGCGC AGCAGACGCT CAACGAGGAG CACGGCAGCT GCG

53

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2742:

TGAAGAAATC GCACACACTA TCGAACGCAG ATCGCACATC GAATGCATCA GAATCAGCTC 60

## (2) INFORMATION FOR SEQ ID NO: 2743:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2743:

TATCACCTCT TTTGCATATT ATTAGAATAT ATAATGATCT TTATAGAAAG GAAAGAAGAA 60

GAGTTATCAT nGCGATATCG CCCAGCGCGT CGTACACTAT GCCATGAATT ACACAATCAT 120

GCCTC 125

## (2) INFORMATION FOR SEQ ID NO: 2744:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2744:

GAATTTCCCC CGAAACCGGG AAAAATTTTT CCAACCGGT GGCCTTCCCC CGTTCCCGT 59

## (2) INFORMATION FOR SEQ ID NO: 2745:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2745:

TTTTCCTTAA GTTAGTTTTT TTATTGGGCC AAAACCGGCC CCAGGAATTG A 51

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 55 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2746:

TAATTGGTC ATAATGTTGT TTCAGATGAA ATGCTAACAA TACTGATT ACAGT

55

(2) INFORMATION FOR SEQ ID NO: 2747:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 64 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2747:

ATGGTGAAT GGGATTAGG TGGATGGCCC CCCCAACCAG CCGGCCTTT TTAAGGAAC  
TTGT.

60

64

(2) INFORMATION FOR SEQ ID NO: 2748:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 78 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2748:

AACAAGAGTT ACATTGGTTG TGGAAATCAT CGGTTTAAAT TAGTCCAAAA GGATGGATTC  
AATCGGTAGG GGGGTAAG

60

78

(2) INFORMATION FOR SEQ ID NO: 2749:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 54 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2749:

GCAAGTGGCG GAGTCACACT TATAGACAAG AAGTACGACA TCTTGATGT GGTG

54

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 58 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

5

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2750:

10

TATTTAGATT CAAAGCATCA AATTGGTTTC GTACCTTTT GCACATCGGT TGGGATAA

58

- (2) INFORMATION FOR SEQ ID NO: 2751:

15

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 79 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

20

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2751:

25

GGAAAACCCC CCAAATTTTC CCCCCCGTT GGGAAAAGAG TTCCCAAAGT TGAATTAGT

60

TCCCAAACCC GGGAGTTCC

79

- (2) INFORMATION FOR SEQ ID NO: 2752:

30

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 68 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

35

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2752:

40

AGAACCGAGA GATAGTGCCG AGAGAGCGAG AGGTTTTAAT AGAGATGTTT GGCCGTACTA

60

GTTAGCCG

68

- (2) INFORMATION FOR SEQ ID NO: 2753:

45

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 64 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

50

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2753:

ATAATCTATG GGGGACCGT CTGGTAAGGA ACCTGGTTGC CCTGCCAATG AAGCCACCCT

60

55

## (2) INFORMATION FOR SEQ ID NO: 2754:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2754:

ACAAAGGTTT TACGCCCAA TTGTTCACTG GCTAACTGGG CGATGGTTAG TATTGGCAGC 60  
GCAAAAGTGG CAGGGG 76

## (2) INFORMATION FOR SEQ ID NO: 2755:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2755:

ACCTCAGGGA CAATTAAAAG TTTTCTTCG GAATGAATGA CAACAACAAA T 51

## (2) INFORMATION FOR SEQ ID NO: 2756:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2756:

ACGTATTCCC TCGTTCTTAG GTCTTCTAAA CATAGGTGAC TTTTGGTCG 50

## (2) INFORMATION FOR SEQ ID NO: 2757:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2757:

AAATGCTTCG TATTAACGCC TATTTTAGCT CCGTTATAGA CACAACTTAC ACA 53

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 51 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2758:

10

ACACGGCAGC GAATACTCGT TTGGTGAGCC TGTACACATC TAACACGAGA A

51

- (2) INFORMATION FOR SEQ ID NO: 2759:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 115 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

15

20

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2759:

GGGAAAACCA ATTAAGGATT TAAAGGTTAA TTAAAGGGG CCGCCACCGG GTTGGGGATG

60

25

CCCTTTGGGC ACCTTAAGAA AGCCCCGATG GAAAGGGACC GGTACCTTA ACCGG

115

- (2) INFORMATION FOR SEQ ID NO: 2760:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 227 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

30

35

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2760:

TTTGCCAGG CCAATTAATT CCTGGTGGCC AATTAAATTT AAGGGGACCT TTGGGGGAAT

60

40

AAGGTTTAAA ATTGGAAAAT GGTCCAATTT GGACCTTTTG GCCAATTGGA TTCCCGGCTT

120

AAAAAGATTT GGACCGGTAA ATCCCTTTT AAATTACCTC GGGCCanGGC CCAACCAAGC

180

CAAACCAATT TAAATCCGCC TGGAAACCAA CCCATanTTC CTTTACC

227

45

- (2) INFORMATION FOR SEQ ID NO: 2761:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 59 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50

55

ACACTATTGT GCCAGCGCAC CTTGAGGTA TCTTGCATCA CTCAGCTGTT TTTTACTGT

59

(2) INFORMATION FOR SEQ ID NO: 2762:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 68 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2762:

TTATCCTGTT CTAAGCCCG ACGGCTCGGC CACACGATTA ACCTTTAACG CCATCTTGTC

60

CAACCTGT

68

(2) INFORMATION FOR SEQ ID NO: 2763:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 116 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2763:

TGGAAAGTAC CATATAAGTA ATGGTAGTCG TTTCAGAAAG ATATAAATCG TTGGGAAAAG

60

AAGAAATGAC AATTAAATGT AAATATTTGT TCATGTACAA ATAAATATAA TTTATA

116

(2) INFORMATION FOR SEQ ID NO: 2764:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 78 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2764:

TTGTTACAGT GGTGTAGCGG ATCGCACGGC CTTCAACTAA GTGGTTCAAT GCTTGATACC

60

AGTTATGAGT GTTGGTGC

78

(2) INFORMATION FOR SEQ ID NO: 2765:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 112 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2765:

ATATATTCGT ATGCACCTTT TGTAAGGCTT TGTAATACGA AAATTATCAC TACAATGATT 60  
 5 GCTGTAAACGA GTAACGACAT ATATGGCACA CCGTTTTTAT TnGTTTTACC AA 112

## (2) INFORMATION FOR SEQ ID NO: 2766:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2766:

TATTGAAGAT TTTTTCGAAG ATAAAGGTGA CACATATTCA TGTCATGTTT AATATCGTTA 60  
 20 CCTTACGTAA CCATATAAGA CTGTAAGTGG TGTCATATCA TTCGTAGAAC nTTTGAAAT 120  
 GAT 123

## (2) INFORMATION FOR SEQ ID NO: 2767:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2767:

GTCCGCGCCA CGGAATGGCC CACGGGACGA TAAGTGAGGG CACCGACGGC CGAACCCAAG 60

## (2) INFORMATION FOR SEQ ID NO: 2768:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2768:

GTACGCGGAG CACGAATTCC GCGGATCTGG GAGCATCTCT AGGTAAnTTT 50

## (2) INFORMATION FOR SEQ ID NO: 2769:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2769:

CTTAGGTAGC TCAGTGTGTT ATTGAGAGGC CTGTTGGCAG GCCCCGGACG ATC

53

(2) INFORMATION FOR SEQ ID NO: 2770:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2770:

AAATTGATAG CGTGCACAAA CCAGGTCCAT CCACGAACAT GCCAATCCAG CCCAGGAAGT

60

AATTGCCCCG

69

(2) INFORMATION FOR SEQ ID NO: 2771:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2771:

ACGATCATCT GGATGGATAT ACAGAACAGT GTGATTGTAC GTGGTGGGGA AA

52

(2) INFORMATION FOR SEQ ID NO: 2772:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2772:

TTAACAGTAT GATATTATCA CACGTGAATA GGATATGCCA AACTGGCAT CGTTGGGGAT

60

AGCGTAATAC

70

(2) INFORMATION FOR SEQ ID NO: 2773:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2773:

5 AACATTGTAT TCGTGATTAA GACTTCGATC GGTTCAGTAT TCGGCAGATC CACATGTGAC 60  
CATGCTT 67

(2) INFORMATION FOR SEQ ID NO: 2774:

10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 120 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2774:

CACCCTTGTC ATATCACATT TGTATGTGTT AAGAGGGAGC CCCTTTCCCG ATCAACTGGC 60  
20 GATAAAAACA GTTGAAAGT GGGCGGGGGT TATTATTCTT GATGACGGCG GGGTTTTTTC 120

(2) INFORMATION FOR SEQ ID NO: 2775:

25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2775:

AACCGTTGCA GGTAAGCTG GGCAACCAT TCTTCTCTAT TAATGGTTCA 50

35 (2) INFORMATION FOR SEQ ID NO: 2776:

40 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 57 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2776:

CATGTACGGT GTCCACACAA GAAGTATTTA GGTGGTTGTT CCCGGATTTA ACCTGGC 57

(2) INFORMATION FOR SEQ ID NO: 2777:

50 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 51 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2777:

AACGACCCCG GGTTCACCG GGTCCATTA AGCCAAGGGC CAGGGGACCC C

51

(2) INFORMATION FOR SEQ ID NO: 2778:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2778:

TTGTTCCGGC CTAAAAAATT TAAATTGAAC CCAAGGGTTG CCTTGGGTTG GGTAAATCCAT

60

TTTTTGAATA AACCTTTGnC CCTAATGAAT TTTTCCGCCA TTAAAGGGT GTCCGCCAAT

120

CCGG

124

(2) INFORMATION FOR SEQ ID NO: 2779:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2779:

GTAAATTTGG GAATTACCGG AAAATTAAGG AAAGGCCAGT AAGGGGTTTC CAGGCCAA

58

(2) INFORMATION FOR SEQ ID NO: 2780:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2780:

GCACTCCAGC CTGAGCACCA GGGTGAGACC CTGTCTCAAG AACAAAAACA nCAACAnCAA

60

AAAACCTGTT CAAAACTCAC TTCCTGCAGT AATCTTTCCT TGAACAACT CACCCTCTAA

120

TTCCACCTG CAATTGTGTG TAGAAATCCA TTCTCGTGTG TAATTTTGGG CTTATATGCA

180

CACATTGAAA ATCCAAGAGC CAGAAAGAGC TCTAAGGAAT TATCCAGTCC AGCTCTGTGC

240

AGCCTGGGCT AGGACCCAGA TCTTTCCCAT TTCCCTGTTT CAAAAATTTT nGGCACAGGG 360  
TGGCCACCCT G 371

5

(2) INFORMATION FOR SEQ ID NO: 2781:

10

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 133 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2781:

GGGGTTGCCA AAGGGGTGTT AAATTTAAGT CCGATGAAAA TTAAGhAAAA AAATCCCATT 60  
 TTCCCTTCCG GGTCCGTTGT TGGGGCCTTA ATTCCCGCC AATCCAAGTT TGGTGAATGA 120  
 AATTAATTAC CGT 133

20

(2) INFORMATION FOR SEQ ID NO: 2782:

25

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 58 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2782:

GTTCAGTTG ACGCTGGATC ATCTGGTACA CACGTATCCT GCATACTATA GATGTCAT 58

35

(2) INFORMATION FOR SEQ ID NO: 2783:

40

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2783:

GCTAATTATA GGCCGTCAGG CATTACGnGA TCGAATCTGG CAACTCACAA 50

(2) INFORMATION FOR SEQ ID NO: 2784:

50

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2784:

GCCnCnCTCT GTGACACTGT GTATATACAC CCGCGGGAAT ATCTCCAACG

50

(2) INFORMATION FOR SEQ ID NO: 2785:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 111 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2785:

CTTTGTCTGA CATATTGGGG CAGTGATTTT TGGGACGGTT CTACATGTCG AGTACTTTAG

60

TCAGAGTTGT GAGTAGCGGA CGGGTtTACT TGATATACCC TTAATGTGTA T

111

(2) INFORMATION FOR SEQ ID NO: 2786:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2786:

CATGATGATA CTTGCATGTA CGTTGTACGT GAACGTACAG TTACGTTGTC

50

(2) INFORMATION FOR SEQ ID NO: 2787:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2787:

TCAGCAAGTA GTAAGGATAT CAACTATGA TCTATTTGAT GTTATGCCAT AA

52

(2) INFORMATION FOR SEQ ID NO: 2788:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 64 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

GCATCATGGA ATATTAAAC AGCTGATATG TTTGAGTAAT GATTGATTGA CGAGATATGC 60  
GGCA 64

5 (2) INFORMATION FOR SEQ ID NO: 2789:

- 10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2789:

TGAGAGAACT CACAGTCGCC AGCGGCAAAG AACCCGnnAA GATGTGnGCA 50

(2) INFORMATION FOR SEQ ID NO: 2790:

- 20 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 64 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2790:

30 CAGTGTATGG AATCTTGTTT GAGTGTGAGA GTCAAAGACT TGGTGATTGA ATGGAAAAAT 60

TGAA 64

(2) INFORMATION FOR SEQ ID NO: 2791:

- 35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2791:

45 ACAAnGGGTG AAGTTCTCCC ACATGCTGTA TACCGTGGGA TTATTTTAA 50

(2) INFORMATION FOR SEQ ID NO: 2792:

- 50 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 83 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

.ATTCCTATTC AACACGGAT ACATAATCTT TTATATCTTC CTTCTAGTCA TATGATACTG 60  
 GAATAAGTGA TATTTCTTAT AAT 83  
 5 (2) INFORMATION FOR SEQ ID NO: 2793:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 64 base pairs  
 (B) TYPE: nucleic acid  
 10 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2793:  
 15 CATATGTCAT CGTACGTAAT CATCGATGAA ATATCAACAT CTCGACTTAA TAGGTCAACA 60  
 AGAT 64  
 20 (2) INFORMATION FOR SEQ ID NO: 2794:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 57 base pairs  
 (B) TYPE: nucleic acid  
 25 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2794:  
 30 CCCTACTCCG CGCAATAACC GCATTACCAG ATGCGCTTCC ACTGAGGAAC GACGGAT 57  
 (2) INFORMATION FOR SEQ ID NO: 2795:  
 (i) SEQUENCE CHARACTERISTICS:  
 35 (A) LENGTH: 65 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear  
 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2795:  
 AGATAAAGTG TCATCTATAT CCATCTATCA ATATAGATAT GTTTACGGCC GATTTCAATC 60  
 45 CGCAA 65  
 (2) INFORMATION FOR SEQ ID NO: 2796:  
 (i) SEQUENCE CHARACTERISTICS:  
 50 (A) LENGTH: 58 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear  
 55



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2796:

TATACGCCTC ATTACACCCA ATTGGACCCT TTACGTATGG AGTACATTAT AGAATCGA

58

5

(2) INFORMATION FOR SEQ ID NO: 2797:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2797:

15

NGCTAAGAAT TTATAAGAGG TTTCGGCAGA TATATATACG CAAGTATCTG

50

(2) INFORMATION FOR SEQ ID NO: 2798:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2798:

AAGCAGTCTT TCACAAAAAG TGAATAATCA CTAGTTCATT AATTGTCATT TGAACCTTCA

60

30

TATAATGCAT ATTACTTAAT GTACAAGCAA AGATGTATTT ACCTATCAAA GAATTTnC

118

(2) INFORMATION FOR SEQ ID NO: 2799:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2799:

CCATAGAACC TGTGAATACC TATACATATC ATACTGTGGA ATTCGTTACG AGG

53

45

(2) INFORMATION FOR SEQ ID NO: 2800:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

50

55

CCAATTCAGA CTGTTATTCT CTCTTCGTGA TAACCCGTGA TGTTCGTCTG C

51

(2) INFORMATION FOR SEQ ID NO: 2801:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2801:

GGGGGnGCAT ACCGCACCGA AGCATCAGAC GATGTGAGCG ACCTACCTCC

50

15

(2) INFORMATION FOR SEQ ID NO: 2802:

- 20 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2802:

CCGTAGCGCA CATATGACGA GACCAAGGAT AACGTGCAAn GncATATTGT

50

30

(2) INFORMATION FOR SEQ ID NO: 2803:

- 35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2803:

CACGTCATGA ACGTGCAATC AACACAATCA TTTACGAGAT GGACCAAGAC

50

40

(2) INFORMATION FOR SEQ ID NO: 2804:

- 45 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 126 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2804:

TATGGTGTTT ATTTTAGCGC TnGTTGTGCT TTGTCTTCAG CATCTATAAC CTAGTGCGAT

60

55

CTATTG

126

## (2) INFORMATION FOR SEQ ID NO: 2805:

- 5 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 88 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2805:

AAAAGCGCAT ATGGTGTMTT TCTCATATCA CTCCAGGACT CAGCAGCTGG AAGGAGTTAA 60

15 GAAGTAATAA GGTGCCACCC TAAATCCA 88

## (2) INFORMATION FOR SEQ ID NO: 2806:

- 20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 66 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2806:

TGGATCCGGT ACCAAATAGG GACTACCGGG AATGTCCCGG GGGGCCTAAT GCCGAATGGG 60

30 GCAACG 66

## (2) INFORMATION FOR SEQ ID NO: 2807:

- 35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 66 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2807:

CCCGCTAACG TGGGGAAAGT TTTGAAGTTA AGAAGGAATG GATTCCTAAC GGGGCGGGGT 60

45 CCAAAC 66

## (2) INFORMATION FOR SEQ ID NO: 2808:

- 50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 56 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2808:

ACAAAGCAGT ACTGAACTGG TTTCGTTGGA GCCCCTGTTG CTGTTTATTC ACGGCA 56

5 (2) INFORMATION FOR SEQ ID NO: 2809:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2809:

AGGGGGCGTA CAACATAGAT TTGCGAGATA CTCAGCATT CACTTCCATT TAACTTATTA 60

TCC 63

20 (2) INFORMATION FOR SEQ ID NO: 2810:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2810:

30 TTAGGCGCCT GTTCCAACCG CACCCATATA AGGCGGTCGG CTGCACGCAC GACGTATG 58

(2) INFORMATION FOR SEQ ID NO: 2811:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2811:

AAACCCCAAA GGAATTAATT TTCCGGTTTT CCAACCCCTT AAAAAGGGAA AGGCCAAT 58

45 (2) INFORMATION FOR SEQ ID NO: 2812:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

50

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CATCATTAAAG GCAAAAACCTT TCACAAAGTC ATGAGGCGCA AAAGGTATTA TTATAACACA 60  
TCCCGCGTTG GG 72

5 (2) INFORMATION FOR SEQ ID NO: 2813:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 53 base pairs  
(B) TYPE: nucleic acid  
10 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2813:

CCATTTAAAG CGGTACGGGG CTTGGTTCAG GAACGTCGTT AGACAAATTC GGT 53

(2) INFORMATION FOR SEQ ID NO: 2814:

20 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 53 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2814:

TAGTACCCAA TTTCCAGTCG AACCAGGATG GGACCAGAAG CCAAACCAAC GTT 53

30

(2) INFORMATION FOR SEQ ID NO: 2815:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 62 base pairs  
(B) TYPE: nucleic acid  
35 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2815:

GAAAAAAGG CCTTGTTTAC CAAAGGGGCC AATTTTTTTCG GTTCAAGGTC CAAACCTACC 60

TT 62

45 (2) INFORMATION FOR SEQ ID NO: 2816:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
50 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

55

TCTGAATGAC GCCGAAATCC CATCTGAATT CATGGGATTT TCCACTTTCA

50

(2) INFORMATION FOR SEQ ID NO: 2817:

5

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 51 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2817:

CGTTACTAAA GCTACATAGT GCGTCATTTA AGATTATAGC AAGTAGCATA T

15

51

(2) INFORMATION FOR SEQ ID NO: 2818:

20

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 54 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2818:

CATTCAACCAT AATATTCATT GTTCCATTAG CATATCAGGC ATGTCACGTG CACA

54

(2) INFORMATION FOR SEQ ID NO: 2819:

30

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 50 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2819:

GTGTATCAAA TGAGCATGTT nCAATGGTTC AnCATGGCGT TTATGGCACT

40

50

(2) INFORMATION FOR SEQ ID NO: 2820:

45

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 50 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2820:

ACAATTGCGG CTGCTCATTG TGAGCAGAC TTTATCATGG TTGGGTTGAG

50

55

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 102 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2821:

CAGTAGTACG TAAAAATGAA TCACTTGAAG ATGCGTACGT AGATTTTAAA CGTCAGTTCT 60  
AAAAAGTGGG CAATCCAAGA GACGTAACGG AATTTCGAA AA 102

(2) INFORMATION FOR SEQ ID NO: 2822:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 55 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2822:

GAGTACTTAA TCCGGCACCG TTTACTTCTG GGGGCATCGA CTAAGTGGGG CGGCC 55

(2) INFORMATION FOR SEQ ID NO: 2823:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 71 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2823:

ATTGGTTTCT CATAAACACT TTTCTATGAA TTTGTATGTA TTTGTTTATT AAAATCTCTA 60  
ATTCTTATGG A 71

(2) INFORMATION FOR SEQ ID NO: 2824:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 134 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2824:

CCATTGAGTG TGAGTATATC ATCGATCAAT ATGCAACATT TATCAGGTGC ATGTTGCTTA 60

TGGATAATTG AACA

134

## (2) INFORMATION FOR SEQ ID NO: 2825:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 57 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2825:

CCAGAATGAT GAGCTACAGG ATCAGCCCAG ATATGCAGGT AAACGGGCCA ACCATTG

57

## (2) INFORMATION FOR SEQ ID NO: 2826:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 89 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2826:

CAATAATGCT GAACAGCAAC GCATCTCATT CTAAATCGC TCAGAATCAC ATCCCATGCA

60

CACATAATAA GTGGCACTTA GCTTAAAT

89

## (2) INFORMATION FOR SEQ ID NO: 2827:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 64 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2827:

CGGATTAGTG GTGTAAACTG GGTGACCCAT ACCACACCTC GCGTGTGTG AAAAAAGGAC

60

TTAA

64

## (2) INFORMATION FOR SEQ ID NO: 2828:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 51 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear



TATACAGAAA ACAGCGTGCC GTTATCCATT ATCACATGAC ATATGTAGTC C

51

(2) INFORMATION FOR SEQ ID NO: 2829:

- 5 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 68 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2829:

GAGATACGGT CTTCGTATAT GATATGTGCA TATTTAGATA GTCATTTATG AGAGAACGTG

60

15

GACGTGAG

68

(2) INFORMATION FOR SEQ ID NO: 2830:

- 20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 58 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2830:

TGATGATTGT TTATGATACG ATATGTAAAT GATAATCATC CAGGAGGTCT AGCATGGT

58

30

(2) INFORMATION FOR SEQ ID NO: 2831:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 54 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2831:

CCTAACAAAC ATAATTAAAC CCATAAATGC ATCCAATGCG GTTAAACCAT GAAA

54

40

(2) INFORMATION FOR SEQ ID NO: 2832:

- 45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2832:

55

(2) INFORMATION FOR SEQ ID NO: 2833:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2833:

GTCTGCTACC CTTTCAGAGC AACATGCTGA GTGTATAATG CCGTGATATAG GGGACAATGC 60  
CATTCACTA 69

(2) INFORMATION FOR SEQ ID NO: 2834:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2834:

AACACCAGCT GGTAAGTATC ACGTTACATT TTGTGTCTTC ATGATTAATA AAAAC 55

(2) INFORMATION FOR SEQ ID NO: 2835:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2835:

AGAGCTTGGA TGCCTTCGT AATTGATGCT CTAGCTCCAT GGGGCCCATG 50

(2) INFORMATION FOR SEQ ID NO: 2836:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2836:

TTTCGTCACT ATTGCTCATG CATAGACATT TGCAATACCG GCAAATGACG ATGGnATATG 60

TTAATGGTCA ATACAGGG

138

## (2) INFORMATION FOR SEQ ID NO: 2837:

5

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 61 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2837:

15

GTTGGCAACT TCAGTCGCTA CTTTAACGCA TCTCACAGTC CTCCTCCCAA AGAGAACGTA

60

T

61

## (2) INFORMATION FOR SEQ ID NO: 2838:

20

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 78 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2838:

30

ACGTGAATCC CGTGAGGCCA ACAGTGATTT GGATAATTAC ATGGATGTTT GACTAATGGT

60

CATTACACCC CAGATCAG

78

## (2) INFORMATION FOR SEQ ID NO: 2839:

35

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 90 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2839:

45

ACTTAAAATC TCCTCTTGCC TAACTTCCAC ATTCTTATCG ATATGAATAC ACCATACGTT

60

TTATAGATAA GTTGATGTTG ATGCATATGT

90

## (2) INFORMATION FOR SEQ ID NO: 2840:

50

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 61 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2840:

TATATTAGT CTGTTATACA AGGTGTATCA CAGCGGTAAT ATGCCTCTAC ATGGCCATAT

60

G

61

(2) INFORMATION FOR SEQ ID NO: 2841:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2841:

GGGCCCCGGC GGCAGGGAGG AAGGGGGCAA GGCGGCGCC AAGACCACGA CCGGCACC

58

(2) INFORMATION FOR SEQ ID NO: 2842:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2842:

TGTACAGGTG CAGTTAGACC GCCTGACGGA ACGAGACGTG CAATTGCCAG CAACGCACAA

60

(2) INFORMATION FOR SEQ ID NO: 2843:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2843:

AAACATGTGA AGTGATCGAG GTATGGACGG AGTAATGATC GCACAAGACA TAGCATCCCC

60

GT

62

(2) INFORMATION FOR SEQ ID NO: 2844:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2844:

ACGATTTAGT TTGAATTTCT ATTAGGGTTT GGTGATTCTA CTACTTCTGA TA

52

(2) INFORMATION FOR SEQ ID NO: 2845:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2845:

GATTATCACA ATTATGCAAA GTTGTCTAAT CGTTAGACCA ATTTCTGTTC AAACACCACA

60

ATC

63

(2) INFORMATION FOR SEQ ID NO: 2846:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2846:

CGTTATATAA GAnCGACATG GAAGCATGAT GAAATATTGA ATACATCATA

50

(2) INFORMATION FOR SEQ ID NO: 2847:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2847:

CCACAGGTGC ATCCGCCTGG TATGGAGCCG GCCAGTCTTC ACTGCTTTCA C

51

(2) INFORMATION FOR SEQ ID NO: 2848:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

AAACTGTCC CAAGCTGTTT TTATTAGAG CAACCAATCC AATTAAACC CCCACCATT 60  
ATTTTAAATA ATACCATTCC AGCGAAAGCC CTTCCANGG TTTTGGATA TAA 113

(2) INFORMATION FOR SEQ ID NO: 2849:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 155 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2849:

CATCTGGAAC TTTTAAATTC CAGAAGGGTT CCAGAAGGTT TCGAAATCCC TCCTAATGGG 60  
CTCCATTAAAC GGATTTTAAA TTTTAAATA ATTTTAGGCC AAAAAATTAA TTTCCAGGAA 120  
AAGTAAGTTT CCAACCGGG TAAGAAATTA CCAAA 155

(2) INFORMATION FOR SEQ ID NO: 2850:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 64 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2850:

CACAACTAA CATAGAAGGG CCATCATCAG GTGCTATTAA ATATCTACGC TAGATTGTAA 60  
ATCA 64

(2) INFORMATION FOR SEQ ID NO: 2851:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 54 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2851:

AATTATTCAT CAATAGCTCT TTACGATTCA CAAATCTAGG TACTTTTCAG ATCT 54

(2) INFORMATION FOR SEQ ID NO: 2852:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 58 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2852:

AAGCCCCCTTT AAAGTGGGCC TTAAAGGAAC GGTGGCGAAA ATCCCCAAAT TCCGGGCA

58

(2) INFORMATION FOR SEQ ID NO: 2853:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2853:

AAAGGTTTCC ATTCGGTCCC ATTAAGATTT TTTTGGAAAT TCCATGGAAG GATGGTTGGT

60

CCTTTAGGCC TGGTAGGTTA TCCTTTTTGn AGGTGGTATC CAG

103

(2) INFORMATION FOR SEQ ID NO: 2854:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2854:

GGCCACGGTC ATTCCTCCAA GCCAACCAGT GGACAAGATG GGTGGAAGGC GCAGG

55

(2) INFORMATION FOR SEQ ID NO: 2855:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2855:

TATTTGGCAT TCAAATAACG TAAACGGATT TTGAAGTAAT TTACATAAAG AGG

53

(2) INFORMATION FOR SEQ ID NO: 2856:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2856:

ACAATTTGAC AATGACTGGG ATGCTGACAC TTGATATGAA GACAATTGAA GAT

53

5

(2) INFORMATION FOR SEQ ID NO: 2857:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2857:

15

AACTGCGTTA CATGCTTTGC TTTTAACTGA ACCCAGAACA ACGGTTTCGG

50

(2) INFORMATION FOR SEQ ID NO: 2858:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2858:

30

CTTTTnTAnC TTCATCTCTA TTATTATTGT CCGAATTACT ACGTGGACAA

50

(2) INFORMATION FOR SEQ ID NO: 2859:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2859:

40

TCCAGGTCGA ATTTATTGCC AATTAGCCTC CCGGGTTAAA AGGGTGGGTG TCGGGTAAAA

60

TCGTAC

66

45

(2) INFORMATION FOR SEQ ID NO: 2860:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

50

55



GGTATCCAGT CCCCCGGAGG GGTGACAAAC TTCCACGCCC AGTGGGGGGA CTACCGTTTT 60  
GGACCAAAGC CC 72

5 (2) INFORMATION FOR SEQ ID NO: 2861:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 58 base pairs  
(B) TYPE: nucleic acid  
10 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2861:

AGTGTCTGAAC AATTAAAGAT ATTGAGTGAC AGGATTGCTT AAGGGCCGGT CGGAACAG 58

(2) INFORMATION FOR SEQ ID NO: 2862:

- 20 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2862:

TTAGCGGTAA ATCCGAAGAA CTAAGAAGAC GTCAAGAAGG GGATATACGC 50

30

(2) INFORMATION FOR SEQ ID NO: 2863:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
35 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2863:

GCAAAANTGA GAGCTCAANC TGCANNAAGC AAATCAACGA AAGATTAGGT 50

(2) INFORMATION FOR SEQ ID NO: 2864:

45

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 246 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
50 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2864:

55

AACTATTCTG GATTGTGCA GTGGCTATGG GGATGAGTGC GTTCCCCTCT TTCATGACGC 120  
AGGCGAACGC CAGCAACGCA ACCACTGATC AATGCTGAGC CAGCTGTAGC CGCCCAGACG 180  
5 GAACAAAATC CGCAGTGGGG GCAAGTGATG CCGGGCGTGC AnGGCGCTGA TnCAgTTcG 240  
TGGCAG 246

(2) INFORMATION FOR SEQ ID NO: 2865:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2865:

20 ACAGATGATA CCTCTTGATC ACTTGCCAGA GATCGTCTAA GTCGTCCTTG 50

(2) INFORMATION FOR SEQ ID NO: 2866:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 51 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2866:

30 AATACCACGC TGACCTTAAT AAGCCATCAT GGGGGAAATC ATGACCGCAA T 51

(2) INFORMATION FOR SEQ ID NO: 2867:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2867:

45 CAACTTGGTA AGTGGTCGTT TTGGGCCCCA CCCTACCCGT TTGGACCTGG 50

(2) INFORMATION FOR SEQ ID NO: 2868:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 223 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
55 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2868:

5 CCCAACCCGG TTCCGGGCCT TAATTTTTTn CTTTTTAAAG GAAAAAAGG AAAAACCGGT 60  
 TAATTCCGGC CCAAAAAnCC CGGAAGTTGG AAACCTTTTT TTAATAAAAA TAATGGACCG 120  
 TCCCAACCTT TGTGCCCCAA AGGTGGCCTA AAGGTTTAAA AAAAACCGTT AAAATCCATG 180  
 10 GCCAGGATCC AGCCTAAAAT TGAAACCATT ATAATTGATA AAC 223

## (2) INFORMATION FOR SEQ ID NO: 2869:

## (i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 66 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2869:

20 TGGACCTTTG GTAATATGAA TTGAATGGTG CTTTGTGGAA ATCGGGAATT CGCCTCGTGC 60  
 CTTGTA 66

## (2) INFORMATION FOR SEQ ID NO: 2870:

## (i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2870:

35 AAnAGCCAnG ATCATGGTAT ATCCATTAG AGACGAGAAG ATCGATGCCC 50

## (2) INFORMATION FOR SEQ ID NO: 2871:

## (i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 125 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 45 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2871:

50 TTATTTGGAC TTACAAGGAG AATAGTCAnT TCTAGGAAAG TGGTGCGAAA GTCACCTTACC 60  
 AATATACGGG GATTATTCAT CCATCGTCTGG TCGGTCATAT GATACGGAAT TAACACGCCA 120  
 CTCCTG 125

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 62 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2872:

CAACACCTGA CGTGATAGA ACTCATCTCT TCAATAACGT CGCTGTCAGG TTACGAAGTC 60  
 GA 62

(2) INFORMATION FOR SEQ ID NO: 2873:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 54 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2873:

TATACATTCC ATTTAACACC TTAACACATG CAACTTACTT CCTCCTCAAG CATC 54

(2) INFORMATION FOR SEQ ID NO: 2874:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 56 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2874:

GCTGAAAGGA GACTTCTGCA GGTGTGATCA CAACTGCAC ATCTACACAA GCCATT 56

(2) INFORMATION FOR SEQ ID NO: 2875:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 112 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2875:

AGCGCGACCG CGAGAAGGGA GGGGGAGCCA GAGCAGCAGC AGGCCCCAGG GCGAAACCCC 60  
 CAAGAGGAGC GAGnAAGAAG GAGGGAAAGC CCAGCAGGGG CGCCCAGGCC AG 112

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2876:

GnGCGTTnnA nCGGTCGCGT AGAGATGTCG GGTCTGTAGT AGATCTGGGG

50

(2) INFORMATION FOR SEQ ID NO: 2877:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 68 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2877:

ACCTTGACTT TGCAGACGAT GATGCTTTTG GCTGGGATCT TCACCATCTG GCAACTGAAT  
 ATGGTTGG

60

68

(2) INFORMATION FOR SEQ ID NO: 2878:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 53 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2878:

CTCCACCTGA TGCATGCCCC CATATCAGGA AAATGATAAC CTCGGACACC TTC

53

(2) INFORMATION FOR SEQ ID NO: 2879:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 75 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2879:

GGGAACTTTG ATCTGCCCTT GAAATCCTGA AAAATGTTTG CAAACGGGAA TGATCTTGTC  
 CCTTGCTTTG AATGA

60

75

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 341 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2880:

AGAGAGGCCG AGATGGCAGA TGAGATTGCC AAGGCTCAGG TCGCTCGGCC TGGTGGCGAC 60  
 ACGATCTTCG GGAAGATCAT CCGCAAGAAA TACCAGCCAA AATCATTTTT GAGGATGACC 120  
 GGTGCCTTGC TTTCCATGAC ATTTCCCCTC AAGCACCAAC ACATTTTCTG GTGATACCCA 180  
 AGAAACATAT ATCCCAGATT TCTGTGGCAG AAGATGATGA TGAAAGTCTT CTTGGACACT 240  
 TAATGATTGT TGGCAAGAAA TGTGCTGCGG ATCTGGGCCT GAATAAGGTT ATCGAnGGTG 300  
 GTGAnTGAAG TTCAGnGGTG GACATCCGTC TATCACGTTC A 341

(2) INFORMATION FOR SEQ ID NO: 2881:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2881:

GCGGTTACTG TGTAATGGCA TTAAATATGA AACGAGCCGA TGGAGCGTTG 50

(2) INFORMATION FOR SEQ ID NO: 2882:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 81 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2882:

CTCATCATTT GTAGTTGGAA AGGTTTATGT ACATTTGGAA AACACCGACA CATGACGTAT 60  
 CTCCATTGCA ATTTACACAA G 81

(2) INFORMATION FOR SEQ ID NO: 2883:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 77 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2883:

5 TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT 60  
TTTTTTTTTT TTTTTT 77

(2) INFORMATION FOR SEQ ID NO: 2884:

10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 104 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2884:

20 ACGGTGTGCT TGATGCACTT GGAAGTGTGA GTTTGGGTGT GACTTTGCTT TGGCTTGCTT 60  
GCTGAATGTT TTGACTATGC ATTGCGTATA TGACTTGnAG CGCG 104

(2) INFORMATION FOR SEQ ID NO: 2885:

25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 127 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2885:

35 AGCAACGTGT CTGTCAACGT GGTGTCATTG GAAAAGGCGT CATGTATTGn CCGGTGGGAT 60  
TTACGTGTAG TCACACATGT GCCCAATTAT TGTTTTGAGG CCAACTTGAG TAGGTTGATG 120  
GTTATGT 127

40 (2) INFORMATION FOR SEQ ID NO: 2886:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 51 base pairs  
(B) TYPE: nucleic acid  
45 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2886:

50 TGAGCGAGTG CTGTGTGAGC GCGAGGTTGT GAGAGTTAGA ACCTTGTGAG C 51

(2) INFORMATION FOR SEQ ID NO: 2887:

55

- (A) LENGTH: 63 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2887:

10 TTGAAACCGC GAACCTGAGT TCTGGTTAAC TACAGTCTGG TATACACATT GAGGGAAACT 60  
 TCG 63

(2) INFORMATION FOR SEQ ID NO: 2888:

15

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2888:

25 AGTAnCATAc nCAACTATCT CAGCATACAA TATTGGrCAC CTCGCAGCTT 50

(2) INFORMATION FOR SEQ ID NO: 2889:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 115 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

30

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2889:

AAAnATAATC CCGTTTTTAT CCCCTACCT AATTAGTGGG AAAAGTACCA ATTGCCAATT 60  
 GGTAAAATAG GTTGCCATAA CGGCCTCCCA AAAGTAAATT CCCTTTTTTG GTTTA 115

40

(2) INFORMATION FOR SEQ ID NO: 2890:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 147 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2890:

AATCGGTCCG TTATACTCTT CATAATATTG TGGCGCAACC ATTTCAACTT TATCTTTTCT 60  
 TATAAATAGC ATCATCGCAA TAnTAAAGAA TAATATCGGA ATGATTAAAG TAACGATAAG 120

55



## (2) INFORMATION FOR SEQ ID NO: 2891:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2891:

```

AACACAACAA GTTGTTAAAG ATGCATTTTT ATCACAACAT AAATCTATTG GACGTAAAGC      60
TCAAGAAGCA TACTTATCAT ATCGTTTAGA ACAAGAGTAT AGTAAAGATG ATATCTTCCA      120
AGTATATCTA AACAAAATTT ACTATTCTGA TGGCGTAACA GGTATTAAAG CTGCTGCTAA      180
GTATTACTTT AATAAAGATT TAAAAGATTT AAACCTTAGCG GAAGAAGCTT ATTTAGCCGG      240
TTTACCTCAG GTTCCAAACA ACTATAATAT TTATGATCAT CCAAAGCTG CTGAAGATCG      300
TAAAAaCACT GTTTTATACT TAATGCATTA TCATAAACGC ATTACAGATA AACAGTGGGA      360
AGATGCTAAG AAAATCGATT TAAAAGCGAA CTTAGTAAAT      400

```

## (2) INFORMATION FOR SEQ ID NO: 2892:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2892:

```

CCTAATTAAA CCTCCATCCA TCCTTTTGAA GGGGGATCTT TAATAAAaCC GGAAAGTTTG      60
GGGGAAAAAT CCTCCATCCT TTGAAGGGGG GGGCTTTCCA ATGGCCTTTA AGAATGGCCT      120
TTTCCAAGCC AACTTTTAAT TCCCCCGGT      149

```

## (2) INFORMATION FOR SEQ ID NO: 2893:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2893:

```

GCCCGAAGTA TTCTTGTAAG TATTATGATA CTCGGTnCTT TTTATGATT ATGTTAATTT      60

```

TTATGTTAGT

130

## (2) INFORMATION FOR SEQ ID NO: 2894:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 65 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2894:

GATGAGACCT GAATTGATTG CAACCCAAAT CGGCATATGC AAATTGCATT AAAGTTGGTT 60  
CAACG 65

## (2) INFORMATION FOR SEQ ID NO: 2895:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 102 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2895:

CGCACAACAC ATTTAGCGAC TCAGATGTCG CGCGAATGGA CCGATATGGC GTGTCTACAC 60  
ATTGTCATAT TGTACGAATA GATGAGAAAT TnCAAAGACC GA 102

## (2) INFORMATION FOR SEQ ID NO: 2896:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 69 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2896:

ATTAAGTGAT GGGCTAATGT TTACGCCCCA ACCAAAGGTT TCCAAAGAGC CCTTGTGGG 60  
CCTGTGTTG 69

## (2) INFORMATION FOR SEQ ID NO: 2897:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 80 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2897:

ATTGAATTAA TGTCCCAACC AAACGAATGG TTGCCCTTTT TCCATCCAAA GGGGGCTAAT 60  
TGGGAAGGGT ATTGGTTCCC 80

(2) INFORMATION FOR SEQ ID NO: 2898:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2898:

CAAATCCTGG AGATGAGCGT AACCAAAAAT AACGTTGAGA AAATGACCAC ACA 53

(2) INFORMATION FOR SEQ ID NO: 2899:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2899:

ATCGTGAACC TCTCATCCAA TCACTCATGT GAGTGAATTG GATGACCTGA A 51

(2) INFORMATION FOR SEQ ID NO: 2900:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2900:

AGCTTTCAGG GCTATATCAG ACCCAGCAT TCATCCACGT GAATGAAACA CG 52

(2) INFORMATION FOR SEQ ID NO: 2901:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

GGTACTGACA GAGGGACAAG GTGGAAAGGn TGCCAATGTA AGAATACGGT

50

## (2) INFORMATION FOR SEQ ID NO: 2902:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2902:

TGTCTGGAAT TCAGGTGAAT TGATGCGGAG ATTTAGGTGA TTAAGGAGTG TTGATTATGA  
AGATGACCAC TT

60

72

## (2) INFORMATION FOR SEQ ID NO: 2903:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2903:

CATGCCAAAG CAGTAGGCAA GCCGCTTAGC AAGCCAAAAA CGTCAGCCCA

50

## (2) INFORMATION FOR SEQ ID NO: 2904:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2904:

TTGATGTTAC CTGATCGCAA TCTTGACCAC CTGGCAGGGT CTCATTGTTG GGTATCGA

58

## (2) INFORMATION FOR SEQ ID NO: 2905:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2905:

GCGGTCTAT

69

## (2) INFORMATION FOR SEQ ID NO: 2906:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 53 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
10 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2906:

15 ATTCCATTAG GTTCAATTAA AAATTAACGG GGTTATGGTT CCGGTAATTC GGG 53

## (2) INFORMATION FOR SEQ ID NO: 2907:

- 20 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 57 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2907:

25 AAAGCTAAGA AAGGAGGATT AGCTGGTAGT GGAGGAATGT TAAGTGAGGC TGGTGAT 57

## (2) INFORMATION FOR SEQ ID NO: 2908:

- 30 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 86 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
35 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2908:

40 GCGAATGGCG CATGAACGTG CACATCAAAT GAACTGCAG GAAATCAATT AGCACGGATA 60  
TGGCATAAAG ACAATGGTAA AAGTGG 86

## (2) INFORMATION FOR SEQ ID NO: 2909:

- 45 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
50 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2909:

55

## (2) INFORMATION FOR SEQ ID NO: 2910:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2910:

GAATTTGTTT CGAGGTATCG AGGACTACGC TTATAAGGTG CTTACAGATA CATTTCATCAT 60  
TAATGGCGTG TGCTGCTGTA TGGGTTATAC TGTTACACAGG TTTAAGAGA 109

## (2) INFORMATION FOR SEQ ID NO: 2911:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2911:

TTGTCCCAT AGGGAGAAAT AATTCGCCT GGGCAAACC AAATCCACGA GCTTCTAAGG 60

## (2) INFORMATION FOR SEQ ID NO: 2912:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2912:

TAGATGTATC CAGCTGACAT TAGCTATTGG TAAGGTAACG GCTTACCAGG CAACG 55

## (2) INFORMATION FOR SEQ ID NO: 2913:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2913:

GCCATGAGGC CCACCCATCC ATGTTTATGG ATGGTGGATT GGGGAATTAC TTGTTTCAA 60

TCA

123

## (2) INFORMATION FOR SEQ ID NO: 2914:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 58 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2914:

ATCCGTAATT CTGGCCTACC AAGGGTTTAG GCCAATGGGC CATTCTTTTA TTAAACCC

58

## (2) INFORMATION FOR SEQ ID NO: 2915:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2915:

TGGTGCGACA GTGGTAGGCT TTTTACGGTn TGChGGCGAG AGTTCTGTAG

50

## (2) INFORMATION FOR SEQ ID NO: 2916:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 68 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2916:

CTGTTACGCT ATGCCCCCA GTTGTATGTT GAGTGAATC GTGTTTTTCG ACCTGCCTTT  
GCTTTTTT

60

68

## (2) INFORMATION FOR SEQ ID NO: 2917:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 65 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2917:

GGAAA

65

(2) INFORMATION FOR SEQ ID NO: 2918:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 101 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2918:

AAATTCCAAT CCTGGAATG GGATTCCATG GTnTTCGGAA AAATCCGCCA CCCCCAAAAA

ATAAATGGGT CCCTTCCCTT GGAAATATTA CCTTTACCAG G

(2) INFORMATION FOR SEQ ID NO: 2919:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 75 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2919:

TAATAAATCC ATGACCACCG TCACGACGAT CTGACTGATA AACTAATGAC ATATGACTGG

TGTACACACC GTATG

(2) INFORMATION FOR SEQ ID NO: 2920:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 56 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2920:

CTTGGATTGA CCATCATTAG TTTTGGTCAC TCTAAGTTGT ACTGTCCGTT GTACAA

(2) INFORMATION FOR SEQ ID NO: 2921:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 65 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear



GCTCATTGCT TGTATATTAA TCCCTGAAAT TGACCGTGTA TATCCCGTCG ATCTATCTTG 60  
TCCTG 65

5 (2) INFORMATION FOR SEQ ID NO: 2922:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 50 base pairs  
    (B) TYPE: nucleic acid  
10     (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2922:

GCAATATTCT AATCTGTATG TTACAGCACA TGGATATAGC ACATCCGGGC 50

(2) INFORMATION FOR SEQ ID NO: 2923:

- 20 (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 54 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
25     (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2923:

30 TGTGATTTAA CAGGATTACA CAGGTGTACC AGCCGATAGT TGATTAAGCT TCTT 54

(2) INFORMATION FOR SEQ ID NO: 2924:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 50 base pairs  
35     (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2924:

ATCCTGGGAA GTGCTGAAAA ACCACTnCAC TAAAGGCATA GGanCCACAC 50

(2) INFORMATION FOR SEQ ID NO: 2925:

- 45 (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 52 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
50     (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2925:

55

## (2) INFORMATION FOR SEQ ID NO: 2926:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2926:

TTGGTCACAT TTATTCTCGT GTTGTGCCGT TCTTCTTCAG TACTAAAGAC AAGGTGATTC 60  
 GG 62

## (2) INFORMATION FOR SEQ ID NO: 2927:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2927:

CAAAAGGCTA TCCCACCTGA TTGCAAAAG GAACTGGACT GCAAGGGAAG TCTCAG 56

## (2) INFORMATION FOR SEQ ID NO: 2928:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2928:

TGATCTTGCT ATTTAGTTGC GGCTTGGATT CATTTGGCAT GGTTAAGATT AAATTAGATG 60  
 CTTCAATTCAT TCAAGATTTC TTCATGTTAG CATTCTTTAC GACAATCGGT CTTGGTGAT 120  
 CATTGAAATT ATTTAAATTA GGTGGCAAAG TCTTGCTATT ATACTTTATG TTTTGTGCTA 180  
 TCATTTTCAGT CATTCAAAAC ATAGTTGGTG TATCACTAGC AAAAGTATTA AATATTAAAC 240  
 CTTTGTTAGG ATTAACAGCA GGTTCATGT CTATGGAAG CGGTCATGGT AATGCTGCTG 300  
 CTTATGGTAA GACAATTCAA GATTTAGGTA TTGATTCGGC ACTGACAGCG GCTCTTGACG 360  
 CTGCAACTTT AGGTCTTGTA TTTGGAGGGC TATCGGTGGT 400

## (2) INFORMATION FOR SEQ ID NO: 2929:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2929:

10 CTGAACCGAT GCGCACTTT GCTACGCCAC CTACAGCAGA TCCCAngGGG GgGAAGCTT 60  
 ATACTGAAGC TCTACGTTCA ACATTTTTCC ATTGGGGATT CCATGCTTGG GCTGTTTATG 120  
 GTGTTGTTGC GTTACGTTTG GCATATTGCG AATTCCGTAA AGGTGAACCA GGTTTATTAT 180  
 15 CTAGAACTTT ACGTCCTCTT TTAGGTGATA AAGTAGAAGG TCCTATTGGG ATTTTTATTG 240  
 ACGTTTTATC TGTATTTGCG ACAATCGTTG GGGTAGCCGT TTCGTTAGGT ATGGGTGCTC 300  
 TACAAATTAA TGGTGGTTTA CATTACTTGT TCAATGTTCC AAACAATACG TTTGTACAAG 360  
 20 CGATTATCAT CATTGTTGTT ACTATCTTAT TTATAGCAAG 400

## (2) INFORMATION FOR SEQ ID NO: 2930:

- 25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2930:

ATGTAGATCT ATATGATGAC TTTTACAAG ATCCATCATC TGTACCAGAA GATTTAAAGT 60  
 35 CTTATTACAGC ACAATTAAGA ATGATGACTC AATTGTACCA GCTTTAAAAA GTACAAGTAG 120  
 TCAnAATAGC GACGGCACAA TTAAGCGTGT CATGCGTTTA ATTGATAATA TTCGCCAATA 180  
 40 CGGGCATCTT AAAGCCGATA TTTATCCTGT AAATCCTCCA AAAAGGAAAC ATGTACCTAA 240  
 ATTAGAGATT GAAGACTTTG ATTTAGATCA ACAGACTTTG GAAGGTATAT CAGCAGGAAT 300  
 TGTTCAGAT CACTTTGCCG ACATTTATGA TAATGCCTAT GAnGCAATTT TAAGAATGGA 360  
 45 AAAACGTTAC AAAGGnCCAT TGCATTTGAG TATACnTAT 400

## (2) INFORMATION FOR SEQ ID NO: 2931:

- 50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

55

GGTTATACAA TCTAGAATCG CATGATAATT TAATGCTACA AATCGATAGT ACAATATATC 60  
TACCGTGAAT AACTGTGCAA ATAGTGACGT TGTAGCCGCC ATACGCATTT CATTTTCATC 120  
5 AGTTCTGCCA TAAATCAATG CATAGTCTGC AATTTGAGCC ACTGGATTAT TAGCTGTACT 180  
AGATATAGTT ATGATGGGAA TACTGTAATG TGTGGCCACC TGTGCAATTG ACTGCAATTC 240  
ACTATGGACT ACCTTGGAAT CGTCACAAA ATCATGCAAT CTCTATCATC ATGCGTCGCA 300  
10 AATGTTGACA CAAGTGAAAT GCGTTTCCAT GTAATAACCT GACATTTGAA GCCATACGAG 360  
ATAACTTTGG AAAAAGATCA CCAATAGnCC AACTCGATGG 400

15 (2) INFORMATION FOR SEQ ID NO: 2932:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 392 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2932:

25 CTTTCAGTAG CAGCTACAAT TGTCTTTAAC ATTTAAGTTT AAAGCTGTAT GTGTCAACCG 60  
CAAATACCGA TAGCCATTCA CTAATGAAGT TTCAACTAAT TTAGTACGAT CTGACAATAA 120  
30 CTTTTTGTA TCTTGGGCTG CTTTCAGCTGA TACAGCAATA TTTCTCATTG TTTTAACAGC 180  
TTCTTCAGGA TATAAACCAG CAGCAGTTTC ACCAGATAAC ATTACTGCAT CTGTACCATC 240  
ATAGATTGCG TTGGCAACGT CACTAGCTTC TGCACGTGTA GCACGTGGGT TACGTTGCAT 300  
35 AGAATCTAAC ATTTGTGTAG CTGTAATAAC TGGTTTACCT AATTGTnAC ATTGTCTGAT 360  
TAAATCTTTT TGAACCATTG GGACTTTnTC AG 392

(2) INFORMATION FOR SEQ ID NO: 2933:

- 40 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2933:

50 TGA CTATGGT ATCGCATGTT GTGTATCAGC GATGACAATT GGTAACAAA TGCAATTCTT 60  
CGGTGCACGT GCGAACTTAG CTAAACATT ACTTTACGCT ATCAATGGTG GTAAAGATGA 120  
AAAATCTGGT GCACAAGTTG GTCCAACTT CGAAGTATTA ACAGCGAGTA TTAGAATATG 180

ATTAAATGTT ATTCACTACA TGCACGATAA ATACAGCTAT GAACGTAATT GAAATGGCAT 300  
 TACATGATAC AAAAAATTGTA CGTACAATGG CAACAGGTAT CGCTGGTTTA TCAGTAGCAG 360  
 CGGACTCATT ATCTGCATTn AATATGCACA AGTTnAAACC 400

(2) INFORMATION FOR SEQ ID NO: 2934:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2934:

AAAATATGCC ATGACTGGCA TGACAAGAAT TGGACGTTAG AAGCATCTCA AACTGGTACG 60  
 TTCAGAGGTC GTAACnTAA CTTCAATGGT GAAGGATTCT CACGTCAAAC ATTTAAAGTA 120  
 AATGCCGTTA GTCAAAAAGA CTACGACAAA TGGGTGAAAG AAGTTAAAGG TAAGAnAACG 180  
 TTAGATCAAG ATACATTTGA TAAACAATTA TTACCAAGCA CACCTAATAA AGCTTTAGAA 240  
 TTTAATGGTA CACATATGGC GTTTGTTGAT CCAGCAGCCG ATCCAGAATA CATCTTCTAT 300  
 GCATATAAAC GTTTCAATTT CGGATTGAAG GTCCCAAAC TCACTAGTGA GGAAATATG 360  
 TTTAAGGTGT ATCAGACAAA CCCTTAATAC CTGCTCGTGA 400

(2) INFORMATION FOR SEQ ID NO: 2935:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2935:

ATGGAGTATA CAACTACTTC GGCATTGGCG CTTACGACAA CAATCCTAAC TACGCAATGA 60  
 CGTTTGCAAG GAATAAAGGT TrGACATCTC CAGCAAAGC AATCATGGGC GGTGCTAGCT 120  
 TCGTAAGAAA GGATTACATC AATAAAGGTC AAAACACATT GTACCGAATT AGATGGAATC 180  
 CTAAGAATCC AGCTACCCAC CAATACGCTA CTGCTATAGA GGGTGCCAAC ATCAAGCAAG 240  
 TACAATCGCT AAGTTATATA AACAAATCGG CTTAAAAGGT ATCTACTTCA CAAGGGGTAA 300  
 ATATAAATAA AGAGGTGTGT AAATGTACCA AATAAAAGAT GTGAAACGAG AATTAAAAAT 360  
 GATGGTGTG ACTTAGGTGA CATTTGGCTG TCGTTTTACA 400

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2936:

AAACAATACA AACAAAAGAA AGTCAACCAA GGATGGATTC CTATTTTAAT CCTTGGTTGA 60  
 CTCTTATTTT ATTTAAATTG TAGAACCTAG AAAATAAAGT TTAATTAAAA GCACCAATCA 120  
 TTTCTACTTT GAAATCTAAG GTTTCTAAAA TAGCAATGAC TTTCTTTATA TCGGTTGTAA 180  
 TTGCAGAATC AGCCTGAACG AAAAATCGAT ACATACCTAA TTGTGTTTTT AAAGGACGAG 240  
 ACTCAATCCA GGGTAAATTA ATATTAAACA AAGCAAATGT ATTAAGCACA CTTGCTAACA 300  
 ACCCGGGTTA TCATGCATTG GTGTAATTAA AACATCAAT GGTGTCGCAT TTTGATCAAA 360  
 TGCTGCTGAT TTTTATAAC TAAAAACGTG TCAGGTATGT 400

(2) INFORMATION FOR SEQ ID NO: 2937:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2937:

TTATTATCTT GATACATTGA GTGTATATTC CATTTTCCAT GAGGCGTTAA ATAACGCATA 60  
 CCAAAGCATC TGTACCACCT TTAATTTTCT TATCTCTATT CCCAAATACC ATTGGCGGCA 120  
 ATGTCGGTTT ATATACTGGT AAGCTCTCCC CAAATTGTTG GAAAACTTCG TGATCCACAT 180  
 AATAACTTTG GACGTCCTGT TAATGTTCTA AAAGGTACTA GACGTTCTAT ATTCGTTGTA 240  
 AATGGTGGAA TATCGTCGAC CTTGTTTATT TGAACCGGGG AATACTGCTG TCGGTATTAC 300  
 TTCTCGTGGT TGTGGAAGTT ATATTTAAAA ACGGAAATTT TCTCAGCAGC GntTTCGTTA 360  
 GGAAATATCT TTAAACGGGC ATTCCAGTTT GTTCntCGGG 400

(2) INFORMATION FOR SEQ ID NO: 2938:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2938:

5 TATCTCTTAA AGCCGGTGAT GGTGGTAATG GTATTACCGC ATACAGAAGA GAAAAATATG 60  
 TACCATTTGG TGGACCAGCT GGCGGTGACG GTGGTAAAGG TGCTTCAGTC GTATTTGAAG 120  
 TGGATGAAGG TTTAAGAACG TTATTAGATT TTAGATATCA ACGTCATTTT AAAGCAAGCA 180  
 10 AAGGTGAAAA TGGCCAAAGT AGTAATATGC ATGGTAAAAA TCGGGAAGAT TTAGTATTAA 240  
 AAGTTCCACC TGGTACAATT ATTAAAAATG TTGAAACAGA CGAGGTTTAG CAGATCTTGT 300  
 TGAAGATGGT CAAAGAGCTG TAGTAGCGAG GGCGGTCGAG GTGGCCnAGG TAATTCACGT 360  
 15 TTTGCAACAC CTAGGAAACC CTGGCACCTG GACTTCATGG 400

## (2) INFORMATION FOR SEQ ID NO: 2939:

## (i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 384 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2939:

CTAACCTCGA GTTCGTATTA TGCCCAACCAC ATGTCTGCTG GCTTGTCGTA AATATTAAACA 60  
 30 GATTTCAAAG TTTGACAAGC TTTTGGAAA CCTTCTTCTA CTGACATAAT AGGATCTTCA 120  
 TGTTC AATAC TTAATACATA ATCATATCCA TTAATAATAA GTTGACTTAT GATATCTGCC 180  
 CATACATATG GACTATGTCC TAAGCCAACT GTACGGAATG TCATGCTCTT GTCGCAACGT 240  
 35 TACCATATGG TTGCATATCA GTTAGACCAT ACATATTTAC ATTTTCTTGG ATTAATATAC 300  
 GTATCTTTAG CATGGAAGTG ATGAATTGCA TTTGCTTGGn CTAATATGCG AATCGCAGCC 360  
 AATTGGGTCA ATAnCnTGGC CACC 384

## (2) INFORMATION FOR SEQ ID NO: 2940:

## (i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2940:

50 TTTTCATATTT TTCTATTAAT GATTCATATT GTAGGGTGAT TGCAATGTCA TCTAAGCCAT 60  
 TTACAAGTTT ATTCTTCCAA GTTTCATCAA TTTCAAATG GAAACGCTTG TCTGGTGATG 120

CACTTTTTTC TAAACGATA GGCAACATCG CATTITTTAGT GCAATTCATA TAAAAATATGT 240  
 CACTGAAACT TCCTGCAATA ATAATATGAA AACCATAGTC CTTAAGAGCC CAAGCAGCAT 300  
 GTTCACGACT TGAACCATAT CCAAAATTAT CTCCAGTnAT TAAATnGGAG GCCCCTTTAT 360  
 ATTGTGGTTT GTTAGGGTTG AATCAGGGTT TnTnGGAACC 400

## (2) INFORMATION FOR SEQ ID NO: 2941:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 409 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2941:

ATCATAATCC ATCGTGCCTC CAAGAAGTAC TTGATTATTT AAAGTTTGTA TTGTGAATCC 60  
 TGTGCACATT GTTCTCACTC CTCTGTACCT TCATTTACTT TAATCACTTT CAAATAAAGC 120  
 TGTITCACTT AAACATACTA TAAAAAATCA ATTATACAAG CAATTAAATTG ATATTCATTC 180  
 TCAATAACTG TGGTATGATA TGTAAGGAAA TCATGACTTA TGTGTGAGTG AACGATCATC 240  
 TATACATCCG TTCACTTCAT CTCATGACTT TCTATATTTA ATTTTACAA GGgAGTGACA 300  
 TCTGTGAATa ACACACAATC TTCACCACGC gTAaTaTtAT TaTTGCGATT ATGTTGTCTG 360  
 CATAACATAT GGTGTGTGCA CAATCATTAT TAnTATAGGA CCTCCGTTG 409

## (2) INFORMATION FOR SEQ ID NO: 2942:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2942:

ATGAAGTGTC AAAAGGTTTA AAAACATCTG AAAGGGGTTT GCACATGTTT TAACTTTTAA 60  
 AAATAAAGGT GGATGTCCAA AATGTCGACC AGCAATCAAC TATTATTTAA ACATGGTTTA 120  
 TCCACATGAT CATGAAGATG AAAGAGAATC AAGATTTGCT AACGAACGTT ACCATGCGAA 180  
 TATTCAAAAT GATGGTACAT TTTCTGTTAT ACCTCAAATG CGTGGGGGTG TTACAGATGC 240  
 AGACCAACTG ATTCGTCTAG GAGAAGTGGC TAAGAAATAT CATGTGCCAC TAGTTAAAGT 300  
 GACAGGTTCA CAACGTGTTG GTTTGTATGG AGTTAAAAA GAAGATTACC AAATATATGG 360



## (2) INFORMATION FOR SEQ ID NO: 2943:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2943:

ACCTGGAAAT GTATGTGCCA TCTCTTTAAG CCAATCAGTA TCTTGAATAC CTTTCGTTCC 60  
 AACTATGCAA TAATTAATCC CTGCGGCAAA GTAGTCCATG ATTGTGACTT CGTACGAATG 120  
 CCACCACCTA CTTCAATATC TTTGGTTGTT AATCTCCTCA ATGACTTAAT ATAATCAAAC 180  
 TCTCGGGCAT GCTGTGCCTT AGCACTCATC AAGTCGACGA TATGAATACG ATTCACACAT 240  
 TCAAATTGAC TATAGTAAGC AATACTTTCT TCAGCCGAGC GTGGACATTT TTTCTTCACT 300  
 ATCATATTTA CCCTCTGTTA ACCTCACACT TGTGACCCA ATCAAATCAA TCGCTGGGCC 360  
 ATAATTCAAT CATTTnATAA ATCCCCCTTG TATTGGCCTG 400

## (2) INFORMATION FOR SEQ ID NO: 2944:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2944:

AACAAAAGGG GTCTATCGTC AATCGTTTTCT TGAATAGTGT TGAAAAAATC GGAAATAAAT 60  
 TGCCAGATCC TAGCGTCTTA TTCTTTTTTAA TGTGTGTGGG CTTAGCCATT ATGACATGGG 120  
 TTATCTCATT ATTTAATGTA TCTGTTAAGC ATCCAGGTAC GCATCAAACC ATTTATATTA 180  
 AAAATATAAT TAGCCATGAT GGATTTACGA TGATAATGAA TGATACGATT AAAAATTTCT 240  
 CAGAGTTCCC AGCATTAGGC TTAGTACTAG CAGTGATGAT TGGTATTGGT GTTGCAGAGA 300  
 AAACAGGATA CTTCGATAAG TTAATGATTT CTGTTGTGAA TCGCGCACCA CGTTTCTAAA 360  
 TTTACCGCTA TAATATTAAT GGGnATTTTA GGGAGTCAGA 400

## (2) INFORMATION FOR SEQ ID NO: 2945:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2945:

5 ATTTTACAAG TAACGGTGCA TCACCAGATT CTAATTTAAT GTCATGCTCA GCAGCATTTT 60  
 GATAACCCAA CTTTTCAAAG TAGTCAAAAC AATGGTCTAC AACAAACCGTA CTATACTCTT 120  
 GTGCTTTGGC CGCTCTTCTA CTGCTTGAAC CAAGCCACGA CCTAATTTT GTCCACGTAA 180  
 10 TTCAGGATGA ACTGATAAAG AGGCAATCGC CAAACCATAA TACGTCTTAT CATCACTATT 240  
 AATTTCTACT TCAATTAATA AAACGTGTCC AACGACATCG TTATTTTCAT TTTTCGCTAT 300  
 TACTTCTAAT TCAAATTAT AGCAAGGAGA TTTTCTTAA TGGTTTACTT TCGGCACGTG 360  
 15 CCTGGCCAAC TCGTTTTTCAG GATTATCATC CAACTTTCC 400

## (2) INFORMATION FOR SEQ ID NO: 2946:

(i) SEQUENCE CHARACTERISTICS:  
 20 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2946:

GGAAATAATT ACTTGAGCTA GATAAGTTGA CAGCTGTGCA ATTATTTTCA GCAGCTAATT 60  
 30 GTAAAATTCG CTCTAATCTT GCTGATGAAT GTTCAGGCCC TTGACCCTCA TATGCATGAG 120  
 GTAAGAATAA TGTTAATCCT GAACGTTCTC CCCATTTTGA GCGAGAACTG AATAAGAAGT 180  
 TGTCAAAAAT CATTTGTGAC ATATTTGGCA AAATCACCAT ATTGTGCTTC CCAAATATTG 240  
 35 AAGCTTTTTT TGTTTTCCAC ATTATAGCCG TATTCAAAAC CAACTACTGC TGCTTCTGAA 300  
 GCGGAGAATT GTGTATATCA AATGTCGCTT TTTGANCAGG AGCATGATGT AAAGGTGTAT 360  
 ATGTTnACC nGTTTGCTCA TCATGTnACA CGGCAGCCGT 400

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## (2) INFORMATION FOR SEQ ID NO: 2947:

(i) SEQUENCE CHARACTERISTICS:  
 45 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2947:

AAGTGGCATA AAAAAATCAC ATGACGATAC ATTGTCGTCA TATGACTTTA AATATTATTC 60

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TTCAATTGTG TCACCGATTT TTAATACATC TTCCACTTTT TCAATTCTAT TTTTTGAAAT 180  
 5 TTGTGAAATG TGAAGCAACG CATCTTTACC TGGGAATAGG CCTACAAACG CACCGTATTT 240  
 TTCAATACGT TTAACAGTGG CTTGGATAAG TTTGACCTAC TTCCGCTTCA CGTGTAATTT 300  
 CCTCAATGAT TTCACGAGCA CGATTTATCA TAGCTTGATC AACAGCACCC ATAAAGATAG 360  
 10 TACCATCCTG GnCCATATCh AATTTAACAC CnGGnTCCTC 400

## (2) INFORMATION FOR SEQ ID NO: 2948:

## (i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2948:

TTTTCAAGT TTTGCTGAAG GCTTTACACA AGGCTATTTA ACAATGGATG CCATTGCAGC 60  
 25 AATTGCTTTT TCAATGATTG TTGTTAATGC AGTAAACTA ACAGGCATTA CTAAAACAAA 120  
 TCAAATATTC AAACAACTT TGA CTGCTGG TTTAATTGCA GCCGTAGCTT TAATTTTCAT 180  
 ATATATTTCA TTAGGTTATA TTGGTAATCA TATGCCAGTA AGTGACATGA CGTTAGATCA 240  
 30 ATTGAAATCC AAAGATCGAA ACATTGGGAC ATATTTATTA ACGACAATGG CTTCAACAGG 300  
 ATTTGGTCAT CCGGAAAATA TTATTGGGCA TCATTGTGGC GCTGGCATGC TAACTACAGC 360  
 ATGCGGGCTA TGGTGCAATT CCTGAATATT CCATAGATCG 400

## (2) INFORMATION FOR SEQ ID NO: 2949:

## (i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2949:

45 CATGGCTTCA GATTGTTTGA ATTGAATGGA CAATTTTGGn TTCTGTCCAA AATTCTTACA 60  
 AAATCTTCTA CCGATAAACT ATCAAGTTCA ACTCTAATCG GAAAAACGAC CTTGCAATTC 120  
 50 TGGTATCAAG TCACTCGGCT TAGATACATG GnaAGCTCCA GCACCTATAA ACAGCATATG 180  
 TTCAGTATTC ACAGTACCAT ATTTGGTTTG AATAACGCTA CCTTCAAGTA TAGGTAAAAT 240  
 ATCTCTTTGA ACACCTTGTC TTGAGACATC TTGACCACTA TTATGATTAT TCGTCGCAAC 300

GTTAGCGCTT TCTTGATCAn TTAGTTCATC CGCATAACTA

400

## (2) INFORMATION FOR SEQ ID NO: 2950:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2950:

TTGACTTTGT AACTAACTA CTCACTCGAC CGACTCAACT GTTTAAATGT TTCAGATGGT 60  
 TTAAGTCTAA ATACTACGTA TAAATCACCA GCAGGTCCTC CATTACGCC TGGAGAGCCT 120  
 TCACCAGCTA ATCTAATTG TTGTTTATTG TCGACACCTT CAGGTACTTT CACTTCTAAT 180  
 TTAAGTGTG TATTTTCAGT ACCTTTTCCG TGACATGTTG GACAAGCTTC TTCAAATTCT 240  
 TGACCACTTC CATTACATT AGGACAACT TGTTCACTAC GAACTCTACC TAAAATTGTG 300  
 TTTTGTCTA CAGCTACATG ACCAGCGCCA TTACAGTAAC TACAAGTCTT TTTACTTGTT 360  
 CCAGGCTTTG CACCATCACC ATGACATGTT TCGCATGTnA 400

## (2) INFORMATION FOR SEQ ID NO: 2951:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2951:

CAATGATTTT AAAAGATGCA ATAAACCAA ACTTAGTACA ATCAATTGAA GGGACACCTG 60  
 CATTAGTTCA TGGTGGACCA TTTGCGAATA TCGCACACGG TTGTAAGTCA ATTTTAGCAA 120  
 CTGAAACAGC ACGTGATTTA GCTGATATCG TTGTAACGGA AGCTGGATTT GTTTCAGACT 180  
 TAGGCGCTGA AAAATTCATG GACATTAAAG CGCGTGAACA GGATTTGATC CGGCAGCTGT 240  
 CGTTGTGTT GCGACAAATC GTGCGTTAAA AATGCATGGT GGTGTAGCGA AAGATAATTT 300  
 AAAAGAAGAA AATGTAGAAG CAGTAAAAAG CAGGAATGGT TAATTTAGAG CGTCATGTTA 360  
 ATAATATTAA CAATCCGTG TAGAnCCGGT TGTGCCATA 400

## (2) INFORMATION FOR SEQ ID NO: 2952:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2952:

	TCAAGTAGCA AAAGAAACAG GTGCTTCAGT TATCGGTATT GATATTGGTC CACAAGCCGT	60
10	TGACCTAGGG CGCAGAATCG TTAACGTCTT AGCACCAAAT GAAGATATAA CAATTACGGA	120
	TCAAAAGGTA TCTGAACTTA AAGATATCAA AGATGTGACG CATATCATAT TCAGCCGACA	180
	ATTCTTTTAA AGTACAGCAT TTTAGAAGAA TTATATGATT TAACAAATGA AAATGTCCGT	240
15	AGTTGCAATG CGCTTTGGTG ATGGCATCAA AGCAATATTT AATTATCCGA AGAAACAGCG	300
	GAAGATAAGT GGGCCATGTG TGAATAAACA TATGAGACCA CAGCAAATTT TTGATATAGC	360
	ACTTnATnAA AnAGCCGGCT ATAAAGTnGG TATTACGGAT	400

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(2) INFORMATION FOR SEQ ID NO: 2953:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2953:

	CGCAATTCAC AATAACATTA AATAATTTTT GGTCTCATAT TTTCAAAAAA CATACTGTTA	60
	TTATCCCATG GgntTAAAAA TATCATTAGT ATATAACGA AACACTTTAC GATAAATGAT	120
35	ATCTGCAAGC CAAGCTGTTA CAAATGGTAC AACAAAGAAC GCTACTACAA TTAGTAAGAC	180
	ACTCAACCAA GCAGAAATCAA CCTCCATAAA TTAAATGCA TTAATCGGTC CTACCATTCC	240
	TATAAAACCA AATCCAGCTG ACTCTTTTCGT TCCATGAATA CCTACTAATG CTGATACCAA	300
40	ACCTGATACA ATGGCTGTCG TAnGGGCGGG GngCATAAGA ATTGGATATT TCACCATATT	360
	AGGTATCATC ATTTTAAACG CTCCAAAGAA GACCGGATAA	400

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(2) INFORMATION FOR SEQ ID NO: 2954:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2954:

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AACACTTTAA TGGAGATTTA GCAGGCACTG TTACACTGAC AGCAGGTTTA GGTGGTATGG 120  
 GTGGTGCGCA ACCGTTAGCA ATTACTATGA ATCATGGGGT AGCAATTTGC GTGGATGTTG 180  
 5 ATGAAACACG TGTTGATAAG CGAATTGATA CGAAATACTG TGATGTTAAA ACAGCTGATT 240  
 TAGATGAAGC ATTAAAATTA GCAGAAGAGG CGAAAGAACG TGGGAGAAGG ATTATCAATC 300  
 10 GGGTTAATTT GGAAATGCTG TAGACATCCC ATCCAAGCGG ATTCTAGGAA AAAGGGTTTT 360  
 AAAATTGGAC ATTAATTACT GGnCCCAAAC CAAGTGCCCC 400

## (2) INFORMATION FOR SEQ ID NO: 2955:

- 15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2955:

TTCAGAATAC GAGCAATGTC AGTTGCAGTG TTTAATAAAT TTTGTTGCT ATTTTGTAGG 60  
 25 CATCTTCTAA AGTGCTAGGT GAAGAGATTA TAGAATAGGC ACTATCAATA CCGAAATCGT 120  
 AAACATGTTG ATAATTTTCG CCTAGACTGC CACAAATCGC GATGACAGGA ATATGATATT 180  
 30 GTTTTGCAAG TAACGCAACG CCTACGGGTG TTTTACCAA GATGGTCTGA TAATCCATGC 240  
 GTCCTTCTCC AGTAATAACG AGGTCTGCAT CTTTAATTCT TTGATGAAAA TCTGTAATGT 300  
 CAAAGACGAC ATCAATACCT TTTGTTAAAG TTGTCTCACA AAACGnTAAT AATGCTGCGG 360  
 35 CCATACCGnC AGTGCACCAG AACCTGGTAT TTGGTTnACG 400

## (2) INFORMATION FOR SEQ ID NO: 2956:

- 40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2956:

AATACGTCCT TTATATAATG TTAATAACCA GTTAAACAAT TTCACACCAG TTGGAATACC 60  
 AATCAGCATT GTTGAAATTG AGAAGAATGA GTTGATTAAAC GCACCAATTAC CCATTGTGAA 120  
 50 GAAATGGTGA ACCCAAATA AGAACTAAG GAACGCGATA CCGGCAGTTG CCCATACCAT 180  
 ACTTTGATGT CCGAATAAAC GCTTACGAGC GAATGTCGGG GATAATTTCT GAGTAAATAC 240

CCAAAGCATT GGGCATACCG CCATGTGGCA CTGTGGAAGA ATGCTGTGTC CAATATTCCG 360

nTCATTGGTh CATTAAATGGC TAACGCTAAC GGTTTAAAGG 400

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(2) INFORMATION FOR SEQ ID NO: 2957:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 394 base pairs

(B) TYPE: nucleic acid

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(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2957:

TAGTAATTAA TACGATGTCA GCACCTACTG ATTTTGCTTT GTCTGCTAAT AATCTTAAAT 60

GTTCCGTGGA CCTGAACCAG AGATAATTAC AAATACATCA TTCGACTTAA TCGCAGGTGT 120

20

CGTTGATTCT CCAACAACAT GTGCCTGTTT GCCGAGCTGA TTTAAGCGCA TTGCAAAACT 180

ATTGCCACG AATCCTGGAA CGTCCTTTCG CAGCTACAAA TATATGTTCA GCATGTAGTA 240

TTTTGGGATG CAAAAGTTGG AAAACTCCAT CCGnTTCAAC ATGTGACAAA GTCATCTTTG 300

25

AATTCATCTA GAnTTAATTG ATAGTCACTA AnTTTAGCCA TATTACTTAC CTTCGGTTGC 360

CAGCGCGACC ATTGTTTCGC AGCTTCTTAC TGGG 394

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(2) INFORMATION FOR SEQ ID NO: 2958:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

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(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2958:

AATTATTCTA CCTATAATTA AAAATGCTGG CAAAGGTGTA ATGATGATGA GTAATGAACC 60

TACAACATTT AATATCAATC CTACATAAGT AATTTTGACG CGACCAAATT TATCAGCAAC 120

ATCACCAGCA CCTACGATAA ACAAACCAGC AAATAAGGCA GATAAGCTAA CAGCGATTAT 180

45

TTATCGTTCC AACGTCACTA CTATATGTTG ATTGTAATGG GACAACAAGA TTAACAAGTG 240

ACTGCGCGAA TAGCCAAAAG GTAATAACCC CTAAAACGAT ACCCAAAGC AATCGGTTGT 300

TCACCTCTTA AATTGTTTTG ATGTGTCCnT GGATTAGGAT AAGCCTCCTA TGTTTAGGAA 360

50

AAACAATTTT TAATATGGTA TATTAAGGAN ACATTTCTTT 400

(2) INFORMATION FOR SEQ ID NO: 2959:

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(A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2959:

10 CTCTTTTCTC AACATCAAAG AACATATGGT TTTGTTTCAA ATATTCTTTT ACTAGCGCGA 60  
 TATGTTTCGTC TGATCTACCA GTTAACTTCA TATATTTAAG AGATTCATCA TCAACTGGGA 120  
 AGAATCCGCA AGTTGCTCCA TACTCTGGTG CCATGTTTGC AATTGTAGCA CGGTCTGCTA 180  
 15 GTGGTAAATG TTGTACACCT GGACCAAAGA ACTCCACAAA TTTACCAACA ACACCTTTTT 240  
 TACGTGGCTC TTGAGTTACT CTTAACGCTA AATCAGTTGC TGTTCGCCT TGTGGTAATG 300  
 AATTTACTAG TCGTACACCA TTAACCTCTG GAATTGGGGA AATAGGAGGG TTGTCCAGGC 360  
 20 ATTCCAGCTT CAGTTTCAAT ACCACCAACA nccctcctag 400

## (2) INFORMATION FOR SEQ ID NO: 2960:

## (i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 380 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2960:

ACGTCAAATG TAATCACAAT CGGAAAGTAT CGTGACAATG CATATATAAC AGGGAGGGTT 60  
 35 TAAATATGAG TTACTAAGGG GATTTTTAGA TTTAGGTGCA CTGTTTATTT TACCGGTTGT 120  
 CATATTCTTG CTGGCCTAT TCTTTAGGCA GAAAATTGGA GCGGCATTTA GGTCTGGTTT 180  
 AACAAATAGGT GTGGCTTTTG TAGGGATTTT CTTAGTCATC GATTTATTAG TTAAAAATTT 240  
 40 AGGGCCAGCA GCACAAGCGA TGGTTAAAAA TTTAGGCGTC AntCTGAATG TGGATTGATG 300  
 TAGGTTGGCC AGCAACATCA TCTATCGCTT GGGCATCATC TGTnCGCnCC ATTTTATTAT 360  
 TCCACTCGGG ATTCATAGTT 380

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## (2) INFORMATION FOR SEQ ID NO: 2961:

## (i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 358 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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GGCCATTGGT CGAACTTACG AAGAATCATT GTTAAAAGCA ATTCGATCAC TTGAGTATGG 60  
 TGTGCATCAC TTAGGATTAC CAAATGGTGA AAGCnTCGAT CTTGATTATA TTAAAGAACG 120  
 5 TATTTACAC CAAGATGATG GACGATTATT TTTCATCGGC GAACAATTAG AAGAGGCACA 180  
 ACAGTAGAAG AAATTCATAA TATGACTCAG ATTGATTACT TCTTCTTACA CAAGTTCCAA 240  
 AACATTATTG ATATTGAGCA TCAATTAAAA GAGCATCAAG GTGATTTAGA ATATCTTAAA 300  
 10 TATGChAAAG ATTATGGnTT TAGTGGTAAA ACAATAGCGC ATCGCCTTAA TATGACGG 358

## (2) INFORMATION FOR SEQ ID NO: 2962:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 364 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2962:

TTTGGGCATC ATTAGGAAAA TTCTTTGAGC AACTTTAGTG TCTACTGGGT AATACAATTT 60  
 25 TATCACCATG TTTTCTAAT AAATCTTTTG CGAATCGATT TTATCTTCTT CTAATAATGA 120  
 AATACCAATT TCTTTACCTT GCGCTTTTAA GAAAGTATAA GCCATACCTC CGCCGATGAT 180  
 AATTTTATCA GCTATGTTAA CTAAGTTTTT GATGACATTA ATTTTGTCAG ATACTTTTgn 240  
 30 GnCACCATAA ATAGCAACAA CTGGTTTATG TGGATCGTTA ACTACGCCGC CAATAAACTT 300  
 AATTTCTTTA TCCATTAAGA ATCCAGCTGC AGTTTCTAAA TGTGTAGAAA TACCAACATT 360  
 35 ATTh 364

## (2) INFORMATION FOR SEQ ID NO: 2963:

40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 372 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2963:

GTTGATTCT TGAAAGATAA TAAAAAATTC AAAGAAATGG GATCTAGGAT TCCTAAAGGT 60  
 GTCTTACTTG TTGGACCTCC AGGTACTGTT AGAAACATTA CTTGCTAGAG CGGTTGCAGG 120  
 50 TGAAGCTGGC GCACCATTCT TCTCTATTAG TGGTTCAGAC TTTGTAGAGA TGTTTGTGG 180  
 TGTTGGTGCG AGCCGTGTTT GTGACTTATT CGATAATGCT AAGAAAAACG CGCCTTGTAT 240

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TCATGATGAA CGTGGAACAA ACCCTAAACC AATATTAGTT GAAGGATGG TTTCGGTGG 360  
 AAAATGAAGG TG 372

(2) INFORMATION FOR SEQ ID NO: 2964:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 382 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2964:

TTAGCAGAAC GCCCACAAAA CCTATCTCTT GCTGTAAAAG AATTTGTGAA nCTGCTGGCT 60  
 TAAAACGTGT TGGCATAATT GCAGCTTTAG GAGCTACAGT TATGTTAGGT TTAAGTACAA 120  
 TTAAAAAATT ATGCCGTAAA TAGAGCAAGA CATAACAAT AATTTAGGAG TCTGGAACAA 180  
 TAATCAATGT TCTAGGCTCC TAAATGTTAT ATTGGCAGTT CTGAAACATT TATAAATCTT 240  
 TGATTATGAA CTCACAACAG TGCTCTATGC TTTTATAGAT TTTAATAAAT TAGCCATTTT 300  
 AATTGCACTT ACTGCTGCTT CACACCCTTT ATTGCCAGCT TTCGnACCTG CnCCTTCCAC 360  
 AGCTGGGCAA TACTGCCAGC CG 382

(2) INFORMATION FOR SEQ ID NO: 2965:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2965:

GGGAATCATA CAATCATTAC CAATAACAT GTTACTTATC ACATGAAAGT CGGTGATGAA 60  
 ATCAAAGCAC ATCCTAATGG TTTTATAAT AACGGTGGTG GACTTTATAA AGTTACTAAG 120  
 ATTGTAGATT ATCCTGGTAA AGAAGATATT GCGGTCGTAC AAGTTGAAGA AAAATCAACG 180  
 CAACCAAAAG GTAGAAAATT CAAAGATTTT ACTAGCAAAT TTAATATAGC ATCAGAAGCT 240  
 AAAGAAAATG AACCTATATC AGTCATTGGT TATCCAAATC CTAATGGAAA TAAACTACAA 300  
 ATGTATGAAT CAACTGGTAA AGTACTATCA GTGAATGGAA ATATAGTGAC ATCTGATGCG 360  
 GTTGTCCAAC CTGGCAGCTC TGGTTCACCT ATATTAAATA 400

(2) INFORMATION FOR SEQ ID NO: 2966:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2966:

10 TGGGGATTCA CAGGCTAATA CATTTGACTT TATTAGCTGG TGGCGGTAAC GCGCGCTGAAC 60  
 TTTAAATGCG ATTCAAAGTG CTGCAATTAT AAGTGCAATC CCATTCTCCT TTGTCGTCAT 120  
 ACTCATGATG GTAAGTTTCT ACAAGGATGC GAACCAGGAA CGTAAATTCC TAGGTTTAAC 180  
 15 ATTGACTCCG AATAAACATC GCTTACAAGA ATATATCAAG AGTCAACAAG AAGTTATGAA 240  
 TCTGACATTC TTGAAAAGCG TCAGTCACGT GAAATATAGA GAAAAAAGAT AACTAATAAA 300  
 GTTTAGTTAA GTATTTTAAT AACAAAGTAGT ATGTCATTCT AGTAGCTAGA ACGGTnATAC 360  
 20 TACTTGtnTG TTTTGTGGA AATTGAGTAT TTCAAAGGTT 400

## (2) INFORMATION FOR SEQ ID NO: 2967:

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 387 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2967:

ACGAGGAATT AGTGAAGTAC AATATTATCG GTGGTTTTGA TTTAGGTGTT GTTTCAGACG 60  
 35 ACTTTAAAAA TCACATGTTA ATAGCTGTAA CTGAATTAAG AACAAAAGAT GAAATCGATA 120  
 CATTTGTAGA AAAGGCTGGT GAGTTAAATG ACTAGTAAAT CAAGTCCATT AATTTTTGAA 180  
 AGATCTCGTG AAGGCAGATA TGCATATTCA TTACCAAAAA GTGATATTAA AACAAATTCT 240  
 40 GTTGAGTCAT TGTTAGATGA TAAATTTATT CGTAAAAACA AAGCGGAGTT TCCTGnAGTT 300  
 GCTGGAACTA GACTTnGTAC GTCATTAATC CTGGACCTTT CCAAATAAAA AATCCGGnG 360  
 GTAGACACCG GGTTTAACCC ATGGGGT 387

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## (2) INFORMATION FOR SEQ ID NO: 2968:

## (i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 806 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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AACAAGTGCA	AGTGAGTCAA	CATCAGAAAG	TGCGTCAACA	TCAGTCAGTG	ACTCAACAAG	60
TACAAGTAAC	TCAGGATCAG	CAAGTACGTC	AACATCGcTC	AgTAACTCAG	CAAGCGCAAG	120
TGAATCCGAT	TTGTGCTCAA	CATCTTTAAG	TGATTCAACA	TCTGCGTCAA	TGCAAAGCAG	180
TGAATCCGAT	TCACAAAGCA	CATCAGCATC	ATTAAAGTGAT	TCGCTAAGTA	CATCAACTTC	240
AAACCGCATG	TCGACCATTG	CAAGTTTATC	TACATCGGTA	AGTACATCAG	AGTCTGGCTC	300
AACATCAGAA	AGTACAAGTG	AATCCGATTG	AACATCAACA	TCATTAAGCG	ATTCACAAAG	360
CACATCAAGA	AGTACAAGTG	CATCAGGATC	AGCAAGTACA	TCAACATCAA	CAAGTGACTC	420
TCGTAGTACA	TCAGCTTCAA	CTAGTACTTC	GATGCGTACA	AGTACTAGTG	ATTCACAAAG	480
TATGTCGCTT	TCGACAAGTA	CATCAACAAG	TATGAGTGAT	TCAACGTCAT	TATCTGATAG	540
TGTTAGTGAT	TCAACATCAG	ACTCAACAAG	TGCGAGTACA	TCTGGTTCGA	TGAGTGTGTC	600
TATATCGTTA	AGTGATTGGA	CAAGTACATC	AACATCGGCT	AGTGAAGTAA	TGAGCGCAAG	660
CATATCTGAT	TCACAAAGTA	TGTCAGAATC	TGTAAATGAT	TCAGAAAGTG	TAAGTGAATC	720
TAATTCTGAA	AGTGACTCTA	AATCGATGAG	TGGCTCAACA	AGTGTCAGTG	ATTCTGGCTC	780
ATTGAGCGTC	TCAACGTCAT	TAAGAA				806

## (2) INFORMATION FOR SEQ ID NO: 2969:

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(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 351 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2969:

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ACCATCTACT	CCGTTAATAG	TTACACTGTT	ATCATTGGTG	TTTGGACTTT	CAGCCCTTGC	60
ATCTAAAAAT	ATAAGCTGAT	TAAAATCTGT	TATTACTTCT	TCCTTGTAAC	CATCTATGAT	120
TTTTACAAAA	GATTGCATTA	ATTAGTCAAA	CCTCCCATAT	AATTATTTGC	ATTGCTCTA	180
TGCCCCACTTT	GTTTTGACAA	TATTTTTTCT	AAACCTCTAA	TTGCATCATT	AGAACCTAAG	240
GATTATCCTG	AGAAGAAACA	GTTTGAATCA	ACGCATCTGT	TAATTnATTn	CCTTTATCAC	300
TTAACATAAC	AATTTGGTTC	AACAATTTnC	AACTGTAGAA	GTATCATTAT	T	351

## (2) INFORMATION FOR SEQ ID NO: 2970:

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(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 359 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2970:

AGTGCTTGAT GAATTTTGAC CACAAATTCA AATGTATCAG GCGTTTCTTT TATCCATTTT 60  
 AATATATTTT TTTCCGGTTG TATCGCATAG TATGTGCGAT CTAATTCGAC AACCGGAAAA 120  
 TGTCCAGCAT ATGTTTTAAG TTTATCGGTT TGGCGTTCTA AATCTTCATA TAATGAATAG 180  
 TGATCACCCC AACCTGTTAA TCCGATGTTT ATCATATATA TCACCAATGT CATCATACCA 240  
 TATAACTTTT ATCATAATCA TTTCAGCGAA CTTTAGTTTG ATGTTTTTGC TTGATTAAAA 300  
 TCTTTTCGGC GAnCCTCAGC TTGATGTTTT TCGTTGATTA AATGGTAAAT AGnnACGCA 359

## (2) INFORMATION FOR SEQ ID NO: 2971:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2971:

CAGACGGTCA AGAATCTTAT ACTTATCAAA ATTTATACTG TGAAGCGAGT CTATTGGCTA 60  
 AAAGACTCAA GGCTTATCAA CAATCTCGTG TTGGGCTATA CATAGATAAT TCGATTCAAT 120  
 CGATCATTTT AATACATGCA TGTGTTGGTGG CAAATATTGA AATTGCGATG ATTAATACAA 180  
 GGTTGACACC TAATGAGATG ACGAATCAGA TGAAGTCAAT CGATGTACAA TTGATTTTTT 240  
 GTACCTTGCC ACTGGAATTA CAGGGTTTCA AATTGTATCG CTGGGTGATA TTGAATTCGC 300  
 TGGAGGGATA TTACAnCGAn CAGTTGTTGG GCAACACAAT GGGTATCCAT TTGAACCATC 360  
 GGATGnAACT TTGTGCCGAA GGTGCGCTCC ACATnTAATG 400

## (2) INFORMATION FOR SEQ ID NO: 2972:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2972:

TCAACCGCTT TACAGCCAAC CGGCGACGCT GACATGGATC GCCTGGCCCA TGCCCACGCC 60  
 TTGGCGCCAT CATTATTAAT TGCTGCAGTT ACGGTATCTT TAATTGCGTT AAATAAACCT 120

AAATCACCGA AATGTTATTC GCTTAACGTT TTGTTGTTGT TATTTTAAAA TAAATTTGAT 240  
 GCAATTAGTT TGTATTATCCG CACAACATCT TATAATGTAC TTAAGTGTAT TTAAAGAGA 300  
 5 AAAGAAATAC AGTTAGGCAT TCAAACTGT ATTTAACACA ATTAAGTTGC CTGAATTCGT 360  
 ATTTAAGTCT TATTGAACCT TTTTnAGATA An 392

## (2) INFORMATION FOR SEQ ID NO: 2973:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2973:

20 ATTGCAATGA TAGCAATCGG AATCGCACCT GCTAAAATAA ACGTTGTGCC ATCCGTCGCA 60  
 TTTGTACCAC GAATCACAAT GTCACCAAGC GTAGGTGCTC CTATAAATGA TCCAACGGCA 120  
 ACAACACCTA TCGCAACAAC CAAGGCAATA CGAATGCCAC CGATAATAAC CGAAACAGAT 180  
 25 AACGGTAATT CAATCATTCG TAGCACTTGA TTGCGTGTCA TTCCCATACC TTTGCCAGCA 240  
 TCCTTAATAT TCGCATCAAC ACTAGCTATA CCAGTATAAG TGTTTTTATA ATTGGAAGTA 300  
 ACGCATATAA AAACACTGTT AAACACTGT TCTGAnCTAG CCTGACTACA TTAAATAGTn 360  
 30 ACATTGCATG ACTGGACTGn TGGATATATT GCATGGATnC 400

## (2) INFORMATION FOR SEQ ID NO: 2974:

- (i) SEQUENCE CHARACTERISTICS:  
 35 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2974:

GTATTCTTTA GGTAATGCAA CTTTAAATCC TTAAATATCT TTACCAATTT CAGATGTAAA 60  
 45 GTCTACATCA TCAACTGGTG CACTTGTAGA GTCATTAACA TCTGCACCAG AAATAGCTTC 120  
 TAATACGATT GCATTATCTT TTACATTTCT AGTCAATGGA CCAATTTGGT CTAATGAAGA 180  
 TGCAAAAGCA ACTAATCCAA ATCGAGATAC ACGACCGTAT GTTGGTTTCA TACCGACAAC 240  
 50 GCCACAATAT GGCAGCCGGT TGTCTAATTG AACCACCTGT GTCTGGAACC TAAGCTAAAT 300  
 GGTACTAAGC CAGCTGCAAC TGCTGCTGCA GATTCCACCT GAnGGAACCA CCTGGGCACG 360

## (2) INFORMATION FOR SEQ ID NO: 2975:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2975:

GAGATCGCGG GTTCGATTCC CGTCGAGACC GTACAAATGC CTATCCAAGA GATAGTTTTG 60  
 TTTTGCCTTT AATATTATAT TAATAAAAGA TATATGGACG AATGATAATC ATATTGATTT 120  
 ATCTGTTTCG CCATTTTCTT TAAAATGTAT GAACCTCAAG TAACTTAGTG GTTGGATATG 180  
 AAAGATAAAC GTnGACAATA AAATCTTTAT TAGACGTACA AACATATGCT ACTGTCAACA 240  
 TATTTCTTCG TTGTGATATG CCACCAGTCC TCCATAACAT CAATTGTTAA AGTAACGAAT 300  
 AACGAATAAT GATATTTnAT TTCTGAGCCA TGACGTGCCA CTAGAAGTTG CCCATTATCC 360  
 T 361

## (2) INFORMATION FOR SEQ ID NO: 2976:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 356 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2976:

TGCTGCTTCT GAAGCGGAGT AATTGTGTAT ATCAAATGTC GCTTTTTGAT CAGGAACATG 60  
 ATGTAAAGGT GTATATGTTT CACCTGTTTG CTCATCATGT AACACGGCAT GCCTATGACT 120  
 GAATGTACCA CGTTCACTAT CTTGACCAGT TAAGCGAATC GGTGTACCAT CTTGTAAAAT 180  
 TGTCGCAAAT GCAAGTnGTT CTGCTTGTGC CCAATCAACT AAACCATCTT CTTTATTAAA 240  
 CGGCTCATGA CGCTTCTCAA GAACTTTGTT TAACTTTTTn CAAAATGTTA AAGCCATCCG 300  
 GATATGTAA CAATGCATCA TTATTTCTTT CAAGTGATCC AAAAGTAAAG GnTTGT 356

## (2) INFORMATION FOR SEQ ID NO: 2977:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2977:

CTTTAGAGCG ACACCTAGTC ACTGCAGCAA GCTATTTCTT TATTGCTAT GCTATAnATC 60  
 5 GTTAATTACT AGACCTATTG CTGGTAGATT GATGGATGAT AAAAATGAAA ATATTATTGT 120  
 CTACCCAGCA TTTATCATGC TTTTCCTTTC ATTTGTATGC TTAATTTCAA GCTATCAAAG 180  
 CTGGTTAATA TTAATTGCTG GTGCTTGCCT AGGTTTAGGG TATGGAAATT TATCATCTGC 240  
 10 AATGCAATCT ATTGCGATAA AAGTCTCACC CCCGATTAAA TATGGTATCG CGACATCTAC 300  
 TTTTACGTT GGTCTAGATG CCAGGTGTCG GCTTCGGTCC AGCATTCTTT GGGTTAnTTA 360  
 15 CGCAGnGTTT T 371

## (2) INFORMATION FOR SEQ ID NO: 2978:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 365 base pairs  
 20 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2978:  
 TTGTAATTTT ATGATTACAC CTCAATTGTT CTTGTTGTTA AAACCTCAATA TTTAATTGTC 60  
 TGCGCTCAAT AATTTGTTGT TTAAGTTGCT CAATATGATT TGATTGGAAT TCTTCCAATA 120  
 30 ATGCTTTTGC TATTTCAAAT GCTACGACAT GTTCGCAGAC GATACTTGCT GCAGGAACAG 180  
 CACAACATATC AGAACGTTCA ATTGTTGCTT TAAAGTCTTC TTAGTATTA ATGTCTACTG 240  
 AATTTAATGG nTTATATAAC GTTGGAATTG GnTTCATTAC ACCATTACGA TAATTGGCAT 300  
 35 CCATTGACAT ACCGCCTCTA ACCACCTAAG TGATTAGAnC ACGATAATAC CAATTCATA 360  
 TATAT 365

40 (2) INFORMATION FOR SEQ ID NO: 2979:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 45 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2979:

50 TGATTATATA AATCTAACCA GCCAAGTTTC GTCTGCGGTG AGACATTGAC ATTAATTGCT 60  
 GCAGATAATG ATTTAACAAAC ATGTGTGGCA TGTGATTGAT TAACGATGAC AATATCATGT 120

55



TGGCGATGGG TAACATTGTT AACATTGCTT CATTTAAAAC GATATCGAAT TGATTGTCAT 240  
 CAAAGGGCAA TTAAACAGCA TTCGCTTGTT GAACTTGAAT ATATGATTCA nGACCTGCTG 300  
 5 CGGAAATGTT TTCCGTGCTT TTTCTAAGCC TTCnTATTAT ATCAACGCCT GAnGTGACAC 360  
 CAnAGTGTGA GCCAGATAAA TAGAGGTGTG CACAGATACA 400

## (2) INFORMATION FOR SEQ ID NO: 2980:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2980:

TTTCTGCTTT TGATAATCTT TCATCAATGC AAAAGCTACA TTGGACAGTC CTATAATGGA 60  
 AATAATGTTT ACAATTGCCA TTAAGCCCAT AAATAAGTCT GCCGTATTCC ATACTGTTTC 120  
 TGTTTTTACA ACTGCACCGA CAAAGACAAG TACTACAACA AGACATCTAA AGATAAATAA 180  
 25 TATTACACGG TTTGTTGATA AAAATTCAAT ATTAGATTGA CCGTAATAGT AATTACCTAC 240  
 AACAGATGAA AATGCAAACA GTGnAACGCT TATTGGTTAA GAAAATACCT CCAGCAGAAC 300  
 CTAAATGCTC CTTAAGTGCC GATTGGGTAA CTGCAACACC nTGGAGGGCG TTTATCACCA 360  
 30 AATTTnCGTC CCGAATATAG TAAA 384

## (2) INFORMATION FOR SEQ ID NO: 2981:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2981:

AATTCTAACG ATATCACCAT TTTTACAACC ACGTTCTCTA AGCGCATCAT CAATACCCAT 60  
 45 CGAACGCATT TGACGAGCAA ATCGACGTAC TGCTGGATCA CTGTTAAAGT CAGTCATTTT 120  
 AAACATTCTT TCAATAGCAT TACCACCTAC CACATAAGCA CCATCATCAT CTCTTGGAAG 180  
 TTGTAAATTT ATCTTGTGAC GGTGTATGTT TATATAATAC TCGGTTAATG CCAACTGACT 240  
 50 CCTCTTCTTC AACTGTGGAG TCAACATCTT TATATTCTTC TGAATTTATC TGCTTATTGC 300  
 ATATGAATAA TTGnnCAATG ATTATCACGC GTTATTGTTG GAAACTGGGA TTAAGTGGCA 360

## (2) INFORMATION FOR SEQ ID NO: 2982:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2982:

CCTCAACCGC TTTACAGCCA ACCGGCGAGC GCTGnACATG GATCGCCTGG CCCATGCCCA 60  
 CGCCTTGGGC nCATCATTAT TAATTGCTGC AGTTACGGTA TCTTTAATTG CGTTAAATAA 120  
 ACCTTCCATT GAAAACACTC CTTAAAATTT AAATTTGAAG ATAACAAAAA CGTGCCTACT 180  
 TTnTGAAATC ACCGAAATGT TATTCGCTTA ACGTTTTGTT GTTGTATTAT TAAAATAAAT 240  
 TTGATGCAAT TAGTTTGTTT ATCCGCACAA CATCTTATAA TGTACTTAAC TGTATTTTAA 300  
 AGAGAAAAGA AATACAGTTA GGCATTCCAA AACTGTGATT TTAACACAAT TAAGTTGGCC 360  
 TGAATTCGGT ATTTGAAGTC CTAATGGAA 389

## (2) INFORMATION FOR SEQ ID NO: 2983:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 379 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2983:

ATATTCCTAT GACAATGTTT AGGCAACGAT TCCAAGGATT AAGAAAAGAT CAACCGGTAT 60  
 ACTTATGTGA TGCCAATGGG ATTGCTAGCT ATAGAGCCGC TCGTATTTTG AAAAAGAATG 120  
 GATATACAGA TATCTATATG TTTAAAGGCG GCTATAAAAA ATGGACTGGA AAAATAAAGT 180  
 CTAAAAAATA GTTTTTGTAA ATTTAATATA CGATTTAATA AAATCTGAGT GTTAATTGAT 240  
 CATCAATAAC AATACTCAGA TTTTAATTTT TTAACAAAGT CTGTTACTAT ATTTCTCTAG 300  
 CTTCACTGAT CATTAAACCT TAGTTTCAGC ATAATTAAGG AAGGTCCGnC CCATTTCAT 360  
 CGnGnTCCAT TACCGCCAC 379

## (2) INFORMATION FOR SEQ ID NO: 2984:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2984:

5 ATGCTGAAAA TATGGTGCCG TTTATATGAA TCAATTTGAA TCCGAACATA ATCCGGATAC 60  
 ATATTTTCAT ACATTGGGAC CCGAATTGAC TTCAGCATT AAGCAAATTG ATTATTTTGT 120  
 GGCTGGTATT GGCTCTGGCG GTACATTAC AGGTACGCAC GTTATTTAAA GCAACATCAC 180  
 10 GTGCAATGTT ATGCCGTTGA GCCAGAAGGG TCCGTGTTAA ATGGAGGGCC AGCTCATGCA 240  
 CATGACACTG AAGTATCGGT TCTGAGAAAT GGCCGATATT TTTAGAGAGA CGCTTGTA 300  
 TGGGnTATTT ACGATTAAGA TcNAGATGCC TTTCCGAATG TCAAAGTTTG CTATAATGAn 360  
 15 GGTGTAGTAA GCAG 374

## (2) INFORMATION FOR SEQ ID NO: 2985:

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 464 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2985:

GGAGCCACCA TTGGAGCAnG TTACGGTGGA AAAGATACGG nAAGGTTnGT ATGACTGTAn 60  
 30 GTCTTGATA GAGTAACAAA CCTAATTTGT TAACTCTAGG CCCCATATGT CGCAGTACCA 120  
 TCTGCATGTG TTGTTAcATT GTATGCATTT GTTTTACTTG GCTTCTTGtA TGTCGGGCGA 180  
 GCTCCGTATG ACACTTGACC GTTTGCATGT GTTGTACGT TGTATGCATT TGTTTTCCTT 240  
 35 GGCTGTTTTT GTGTTGGGCG AGCGCCATAT GATACTTGGC CGTTTCCATG TGTGTTACG 300  
 TTATATGCGT TTGTTTTGCT TGGCTTGTTT TGTGTGGAC GAGCTCCGTA TGATACTTGG 360  
 CCGTTTGCAT GTGTTGTAC ATTGTATGCA TTCGTTTCGC TTGGCCTCCT GTATGTCGGA 420  
 40 CGAGCTCCGT ATGATACTTG ACCATTGCAT GGGTGGTACG TnnG 464

## (2) INFORMATION FOR SEQ ID NO: 2986:

## (i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 359 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2986:

AACTATTATA TTAACATACA ATGTAGGGAT GTGATGCGCG TGAAGTTTAG GGATAAAGAT 120  
 AATCGTCAAG TTAATTTGAC ATTTAAAAAG GATAATGAGA TAGCAGATGG CAATCATGTG 180  
 5 CTAGCTATTC CAACGTTTAA AAATCAATTG CTTTTTACCA AACATAATTT ACGGGGGATT 240  
 GAATTTCTCG GTGGTAAAAG GGAACGCGGG GAAAGTAGT GCTGGAAGCA GTTACACGTG 300  
 AATTATATGA AGAAACAGGC GCCAAATTGA AAAATGnTTA TTACATAGCA CAATGTnCC 359

(2) INFORMATION FOR SEQ ID NO: 2987:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 15 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2987:

TAGAATTCTT CTAATGAATG AGCTTCTTTA GAATGATAAC CATAACGAAT TCCGTCAAAA 60  
 CGAGAAAGGT TTGACGAAGC TTCTGATGAT GCAATCACGT AATATGATGG AATACCAAAT 120  
 25 TTAGTATTTG GCAATGATAC TTCCTCAACG ACAGCACCTA AAGATTTTAA AGTTTCTACA 180  
 GCGTTTTGAA CTGCTTCTTT TACGTCATCA GCTACACCTT CACCTAAGTA TTCTTTAGGT 240  
 AATGCAACTT TTAATCCTTT AATATCTTTT ACCAATTTCA GATGTAAAGT CTACATCATC 300  
 30 AACTGGTGCA CTTGTAGAGT CATTACATC TGCACCAGAA ATAGCTTCTT AATACGGTTG 360  
 CATTATCTTT TACAnTTCGG GTCATGGnCC CATTTTGGTC 400

(2) INFORMATION FOR SEQ ID NO: 2988:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs  
 (B) TYPE: nucleic acid  
 35 (C) STRANDEDNESS: double  
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2988:

ATTCAATCAT AATTATCAAT CCTTTGTGTT AAATTACTAT ATAAATAGTG TACGnATTTT 60  
 CGAAATTTGT GATCATAAGT TTATTCAATG CTAAACAATA AGGTTGAGAC ATAATCGTAT 120  
 CTCAACCTTG AAATTATTAT ACGTTGACGT CACTAGTCAT TCAGTTTTCT TAATGCTGCT 180  
 50 ACAATCTCTT TTTTAGTATC TTGTACTTCA GAAGCTTGCT TAATCACTTT TGCAGGTGTA 240  
 CCAGCAACAA CTGCACCAGC TGGTACATCT TGTGTCACAA TCGnGCCACT GGCAACAATA 300

nGATTATAAC CGTGGAG

377

## (2) INFORMATION FOR SEQ ID NO: 2989:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 356 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2989:

CCAGGnACCT GGACACGCCG GGTCTTATCA TCAATAATAG TAGCATGACA AATCTACTAT	60
TTTTTCGCTA ATAAGTGGAT GTAATGCTAA TAATGTTGCT GTAGGGAAAC AGCCAGGATT	120
AGAAATGAGC TTCGTTCCAT TGTTATCAAA CGATTGCCAT TCTGAAATGC TGTAATAGT	180
CATGATTCAA ATCATCTTGT GCCTGCAGCA GTTCTTTTGT AATATGCTTC ATATATTTCA	240
CGnTTCTTAA TTCTAAATGC GCCAGATAAA TCGATAACAT GAATACCTTT TTCTACTAAG	300
GGAGGGATAC ATGTTTTTACT TACGGGTGCT GGTGTCGCAA AGAAAATTAC ATCAAn	356

## (2) INFORMATION FOR SEQ ID NO: 2990:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 349 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2990:

TCATTTTCCA AGTGAGACTC TGCTCTTGCT TTGGCTAATT TAGCTCTTTC AACATCAATT	60
TCTCTGTCAG TTTCTGCAGT CTGAACAATG ATTGAACTT TATCTTTTCT AACTTCAACA	120
AAGCCATCGC TTACAGCAAT ATATTAGTT CCATCGTGGA AATTTCACCTT TTACAAAGCC	180
TGTTTTTAAA GCAGCTACAG TTGGGAATAT GTCCACTCAT GACACCTATC TCACCAGCTG	240
TTGTTTGCAT AACACGAGT TCAACATTAT CACGATTGTA AACAGAACCA TTAGGAGTGA	300
CAATATCTAG GTTTAAATGT CCATTATCCA TTCCnCCnGA ATTGGnTGA	349

## (2) INFORMATION FOR SEQ ID NO: 2991:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 363 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2991:

5 ATGCCACGT TCATGCCAAT AGCTGTCGTA GTCGCATTTT CACGTTCTAG TATTGCATTT 60  
 TTTAAATGCG ATGTGTGCTC TACATAACGG CAAATTTTAA GTTTATGAAT CAACATATCA 120  
 ATTGCTTCGT TTCGAGACAT GTCGTGGATC AGTAATTATC ATAGTTTGTT GATCAAAAAC 180  
 10 ATGAGAAGGT TTATTGAGAT GTGAATGTTT CGCGGTGTTA TCTACATTGT CAACCTCTGT 240  
 ATCATGTTGT GTAATATCTG TATCATGAAG TTGCGGTGTC GCTGGTGCAT CTACTGCTAT 300  
 AACTGGTGTA TTGCGTTTTA ATAATAGTAC AGTAGTnCAT TGTnGACAAG ACTnACCGAC 360  
 15 TTA 363

## (2) INFORMATION FOR SEQ ID NO: 2992:

## (i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 349 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2992:

AAGTTTATTT TAAAATTCGT AATAAAAATA ATAACTCAT CGAACGATTT AATGGTCTAG 60  
 30 GTTCCATAT CAACTATGAG TACATTAAAT TCAAATTCGA ATCACGTAAC GTAAAAGATC 120  
 AAACAATCCC TGAATAAAAC ACCAAGCAAA TACCCTACAG TACATCATTG GCATGTATTG 180  
 TGGGTTTTTC TACTTTTTGT AAATATTGAn AATTATnAGT AGTTGTTTTT TACTATTAGG 240  
 35 GCAGAATGCT TTACAATAAC ATGCAAGTGT CAATTAAGGG GAGCACTTGC ATAAATAGTA 300  
 TAGGnGAGTG AGTAGTCCTG GCCATTTCTT GGAATTCCTT AATCGGCAC 349

## (2) INFORMATION FOR SEQ ID NO: 2993:

## (i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 399 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 45 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2993:

50 TTTGTGCAAT AAGCGCTTTT TGTTGTTTTG CTTTGTGTC TAATTCATCT TTCGCAACAT 60  
 CTTTAATTGT TGTATCTGCA GTAATACCTT GAATATCAGC AACTGCTTGA TCTTTAATT 120  
 GCGTAACATC ATTAGTTGTT TGTGCATTTA AGATATCTTG ATACGCTTTT TCTTTAGCTT 180

TTGCTTGATT TTGAGTTGTC ACAGCTTGAT CAACATCATT TTTAGCATTG ATTTAACCGC 300  
 TGTGCTGGTT GCGGCTTGAA TTGAATCTTC CAGGCTTCGC TGACTACACA TACACAGTGA 360  
 5 GnGnAATATT TCGGCTGAAC GCGTGCATGT GAAngCTCT 399

## (2) INFORMATION FOR SEQ ID NO: 2994:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 326 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2994:

AATGACAGGA ATCGTCGTTG CCTTTACTAA TTGACCAGTT AATTCAAAGT TAGGTCCGGA 60  
 20 CATTTTGCCA TCTTTAGCAA TATCAGTATA TATAATGCCG CCAAGAGGTA TATCCGATAA 120  
 CCGTCTCACA AACTAAATAA ATTTAACTCT GTGTCCTCTT CCCATCCGTT CACTTTAATA 180  
 TCTTCTCCAT AGGCATCAAC AGATAAATAA ATGCGACCTG GAAATGTATG TGCCATCTCT 240  
 25 TTAAGCCAAT CAGTATCTTG AATACCTTTC GTTCCAATA TGCAATAATT AATCCCTGCG 300  
 GCAAAGTAGT CCATGATTTG TGACTT 326

## (2) INFORMATION FOR SEQ ID NO: 2995:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2995:

CTAATGCCGA TGAGCAAAAC ACAAGCATTG GAAATTATTA AAAAAGTTAG GTACGTATAC 60  
 AACATTGATT TTGATAAACC GAAGTTAGAA ATGTGGATTG ATGTATTAAG TCAAAATGGA 120  
 45 GATTATCAAC CAACTGTAAA AGCGGTAGAT GTTTATATCA ACAGTAACAA CCCGTACCCG 180  
 CCTAACTTAC CAGCAATCAT GCGTAAGGAA CCTAAAAAG TATCTATCGA GCCAGTAGAT 240  
 AACGAAACCG CTACACACCA TGGGAAAATG CAGAATGACC CGAATTGTCA GACAAGGAAA 300  
 50 ATAGCGCTAG ATAGTTCATG AATAGTTGGC AGATTGGGGC GAACGATGAT ACGnCATTCG 360  
 ATTGAAGTCA TATCGTCGTA CTTAACACCG GACGTTnGAA 400

## (2) INFORMATION FOR SEQ ID NO: 2996:

(A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2996:

10 GAATGTAAGT GTCCCTTAAG CATAGTGCTC CCACCTTAAA TTTTGTACA TACTTTCATG 60  
 GAATGTACGA GAAATTACAT CTAATTGTTG TTCACGTGTT AATTTAATGA AGTTAACAGC 120  
 GTAACCAGAT ACACGGATGT TAACTGTGGG ATATTCTTCT GGATGTTCCA TTGCATCTAT 180  
 15 TAATGTTTCA CGGTAAATA CGTTAATATT TAAGTGGTGA CCACATTGCA TTGCGTAACC 240  
 ATCTAACATA CTAGTTAAGT ACGGTTTGAT CTCTGGnTCT TTACCTAATG AATTGGnACG 300  
 ATACTGATGT ATTGAAATAC CATCCTTACA GCATCGTAAG GGGTCCTAGC CACAGAACTT 360  
 20 ATGAAGAAAT GCACCTTTTn GGCACnGGCA TGCATGGGGT 400

## (2) INFORMATION FOR SEQ ID NO: 2997:

25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 335 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2997:

ATGATATTAA CCTGTTTACA AGATGGTTGA TACTTGCGCA TGAATTGTA ATCTTCAACA 60  
 35 CCATATTATT ATGGTACATA CGAACTGAA AATGAATCCA TAGTTACTGA CAAAGAAAAA 120  
 ATCTTAGTAT TAGGCTCTGG ACCAATTCGA ATCGGCCAAG GTGTAGAATT TGACTATGCG 180  
 ACAGTTCACG CCGTTTGGGC AATTCAAAAA GCAGGGTACG AGGCGATAAT TGTGAATAAC 240  
 40 AATCCAGAnA CAGTTTCAAC AGATTCTCAA TTTCTGACAA ATTATACTTT GAACCTTTAA 300  
 CTGAnGAGGA TGTGATGAAT ATCATTAAAT TTGGA 335

45

## (2) INFORMATION FOR SEQ ID NO: 2998:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 397 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 50 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2998:



GCAGTAACTA ACTTTTGTAC AAAAGGATCA TTTTATCAA CATAATGTGG TGGTTGGACT 120  
 TTACCTAATT TCACTTCAAA GtATTGTTGA ATCTCATTTG CAAAACGATC CATAGCTTTT 180  
 5 TCAAATTCAA ATCCTTCTGG GTAGCGTAAt TGATACCGAA AAGACCTGCG TTTTCATTAT 240  
 CATATGTAAT AACACCAATG TTAGTTGTCA CGTCACCCAT GgACATCTGT ATGGgAATTT 300  
 CATTCCCaNC TTTTTCACCA AAATCnGGAA TTGAAATAAG TGAGCGATTA CGAAATGGCG 360  
 10 ACAAACGCCT GTGGCATTGA TnGAGCAAGA TTnAAGG 397

## (2) INFORMATION FOR SEQ ID NO: 2999:

(i) SEQUENCE CHARACTERISTICS:  
 15 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2999:

AAAGCTGTGT TGGTAAAGAG TTTTGTGAT TTGGTACGCA ATACACGACA CGACTTGGCA 60  
 25 TTCGTTTAGA AAAACATTT GAATACATCG ATACACCTCA TAAATTCAAA ATGGGTGTAT 120  
 CAGGCTGCCC AAGAAGTTGT GTTGAATCAG GTGTTAAAGA TTTTGGTATT ATCTCAGTTG 180  
 AAAATGGGAT TCCAAATCTA TATCGGTGGT AATGGTGTA CAGAAGTTGA AAAAGCTGAA 240  
 30 TTTTAAACAA CTGTAGAAAC AGAAGATGAA GTAATCAAAT TATGTGGTGC TTTGATGCAA 300  
 TATTGAnCGC GAAACAGGTA TATATGcGG AAAGAACCAG CGCCCAGGTT AAGAAGACCT 360  
 GGATTGAAA ATGTnAAAAG AAGTCCTTAC CTGGGCCCCG 400  
 35

## (2) INFORMATION FOR SEQ ID NO: 3000:

(i) SEQUENCE CHARACTERISTICS:  
 40 (A) LENGTH: 506 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3000:

AACGGTAGTA TTACAGAAAG CTCTACTTAT GGTGATAATG ATACACCAGC GCCACCAACT 60  
 GACGAATTAG GTGGTAGTTG GACACTATGG AAAAATTTAG CGCGACAAAG TCCTGAATTT 120  
 50 GGTAATCCTG ATAAGTTTTG CCAAAATATT CCTAAAAAA GTTGGTTTGT TTCAGCAACT 180  
 TCTACAACAA ACAATAAAGA GATTATCGAT ACAATAGAAA GTATTTGTAA ACGTGACCCA 240

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AGTTTTACAA TCAATCGTCA GCMACAGTTT aAAGACCAaC CTGrAAATGA AaTATCTACA 360  
 TGGATTTATG CCTTATATyC AGATGTAAaC GGCGATTATA TTAAAAAGCC AATTACAGAA 420  
 TGTAGTGGTA ATGAAATATG CCAAGnATGG CTGTATCnCT TnGGTGTATC AACTGACAAG 480  
 ATTGAAGACT TAGCAAAACA TCGGTC 506

(2) INFORMATION FOR SEQ ID NO: 3001:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3001:

ATTGATGGCA TCGAAAACT TTAATAAGAC AACAAGTTGA TGAGATATAT GTATATAGGT 60  
 TTGGCATGGA TTTGATTGC AGTTAATTAG AATAGCTCAA TGCTATAAAT GTAAGTAGTT 120  
 GATATGAAGA AACTAATGAA CTAAATGCAA GTATTGTCTA AAACAATCAT TTTATTGAAA 180  
 TTTAGTAGAG CTGAAATTAA TATAACGTCG TTAATTGAAT AACGCTTATG TTATAAGAGC 240  
 ACTCATACCA nACCATAATC ATCTATAGnT ATAACAATTC ACGTATAAGG GGCTGTGTTT 300  
 GGCATAGCCC TTAGGTATAC ACCTAATTCC CATTAAAATA GTAGGGGnTT AAA 353

(2) INFORMATION FOR SEQ ID NO: 3002:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3002:

CAACAAAATG TCTATATGGT AAGTGGTAAA ACGAAAAATG ATGAAGACTA TTCATCAACT 60  
 ATTTTATATA ACAACGAAAA AGAATTACAA AAAATTACTG ATGCTGCTAA AAAGCAAAAC 120  
 GGTGTAAAAT TAACGATTAA AGAAGAAGAA AAACAAAGTG TCTTTGTGAG TATACTTTCA 180  
 ACATTAAATC CAGTTGTAGT CATAGCGTTA TTATTCTTTC TCTTCCTAAG CCAAGCACAA 240  
 GGTGGCGGTA GTGGCGGTcG TATGATGAAC TTTGGTAAAT CTAAAGCAAA AATGTACGGT 300  
 GATnAATAAA CGTCGTGTTC GTTCTCTGA TGTAGCCAGG GGCCAGATGn AGGAAAACCA 360  
 AGGnTTAATT GGAAATTGTT GGTTCCTTGG AAAGGTAATG 400

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3003:

ATAACATCGG CACAGCAGCT AAAATAACCA TACCCAAAAT GANTGTATCT TTAAACGTGC 60  
 ACCGTAAAGn CTTCCGACTA GCCATGTATA AGCTTTGGCA GCAGATAATT GCTTCGTTGT 120  
 AATGAGTAAT CCTTGGACAA GCGCAATAAA CAACGTTTGC ATCGAAATAC CGATGATTAT 180  
 GAGTGTGTGTC GGGCGTATTT GTCCTTTCGT TTGAAACACT AATAGTATCA TCATTGCAAC 240  
 TCGGCCACCT AATACTGCAA ATAGTGGAGT AAATGTATTG TTAAAGGCTG AAAATGCAAT 300  
 AAAGACAACA GCACTTAAGC TAGCACCACC TGTGATACCG CTAATATCAG GTGAGGCCAA 360  
 TGGnnTTTTT TTATACATT TGGCAACATT TAACCACTTC 400

(2) INFORMATION FOR SEQ ID NO: 3004:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 354 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3004:

CTAATAACAA ATGCGATGAT GATTAATACT AATTTACCTG CTGCTAATAC AGAATCTCCA 60  
 AGGAATGAGA AGAATGGTTG ACGTTCAACT TCATTGTTTT TAAGACTGTA GATAATATCT 120  
 TCTTTCTCTT CAACACTTAC TGGATTCAAC AAGCATGACA CAATAATCGC GTTAACGGAT 180  
 ATTTAGTGGA ATTGCCGTTA GTACCACTTC TCCTGGTACC ATTTGTACAT ACGCACCTAC 240  
 AATAGCTCCC GATACAGAGC TCCATTGACA TCATTGCGAT TGTTAATACA CGCATTTCAT 300  
 TnCAGACGTT TTAGTTGCTC ACTTGGATAC GGGCTAANGC TTnCGTGAAT TGCC 354

(2) INFORMATION FOR SEQ ID NO: 3005:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 378 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

GGTCAGCTTA TTGAACAAGG GACACGTGAA TCAGTCTTGC ATCATCCAGA ACATGTTTAT 60  
 ACGAGATTTA TTATCAACGA AGAAGAAGAT TAATGATCAT TTAAACATG TGATGAGGGG 120  
 5 TGATGTACAT GATTAAATT AAAGATGTTG AAAAGTCATA TCAAAGCGCA CATGTTTTTA 180  
 AGCGTCGTCG AACACCTATC GTGAAAGGTG TGTCATTTGA GTGTCCAATC GGTGCGACGA 240  
 TTGCGATTAT CGGAGAAAGT GGTACGGnTA AATCGACGTT TGAGTCCTAT GATATTAGGT 300  
 10 ATTGAGGAAC CGGATAAAGG TTGTGTACCC TTAAATGATC CACCGATGCh TAAGAGGAAG 360  
 TGAGCCGCCA CChATTGG 378

15 (2) INFORMATION FOR SEQ ID NO: 3006:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1785 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3006:

25 ACnTTAGTTG GCCAAGCCTT TATCCGGAAT TATTGGGCCT TAAAGCCCCC TTAGGCGGTT 60  
 TTTTAAGTCT GATGTGAAAg CCCCGGCTCA ACCGTGGAGG GTCATTGGAA ACTGGAAAAC 120  
 TTGAGTGCAg AAGAGGAAAG TGAATTCCA TGTGTAGCGG TGAAATGCGC AGAGATATGG 180  
 30 AGGAACACCA GTGGCGAAGG CGACTTTCTG GTCTGTAACT GACGCTGATG TGCGAAAGCG 240  
 TGGGGATCAA ACAGGATTAG ATACCCTGGT AGTCCACGCC GTAAACGATG AGTGCTAAGT 300  
 GTTAGGGGGT TTCCGCCCCCT TAGTGCTGCC AnTAACGCAT TAAGCACTCC GCCTGGGGAG 360  
 35 TACGACCGCA AGGTTGAAAC TCAAAGGAAT TGACGGGGaC CCGCACAAGC GGTGGAGCAT 420  
 GTGGTTTAAT TCGAAGCAAC GCGAAGAACC TTACCAAATC TTGACATCCT TTGACAACTC 480  
 40 TAGAGATAGA GCCCTThcTT CGGGGGACAA AGTGACAGGT GGTGCATGGT TGTCGTCAGC 540  
 TCGTGTCTGT AGATGTTGGG TTAAGTCCCG CAACGAGCGC AACCCTTAAG CTTAGTTGCC 600  
 ATCATTAAGT TGGGCACTCT AAGTTGACTG CCGGTGACAA ACCGGAGGAA GGTGGGGATG 660  
 45 ACGTCAAATC ATCATGCCCC TTATGATTGG GGCTACACAC GTGCTACAAT GGACAATACA 720  
 AAGGGCAGCG AAACCGCGAG GTCAAGCAAA TCCCATAAAG TTGTTCTCAG TTCGGATTGT 780  
 AGTCTGCAAC TCGACTACAT GAAGCTGGAA TCGCTAGTAA TCGTAGATCA GCATGCTACC 840  
 50 GTGAATACGT TCCGGGTCT TGTACACACC GCCCCTCACA CCACGAGAGT TTGTAACACC 900  
 CGAAGCCGGT GGAGTAACCT TTTAGGAGCT AGCCGTCGAA GGTGGGACAA ATGATTGGGG 960

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TATATTCGGA ACATCTTCTT CAGAAGATGC GGAATAACGT GACATATTGT ATTCAGTTTT 1080  
 GAATGTTTTAT TTAACATTCA AAAAAATGGG CCTATAGCTC AGCTGGTTAG AGCGCACGCC 1140  
 5 TGATAAGCGT GAGGTCGGTG GTTCGAGTCC ACTTAGGCCC ACCATTATTT GTACATTGAA 1200  
 AACTAGATAA GTAAGTAAAA TATAGATTTT ACCAAGCAAA ACCGAGTGAA TAAAGAGTTT 1260  
 TAAATAAGCT TGAATTCATA AGAAATAATC GCTAGTGTTT GAAAGAACAC TCACAAGATT 1320  
 10 AATAACGCGT TTAAATCTTT TTATAAAAGA AAACGTTTAG CAGACAATGA GTTAAATTAT 1380  
 TTTAAAGCAG AGTTTACTTA TGTAAATGAG CATTTAAAT AATGAAAACG AAGCCGTATG 1440  
 TGAGCGTTTG ACTTATAAGn ATGnnnGATA TGTGGAATAT CCATATCTAA AGCTAGATCT 1500  
 15 AAACTTTGTT CAAAATCTTC AATCGTCTGT TTCGGTAAAT GATACATTAA ATCTAACTG 1560  
 ATTGATTAA TACCTGCGTT TTTAGCATTT AACACCGAAG TGTAAATATC TTCAGTATTG 1620  
 20 TGCCTTCTAC CTAAACAGA CAATAACTCC GGCTTGAATG TTTGAACGCC CATTGAAATC 1680  
 CTTTTTACTC CATATTTCTC TAATAGTTGG ACTTTCTCTT TAGTTAACTC ATCAGGATTT 1740  
 GCTTCAAATG TATACTCGCC TGTGATTGTA AACGTATCAC GTATT 1785

25 (2) INFORMATION FOR SEQ ID NO: 3007:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 360 base pairs  
 (B) TYPE: nucleic acid  
 30 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3007:

35 TGCAAAAAAC ACAATAACGA TAAATGTTCC CATTGATCCT ACAGCATCGC GAACATTTTA 60  
 CCTAAGTCTT TTGTATTTTT AATTTCTTTG CTAAATCC CATAAACTAA TCCAGGTACT 120  
 40 AAAAAACGA CAAGAATAAT TAATCCGACA CCGTTAATTA ATGGCGATCG TCTAGTAAGC 180  
 TGCCTGTTTT AGCATTCTT AAAAACTAT GTCAGGAATG GCTGTAATAA TTAATAAAAT 240  
 AATTGnGCTA TGAACGATA TTTGCCATTT TAAAAATGT GCTCTTTGTC AGAATATGTG 300  
 45 AGATGTnCTC ATGGCATCAT GCATTAACT GCATCATATT TTCCTAATCT AGGATAATGA 360

(2) INFORMATION FOR SEQ ID NO: 3008:

- (i) SEQUENCE CHARACTERISTICS:  
 50 (A) LENGTH: 350 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3008:

TTGCCTTCAA ACACATACTT GTAGTCGGAT GATCACCTGT TCCAAAAGnC ATACCTGGGT 60  
 5 CGAGCTCAAT GCAAAGCTCT TCATCCGCTT CTTTAGCATA TGTTTCCCAA CTAGGAACTA 120  
 TTGTGAACTT CTTGACGCT CGGGAATGGA TGGAAATAGT TTTTCCATTC ATTTTCCCAA 180  
 TCCGTCTCTG CAATAATTTG CTCACTGAAT TGAACGTTAT GTTGATCAAG TTCATCTAAA 240  
 10 TTTAATAACT CATCTTTGAA TTTGCTGTCG CAACTGTATC ATCATAAGTG CATTTCAGTA 300  
 AAATAGGCTT nGCAAnCTTA CTCCCTTATC TGGGATAAAG CCTCGGTTTT 350

## (2) INFORMATION FOR SEQ ID NO: 3009:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 383 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 20 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3009:

25 TCTTATATCA CCAGGAATTA AACTGCCTT TTGACCACTT TCTTCAATCA CTTGGCGTAC 60  
 TTCTTGTCa TCTTGTCTT CACTCGGAAG ATAGTTAATC GCTACATCTG CACCTTCTTT 120  
 AGCATACGCA ATTGCTGCTG CACGCCCTAT TGCTGAGTCA CCACCTGTGA CTAAtATTTT 180  
 30 ATAGCCTTGT AAGCGTTGAT GACCTTGGA AGACGTTTCG CCACAATCGG GTGCTGGCGT 240  
 CATTTCAGAT TGTAACCCG GTACCTCTTG TTCTTGTTTT TCaTAATCCG TTGTTTTAAA 300  
 TTTTGTTcNa GGaTCTkGAG CkGCCaTTTT TtGACaYctC CGTATnCGCT TAATGGGTAT 360  
 35 CATTTACCCC AATCTTCCTA AGG 383

## (2) INFORMATION FOR SEQ ID NO: 3010:

40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 388 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 45 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3010:

TAATTCAACG GGAATTTTCC CTTTGAAGTT AACATAACGG TAGGCTGCTT TAACAGCTTC 60  
 50 ATCATCGGGC GCTTCGACAT CTTCTAATTC ATATGCAATG CCCAATGTTT TCCACTTATG 120  
 AACACCTAAC TGATGATATG GCAGAATTTT AACTTTTTCG ACGTTATCAA GAGAATTAAT 180

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TGTCGAATCC ATACCAGGTG GTTTCATATC TGACAGTTTG CGCGCGAAGT TAAAGGATGT 300  
 GTGTATTAGG GCTTTCCCGG TCCATCCAAA TAnGGTTGGT CCATTAAATCC ATAAGGTTTT 360  
 5 AAnAATCnAAA TAATAATCCA GTCCGGTA 388

(2) INFORMATION FOR SEQ ID NO: 3011:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3011:

ACTGCTGTAA CGTCAGTTGA TCTTTTCATT CTTGGTTTAA TTTCTGAGAC GTTACTTGGT 60  
 20 TGnGChAnGC CACCAATTGC CATACCGACA GATTGGAAGA ACAATGCATC AGTTCCACCA 120  
 ACACCAAAGA TGTCAACCAAG TACAACGAAA CCTACATATC CAACTGTAGA TACAATTAAA 180  
 ATACCCATTG CTTTTTTTAAA TTCAGGATTA TCTGATTGAC GTnCATTTTT AGCTTTAAGT 240  
 25 GAAGTAAGTG CTACACCACT AACTAATAAT ATCATGGCGA TTAAACCAAA GATAATTGA 300  
 GTCATTGAAG ACCATTCACC TAAAAGATA ACGCTGGAAT AATGGTGTAC CCAACTAATT 360  
 GGCATACCTG GTAGGAACT GGGCATAGGT ATTTGGATAC 400

(2) INFORMATION FOR SEQ ID NO: 3012:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3012:

TTATCGGATT CGTTAATACT GGCGGTTTAC GCAATAGTTT AGATGTAGAT GATAACAATG 60  
 TGCCTATTAA ATTTAAAGAA GAGTTCGAAC CTAGAAAGTT TGTTTTCACT AACGGCGAAA 120  
 45 TTAAATACAA TAGCAATTC GAAAAAGAAG ACGTACCGAA TGCATCAAAC CAACAAAGTG 180  
 CGTCAGATTT AAGTGATGAG GAACTTCGCG GAATGGTTGC GAGTATGCAA ATGCAGGTGG 240  
 CACAGTAAAC GTATTAACAA TGGGATTAGC TCAACCAAAC GCTATGTTAA CACCACAGTT 300  
 50 GACTGACTGG AACTACCAA ACCAGTACTG AGGGGnCGTT AATAATGAGT GTTTCCACTT 360  
 AAGCATAAAC TTTTGTGGT CTTAAACGGC ATTAGTGTGC 400

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 389 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3013:

10 GGCTGTAATG AAAATCCAAA AGCCAAGCTT ATTTAATTCG CCTTCATGTG TGCCTGAATC 60  
 AATAGTGTTT GTATCATGAC TCATGACTTA CAGCCTCCCT TTCTTTAATA CGCGCTTCTC 120  
 15 TTAATCTAGC TTCAGTTTCT GCAACTTCAG CAGCAGGGAT ATGATATCCG TGATCGATTT 180  
 GGAAACTGCG ATAAATCATA GTACCAAAAA TACCGAATAA ACAAATTAAT GCTGGAATTA 240  
 CAGTTTCGAA AATTAAGAAG AAACCGCCGA TAGTCATAAA GATACCAATC CAGAATCCAA 300  
 20 CAGGAGTAAT GGTGTCGCAT ATGGATGGCC TTGGnAATAA TGGGTTGnCC TAAGTAATGG 360  
 CCGACCAAGG TCCTTTCCAn ATCCACCAA 389

(2) INFORMATION FOR SEQ ID NO: 3014:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3014:

35 AATCGCTTCG GTTAAGTGT CTAACCATTG GTAATAACA TGTGTATGAT CAAGCTGAGC 60  
 TTTAATTTTT TGTGCCTCTT GTGTTTCAGC TTCAGTTAAA TCACTGCTTT CAAGTAATGG 120  
 ATTGATAATA GCTTGAGCAT CTTTTACTGC TTCGACATTG ATGTCAATTT CACGCTGGAA 180  
 40 TTTTTTAGTG AAAAAGTTT GGAAGAT GAAAAGTCT TTCTCGGCGA TAAATGTGT 240  
 TTGCGGCTCC TCTCGTAAAT TGTGGTTAAC AATATCAAAT TCCTGCAATT CCTAACGCAG 300  
 CACTCATACT nGTTGnCAT TGCAATGATG ACGCATTAC AGGGCAACTG CTCAACACAT 360  
 45 GGGCATAAAG TTCCACACTC ATAGGCAACA ATCATGGCGG 400

(2) INFORMATION FOR SEQ ID NO: 3015:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 379 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3015:

ncctatctct GGTGAGAGT CTTTGAGCTG AAAAATGTGA CACACAAAAT TGCAATGGnA 60  
 5 TCAACAAATG TTTCCCATG TGGATGGTCT TGAATAAGTA TTTGGTGTTT AACTTGGTGA 120  
 TTTGCCATGA CTAATACCAT GTCATTTGTA CTTGTATCGC CATCAACAGT AATCATATTA 180  
 AATGTATGGT CAGTCGAAGA TTTTAATAAT TGATGAAGTG TATTCGATTC AATCGATGCA 240  
 10 TCGGTTGTTA TAAAAGCAAG CATGGTAGCC ATATTGGGT GAATCATACC TGAACCTTTG 300  
 GTGCTACCAC CAATTGTAAC GGTTTACCAT CGATTTTAGT GATACAGCGA TATGTTTTGT 360  
 ACAGGTATCA GTGTTAAAA 379

## (2) INFORMATION FOR SEQ ID NO: 3016:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 20 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3016:

CATATAAATT GCTAACGTGC CACCATTAC TAAGGAATTG ACATCCACTT CATTTTCTTC 60  
 TGAATCTTTA AAGTGACCTG TAGAAAATGT CACACTTTTA GCAACTGTAC GCATTGTCAA 120  
 30 ACCTGTCTGC ATAGTAGCAA CTGCTGCGCT CGCTGATGTC ACCCCTGGTA CAATTTCAAA 180  
 CGCAATATGA TGTTCAATTA GTATGTCGAC TTCTTCTTGC ACACGACCAA ATATCGCTGG 240  
 ATCGCCAACT TTAAGTCTAA CAACCTTGTT ATATCGACGC GTGCTTCCAC GATACAGTCA 300  
 35 TTATTTTTCT GCGGAAAAT GTTTGGAAC GGCTTTTACC AACnGGTAA TTCAGAGGCA 360  
 ATCGCAATGn AAATTACGn TCACnAACGG TCATTGGATG 400

## (2) INFORMATION FOR SEQ ID NO: 3017:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 310 base pairs  
 (B) TYPE: nucleic acid  
 45 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3017:

CCTTTTTCTC TTCTTTCATA TCTGCAAACG TGCATCAATT TTAGGATCTA AATCTCCAAA 60  
 TGCTTCTGCA ACTGGTTCAG AGCGTTCATA ATACATACGA ACTTTTGGAT ATAACGCTTT 120

TCATTTAACT GTTCATCAGT ATATTTATCA TATGCTTTTG TTGCTTGTTT TAATTCTGCT 240  
 TTAACACCAT CATCTTTTTT CGATGTCTTT GAATCATCCT TCTTACTATC GTCGTTCCCC 300  
 5 ACATGCAGCA 310

## (2) INFORMATION FOR SEQ ID NO: 3018:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3018:

TCGCTTTGTA AATTCTGGAA CAAAGnCAGT CATGACAACA ATTCGTGTTG CACGTGCATA 60  
 20 TACTAAAAGA AATAAATTA TAAATTTGC TGGATCTTAT CATGGCCATT CTGATTTAGT 120  
 ATTGGTTGCA GCAGGTAGCG GCCCATCTCA GCTCGGTTCT CCAGACTCAG CTGGTGTTC 180  
 AGAAAGCGTC GCACGTGGAA GTCATTACTG TACCTTTCAA TGATATTAAC GCCTATAAAG 240  
 25 AAGCAATTGG AATTTTGGGG TGATGAAATT GCCGCAGTAT TAGTAGAACC AATTGTTGGT 300  
 GAACTTTGGG AATGGnnAAT GCCTCAACCT GGGATTTTGA GGAAGAGGGT 350

## (2) INFORMATION FOR SEQ ID NO: 3019:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3019:

ATATCATGTG CCAGTGAAAG CGGCACTGGn CGGATATGGC GCACATATGG ACATTATGAA 60  
 40 AGAGTACCAA TTAATCATTT TAGCGCCACA AGTTGCGTCT AACTATGAAG ATATTAAGCA 120  
 AGATACAGAT AGATTAGGTA TTAAATTAGC GArGACTCAA GGTGCTGAAT ATATCAAATT 180  
 45 GACACGrGAT GGCCAAGCAG CCCTTGATTT CGTTCAACAA CAATTTGAAA ATTAAGAATA 240  
 GGAGTTTTTC ATATGACTAA AACATTACCT GAAGGATTTT ATTTTGGTG GAGCAACAGC 300  
 AGCATATCAA GCAGGAAGGT GCGACCAAAT TACGGGATGG GTTAAAGGTC GCGTGCATTG 360  
 50 GGGATACGGT ATTTTAGGAA GGAAACTTA TTTGGTACCA 400

## (2) INFORMATION FOR SEQ ID NO: 3020:

- (A) LENGTH: 361 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3020:

10 ACGTTCGTCT TACGTTTAAC GCCATACGGT GTATTAGCAA TTATGGnCCA ACACATTATC 60  
 GACAAGTGAC TTTGGCGCCA TTTGGACTTT AGGAAAAATT CTTAATCGCA TCGTACGCTG 120  
 CATTAAATAC GATGTATATC ATTCACTTAA TTATTTTAAG CCTGTTAGGT ATTAGCCCCA 180  
 15 TTCGCTATGT TAAAAAGACT TTGGAAGTAT TAATCTTTGC ATTACATCA CGCTCAAGCG 240  
 CGGGTGCCTT ACCAATGAAT GTACCAACAC CAACCAGACG TCTAGGCGTG CCAGAAGGTA 300  
 ATGnCAATTT CGCTGCGACA TTTGGAATGG CGATTGGACC AAATGGGTGG GCAAGnAATT 360  
 20 A 361

## (2) INFORMATION FOR SEQ ID NO: 3021:

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 356 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3021:

CAATGACCAT GACCAATTGA TTTGGAACAA TGATTGACAT TGGAGCTATG CATCAAGTTT 60  
 35 GTCTTTAAGA CTAATAAACC CACGAACCAT GTTAACCCCG TGGTGACCA TCACCAATTG 120  
 nCTCGATCTA ATTCAGTTAA TTCAGATTCA TGTTTTTTAA ACGTTTCTTC TAAATTTAAT 180  
 AAACGTGnCT TTCATATCAT TCACTTTCAT TTGTGnCCAC CTCATAAATG TATATTATCA 240  
 40 TATCACTCT TATTAAAGTA TGA CTGTTGT TGGTGCTAAA AATGCTCCAA ATATTCGGTT 300  
 TATTAGGCAC GATAGTTATA GAAAAACCTG ACAGTCTAAA GATGTCATAT AATCAC 356

## (2) INFORMATION FOR SEQ ID NO: 3022:

45

## (i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 332 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3022:

55

GTGTTTGGTC CAATATCCAT ACCTTCTTGG nTCTGCTGGA ATTGAATCAG ATGGTACTAC 120  
 AGTGATTTTG GCATCATTAG nAAAATTCTT TAGTCAACTT TAGTGTCTAC TGGTAATACA 180  
 5 ATTTTATCAC CATGTTTTTC TAATAAATCT TTTGCGAGTC GGATTTTATC TTCTTCTAAT 240  
 AATGAAATAC CAATTTCTTT ACCTTGCGCT TTTAAGAAAG TATAAGCCAT ACCTCCGCCG 300  
 ATGATAATTT TATCAGCTAT GTTAACTAAT AA 332

10

(2) INFORMATION FOR SEQ ID NO: 3023:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 311 base pairs  
 (B) TYPE: nucleic acid  
 15 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3023:

AAAGGTATTC CACAAGAATT AGCTTTGCAA AAATGCCAAA GCAAACAGAA GATGGnACAA 60  
 TTTAAAGTgn CCTACAATCA TGAATGAGGA GGACGCGTAA GATGAGCATT CGCTACGAAT 120  
 25 CGGTTGAGAA TTTATTAACT TTAATAAAAG ACAAAAAAAT CAAACCATCT GATGTTGTTA 180  
 AAGATATATA TGATGCAATT GAAGAGACTG ATCCAACAAT TAAGTCTTTC TAGCGCTGGA 240  
 TAAAGAnAAT GCAATCAAAA AAGCGCAAGA ATTGGATGAA TTACAGGCAA AAGATCAAAT 300  
 30 GGATGGCCAA T 311

(2) INFORMATION FOR SEQ ID NO: 3024:

(i) SEQUENCE CHARACTERISTICS:  
 35 (A) LENGTH: 319 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3024:

ATTAGACATT ACAAGGTGCA GTACGTGCAA CATATTAGAC ATATTGAATT AAGTGGTCAT 60  
 45 GnAAGGTATT GACAGTTAAA AAAGTTGAAC AATTAGAAGA AATCGAGGGC TTAATATTAC 120  
 CTGGTGGCGA GTCTACAACG TTACGTCGAT TAATGAATTT ATATGGATTT AAAGAGGCTT 180  
 TACAAAATTC AACTTTACCT ATGTTTGGTA CATGCGCnGA TTAATAGTTC TAGCGCAAGA 240  
 50 TATAGTTGGT GAAGAAGGAT ACCTTAACAA GTTGAATATT ACTGTACAAC GAAACTCATT 300  
 CGGTAGACAA GTTGACAGC 319

55

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 320 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3025:

GGTGCCAAGC AATAAATATG ACTATGCTCA AACTGAATTA ATGGTGGGTG TGTCGCCATC	60
GTAATTGGAT CGTCTGAAGG CGCATATAAA TGATAGTGCT CTTGGAATAA AGGTAGCATA	120
TGTAATTGTT TGTGTTTACG TATTTCTGGT GGTAAGTTCC GTGAAACCCA ATGTCTATAT	180
TCCCATTAA TACGCTATTT ATAATGTGT CATGTTCTAA TAAGCTCGGT ATGACATGTG	240
TATCAATTTG TAAAATGAAC GTTTGGATAA GGGGAGTAA CATGTGGGAT ACGTCACTCT	300
CATCAAGCCA TG TAGATACn	320

(2) INFORMATION FOR SEQ ID NO: 3026:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 328 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3026:

TCTCAACAAA TGCATCCAGT ACTTAAATTG GCATTATAGT AATTTAAGnA CAATATATCA	60
ATATTTCTCC TTATCCAGCA ACAGCAAATT TATTGGTAAG GTGTACGATT GAACCTTTAG	120
TCAATGAAGC AGGTACATTT GGATTGGCCA GGTGGATTTA CTTCAACTGA GCGCTTTGTG	180
AGAATGGGCA TTTATGAAAG CAAACATTGC TCAAACAAT GATAAAGAAA TGGATTTAAT	240
GAATGCATTT TATTTATTAG ATGCGGTAAA TATACCGATT GGAATTGTAC GTCCGCATGA	300
TGCTGACAAT CACTATACGA TGTATCCA	328

(2) INFORMATION FOR SEQ ID NO: 3027:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 322 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3027:

ATTGAAAATA TGTGTTCTnT GTAAAATTTT AATCGTTCGC CACGATGCTG TTGATAAAAA 120  
 TTCAAAACT GGAGTTGATC TTCTAGTTCA ACATAATCAT CGTAATTAGA CATGTAACCT 180  
 5 TTGATTAAGA TTTCAAGTAC ATGATCTTCG ATAGTATTGn TTTTAACTTG TTGTTGAGCC 240  
 GCTATATCTT CCATCGTGGA ATTGTTCAAG CAATTTTGTA TAAGTAATAT AAGTTTCGATT 300  
 TAATGAATGT AGGTTTCATT AT 322

## (2) INFORMATION FOR SEQ ID NO: 3028:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3028:

CAAGAATCTT ATACTTATCA AAATTATAC TGTGAAGCGA GTCTATTGGC TAAAAGACTC 60  
 AAGGCTTATC AACAACTCG TGTGGGCTA TACATAGATA ATTCGATTCA ATCGATCATT 120  
 25 TTAATACATG CATGTTGGTT GGCAATATT GAAATTGCGA TGATTAATAC AAGGnTGACA 180  
 CCTAATGAGA TGACGAATCA GATGAAGTCA ATCGATGTAC AATTGATTTT CTGTACCTTG 240  
 CCACTGGAAT TACGAGGGTT TCAAATTGTA TCGCTGGATG ATATTGAATT CGCCnCCGG 300  
 30 GcnTATTACA ACG 313

## (2) INFORMATION FOR SEQ ID NO: 3029:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 386 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3029:

CTTCCAAAGA AAAGACCACA GTTTTTGACG CATCAATATG GTGCAATTTT AGAGACACTG 60  
 45 TAGTTGCAGA AGATGGTTCA GTTGACTTT GAAGACAATC GTTATACAGA AACACGCGTG 120  
 CCGCTTATCC AATTAATCAC ATTGACAATA TTGTAGTACC ATCTAAAGCA GCACATCCAA 180  
 ATACAATTAT TTTCTTAACT GCGGATGCAT TTGGTGTAT TCCACCGATT TCAAAGTTAA 240  
 50 ATAAGACCAG CAATGTATCA TTTCTTGAGT GGTTCAC TTC TAAATAGCTG GncAGAGCGT 300  
 GGTGTGACAG ACCTGACCAT CATCTCAACA TGTTCCGnGCA CCGTCTTCCG TACATCnACT 360

## (2) INFORMATION FOR SEQ ID NO: 3030:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3030:

TGATGGATTG GCTAGCAGGT GTTTACATTA ACTCATTAAA TGTTATTCAC TACATGCACG 60  
 ATAAATACAG CTATGAACGT ATTGAAATGG CATTACATGA TACAGAAATT GTACGTACAA 120  
 TGGCAACAGG TATCGCTGGT TTATCAGTAG CAGCTGACTC ATTATCTGCA ATTAAATATG 180  
 CACAAGTTAA ACCAATTCGT AACGAnGAAG GTCTTGTAGT AGACTTTGAn ATCGAGGCCGA 240  
 CTTCCCTAAA TACGGTAACA ATGACGACCG TGTAGATGAT ATTGCAGTTG ATTTAGTAGA 300  
 CGCTTCATGA CTAATTACGT GGTCAITAAA CATATCGTGA TTCAGACCTT CCATGGGnGT 360  
 ATTACCATTA CTTCAACGTG GTnTCGGGTA GAAACTGGGT 400

## (2) INFORMATION FOR SEQ ID NO: 3031:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3031:

nGCGTTTAAT CACATCTTTT TGATAATGTT CCCTTACCAT TTCTTCATGT GCATCTGCAT 60  
 AGTCTTTTCC AAATGGCAAA CTAAACTGAT ATGCAACTTT TAAATAGGCA TCTATATGCG 120  
 ACTCGTCAAC GATGGCAATT TCAACGTcna GTTACGCGGA CAAATTGGCA AGCGCATCAC 180  
 TTTCTATGGC ATACAATTCC ATAATACCTA GTTCAAAATT CATATCTTTA AAACATAGCC 240  
 ATCCAATGGA TTATCAAGTT GTTCATTTTC CGGGAAAACT nAAACGCATA AATGATTTGG 300  
 AACCTTGATT TGTATGTGA 319

## (2) INFORMATION FOR SEQ ID NO: 3032:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3032:

5 AAGAAGTGGC AATTATGATT GATGCTCTAG CTGACAAAGG GAAAAAAGCA TTAGAAGCAT 60  
 TATCTAAAAA GTCACAAGAA GAAATTGATC ATATTGTTCA TCAAATGAGC TTAGCAGCTG 120  
 TTGATCAACA TATGGTGCTA GCAAAATTAG CACATGAAGA AACTGGAAGA GGTATATACG 180  
 10 AAGATAAAGC GATTAAAAAT TTATACGCTT CTGAATATAT ATGGAATTCA ATAAAAGACA 240  
 ATAAGACAGT AGGGATTATT GGTGAAGATA AAGAAAAAGG ATTAACGTAT GTAGCGGAAC 300  
 CAATTGGTGT TATTTGTGGT GTTACCGCCC AACCACCAA TCCCTACGTC CGACCACCTA 360  
 15 TTTTAAAGC CGATGGATTT GCCATTAAAG ACnGGGAATC 400

## (2) INFORMATION FOR SEQ ID NO: 3033:

## (i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 303 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3033:

TAGCGGTAAT CGAAATTGGG GACTAAATTT CGCAAAGCG GGTCGCACGA TATCAGAAGA 60  
 30 GTATAATGTC CCTTTATTAA TGAAGTTTGA GTTACATGGA AAAACAAAG ACGTTATTGA 120  
 ATTTAAGAAC AAGGTGGGTA ATTTTAATGA AAACCATGGA AGAGAAAAAG TACAATCATA 180  
 TTGAATTAAA TAATGAGGTC ACTAAACGAG AGAAGATGGA TTCTTTAGTT TAGAAAAnGA 240  
 35 CCnGAGCTTT AGTAGCTTAT TTAGAGGAGT AAAnGACAAA ACATCTTCTT CGACACTGAA 300  
 TCG 303

## (2) INFORMATION FOR SEQ ID NO: 3034:

40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 340 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3034:

50 CTnCGCTATT TTGTAGGACA TCTTCTAAAG TGCTAGGnGA AGAGATTATA GAATAGGCAC 60  
 TATCAATACC GAAATCGTAA ACATGTTGAT AATTTTCGCC TAGACTGCCA CAAATCGCGA 120  
 TGACAGGAAT ATGATATTGT TTTGCAGCTA ACGCAACGCC TGACGGGTGT TTTACCAAAG 180

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TGATGAAAAT CTGTAATGTC AAAGACGGAC ATCAATGACT TTTGTTGAAA GTTGTCTCAC 300  
 AAAACGnTAA TGAATGCTGC GGCCCATGAC CGGCCAGCTG 340

(2) INFORMATION FOR SEQ ID NO: 3035:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3035:

AAAGAACATG GTGTAGCAAT AGTCTCTGGA GGTGGAAGCG GACATGAACC TGCGCATGCC 60  
 GGTTTTGTG CAGAAGGTAT GCTAGATGCA GCGGTTTGTG GCGAGTATTT ACATCACCTA 120  
 CACCTGATAA AATATTAGAA GCTATTAAAG CAGTAGATAC TGGTGATGGT GTATTACTAG 180  
 TTGTAAAAAA CTATGCAGGT GACGTGATGA ATTTCGAAAT GGCACAAGAG CTTCCAGAAA 240  
 TGGAAGGTAT AAATGTTCAA ACTGTTATTG TTCGTGnCGn CATTGCTGTG ACAAACGnGT 300  
 ACA 303

(2) INFORMATION FOR SEQ ID NO: 3036:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3036:

GGGGAAAGTA AATTAACAGC TGTGTAGAAT AATTAAGGTT TTAATTTATA TAGAACAACT 60  
 TATTGTAAAC TTTTCATTTT TTAAGTTTA CAATGGTGCT ATAATAATGG TCATGAAATA 120  
 CGAAAGGAAG GAAAAAATGA CnACAAAACA GTTAGTATAT ACAGCTTTAA TGACAGCGAT 180  
 TATCGCTAGT TTAnGATTGG TACCGGTAAT TCCACTACCA TTGnCTTCAG TACCAATTGT 240  
 ACTTCAAAC AGTGGTATTT CTTAGCAGGG GCGATTTTAG GACGTAAATA TGGCACATTA 300  
 AGTGTTATCG TCTTT 315

(2) INFORMATION FOR SEQ ID NO: 3037:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3037:

5 GCACCAATTG ACGAAGGAAT ACCGAATCCC ATTGTTCCCTA AACCACCGCT TGTAACCCAT 60  
 TGTCCGTGAT TTTTAAATGG ATAAAATTGA GCTGCCACACA TTTGATGTTG TCCCACGTCT 120  
 GTAGTAACAA TTGCTTCACC ATTTGTAATT TTGCCGATAT ATTCGATTGT TTGTTGTGGC 180  
 10 TTACAAATA CTTGATCTTC TTCACCAAGT TTAAATGGGT GTTTCTGCTT ATTATTTTGA 240  
 CAATGTTTAA CCCAGTCACT GTGTTCTATA GTCTCAACAT TTTTATCATT TAAACCTCC 300  
 AAAAAACCTT TACAGCCnG CAAAAAACC 330

## 15 (2) INFORMATION FOR SEQ ID NO: 3038:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 334 base pairs  
 (B) TYPE: nucleic acid  
 20 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3038:

GTGAGTCCAC ATAATAACTT TGACGTCCTG TTAATGTTCT AAAAGGTACT AGACGTTCTA 60  
 TATTCGTTGT AAATGGTGAA TATCGTCGAC CTTGTTTATT TGAACCTGGG AATACTGCTG 120  
 30 TCGGTATTAC TTCTCGTGGT TGTGAAGTTA TATTTAAAAA CGAAATTTTC TCAGCAGCGC 180  
 TGTCGCTAGA AATATCTTTT AACGGCATT CAGTTTGTTT TCGAGATCT TCATATGGAT 240  
 TTTTGTGnAT AATThACCAT TCGTAGCAGA TGGAAATACT TGAGTATnGG CATCAGCGAC 300  
 35 ATTGACGTGC TGTATCAATA CGTGGACGAT TCGC 334

## (2) INFORMATION FOR SEQ ID NO: 3039:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 327 base pairs  
 40 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3039:

GGTCTGATCG TGGTGAATGA AAAAGGTTCT TCTCTGTAAT GAATTATCTC TTACCGATGC 60  
 50 AAGATATTAT GAGCATGCAT TGCTCAGCAA ACGTTGGTGA AAAAGGCGAT GTTGCAATTAT 120  
 TCTTTGGTCT ATCTGGCACT GGTAAAACAA CCTTTATCGG CTGACCCACA CCGTAAACTA 180

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ATGCAAAAGC AATTAACTCTT TCCAAAGAAA AAGAnCCACA GntTTTTGGA CGCATTCAAA 300  
 TATGGTGCAn TTTTAGAGAA CACTGTA 327

5 (2) INFORMATION FOR SEQ ID NO: 3040:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 305 base pairs  
 (B) TYPE: nucleic acid  
 10 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3040:

GTGATATTCA CGAnCGTTAT TTTCAATATT TGATAAGTAG AAAnTATGAC GATCTTCATG 60  
 AACAGCATCT TGTCTCTCGT CAAATTCAAC GTCATCAAAA CGTTTGAAGA ATGTTTCATA 120  
 20 TGCATCAACA GATACTTCAG TACGGTTATT TAATAATGCT TTATGTGCAG CTTGGATCTA 180  
 AATGATCTTT GTAGCCTTCA ACTnAATGTC GCACTATAAA ATTCACCAAC TGAACCTGAG 240  
 CCATAACTGA ATAAACCGAT TGTTTCCACC AGCTTGTGAA TCTCGATTTT CAAGTGAATG 300  
 25 ATATT 305

(2) INFORMATION FOR SEQ ID NO: 3041:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 317 base pairs  
 30 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3041:

GTTGTGTACC TTAAATGATC AACCGATGCA TAAGAAGAAA GTGAGACGTC ATCAAATTGG 60  
 40 TGCTGTATTT CAAGATTATA CGTCATCATT ACATCCATTT CAGACTGTTA GAGAAATCTT 120  
 ATTTGAAGTG ATGTGTCAAT GTGATGGACA ACCTAAAGAA GTTATGGGAA GTCCAAGCAA 180  
 TTACATTGTT GGAAGAAGTC GGTCTATCTA AGGCATACAT GGATAAATAT CCTAATATGT 240  
 45 TATCAGGTGG AGAGGCGCAA CGTnTGCA nTGCGCGTGC AATATGTATT GAACCCnGAA 300  
 ATATATTTTG TTTGGAT 317

(2) INFORMATION FOR SEQ ID NO: 3042:

- 50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 351 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3042:

5 AATCTTCGAA AAATAATGCA ATGCAGATTC CGAAAAAAC AATATGATAG AAACACCTCA 60  
 ATTAAATACA ACGGCTAATG ATACATCTGA TATTAGTGCA AACACAAACA GTGCGAATGT 120  
 AGATAGCACA ACAAACCAA TGTCTACACA AACGAGCAAT ACCACTACAA CAGAGCCAGC 180  
 10 TTCAACAAAT GAAACACCTC AACCGACGGC nATTAAAAAT CAAGCAACTG CTGCAAAAT 240  
 GCAAGTTCAA ACTGTTCTC AAGAAGCnAT TCTCAAGTAG GTTATTAAAA CACGGATGGT 300  
 GCTAATAGCT TnGCAACAAC GTGGGCTTTA AAATTCTCCA ACTTTAGTTT T 351

## 15 (2) INFORMATION FOR SEQ ID NO: 3043:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 319 base pairs  
 (B) TYPE: nucleic acid  
 20 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3043:

ACGnCCTTAC TGGnTACTTG GTTGATAAGT GTTAATCCAA ATGACGTCCT GCTACGTACA 60  
 GCTTTACGAA TATTTAATGC ACGTGTGATA TTTTGAGAAA ATACACCGCC TGGCTAAACC 120  
 30 ATACTCAGAA TCATTAGCTA TATCAATTGC TTCTTGATCG TCCTTCACCT TAATCACTGT 180  
 TAACACTGGT CCAAATATTT CTCTGTGTC TAATTTGTGA TGATTGTCTG GCACnCAATT 240  
 AATGTCGGCT CAAAGAAGAA CCCTTTATCT AATCCATTTT CAGTTAAGCG ATGACCGCCT 300  
 35 GCTAAAATTT GTGCATCCG 319

## (2) INFORMATION FOR SEQ ID NO: 3044:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 342 base pairs  
 40 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3044:

GTCAATAAT CTAACATTTG TGTATCTGT TAATTAAGTG GntTTTACCT TAATTTGTTA 60  
 CATTGnTCTG TATTAAATCT TTTTGTAACC ATTGGTTACT TTTTCAGGTG GAATTTCAAC 120  
 50 ACCCATGTCA CCACGTGnCA ACCATTAAAC CATCAGACAC TTCAAGAATT TCCGCAATAT 180

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AAATTCACGA ATTTCTAAAA CATCACTAGG TACGACGTAC GAAACTTGCT GCAATGAAGT 300  
 CAACATTTTC TTTAATACCG AAACGGATAT CTTCAGCATC TT 342

5 (2) INFORMATION FOR SEQ ID NO: 3045:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 10 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3045:

TAATATCATG TTGTGCTTTT AGTGCTTCGG CAATTTGTTT TGTACTTACT GACCCAAACA 60  
 ATTTACCACC TTCACCAGTT TTTGCTGATA CTTCAACTTC AATGTTTGAT AACGTTTCTT 120  
 20 TTAATGCTTT ACATCTTCAA TTTCTTGTTG GCGTTCTTGT TTTGCACGTT TTTTCTGTAA 180  
 CTCTAATTGT TTAAGGTTAC CTGGTGTGTC TTCTACAGCA TAATTCTTTT TCAATAAGAA 240  
 GTTATTTGGC ATAACCTACT GGTACTTCTT TAACTTCACC TTTTTTACCT TTACCTTTAC 300  
 25 CTTTAACAnC TGTGTAAAAA TTACTTTTCAT GCAGnTCACT CCTACTTAAA TGTTCGGTAA 360  
 TGCCTGTTGT AATGTGCCAA CGCCnCTCGA CGTGACACCT 400

30 (2) INFORMATION FOR SEQ ID NO: 3046:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 306 base pairs  
 (B) TYPE: nucleic acid  
 35 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3046:

40 AATCACTGTT TCATTACTTG TTCCAAATCT GnATTCAAAC TATTGTTCAA AGATTCTAAT 60  
 TCCGCTTTAT TTTTATCTTT AATCGCTTTT GTCATCGCAG CATCTTTAGn CATCGACTTn 120  
 CTGTTGCAAT AGTTTAATTT TAGAACCCGC ATCTTTACTA GCCAATTTCT CTTCATAAGC 180  
 45 AATTAATGAC TTCGTTAATT GCGAAAGTGT ATCTTTTTGA TTATCATTCG CTTTTGCATC 240  
 TTCAAGCTTT CTCACATCTG CATTGACAG CATTACTTGC ACTATTATCT TCAAGCGATA 300  
 50 ATTTCT 306

(2) INFORMATION FOR SEQ ID NO: 3047:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 306 base pairs  
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(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3047:

ATGGATCATA TTAGCACGTA AAAGAAAATT CTGTTTCATTA TGAAGAAGTG CCAGAnGTTG	60
AATTTAAACG CACATATGTA TGTGAAGATA TGTCTAAATG TATTTGTTTA TACAACGCAC	120
CTGATGAAGA AGCGGTAnTC GCGCGCGCAA AGCAGTTGAT ACACCGATTG ATGGCATCGA	180
AAAACTTTAA TAAGACAACA AGTTGATGAG ATATATGTAT ATAGGTTTGG CATGGATTTC	240
GATTGCAnTT ATTAGAATAG CTCAATGCTA TAAATGTAAG TAGTTGATAT TGAGGAACTA	300
ATGAAC	306

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(2) INFORMATION FOR SEQ ID NO: 3048:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 287 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3048:

GACAGGCTAC GAGATATTTT AAACAAATTT ACATCAAATC CAGTATTAGG TGTTATTGCA	60
GGTATCGTTG TAACTATTTT AATACAAAGT AGTTCAGGTA CGACATTATC ACAATCGGAC	120
TGGTAAChCT GGATTTATGA CATTGAAACA AGCCATTGGA GTGATAATGG GTGCTAATAT	180
CGGAACAnCG GTAACGTCAT TTATTATCGG TATAGATTTA GGCGAATATG CAATGCCAAT	240
TTTAGCATTG GGTGCATTCT TGAATCTTTT TCTTTAAACG CTCTAAA	287

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(2) INFORMATION FOR SEQ ID NO: 3049:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 371 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3049:

CATATAAATA GCGnTACATC GCGCCATTCT TGATCTGnAC ATATCTTTCT TAGGTCCAAC	60
CGTGAATGAT TACGTCCATG ATAACGTACA AACGCAATTT CATTGTGAT TCGATTGACT	120
AAAGGTACAC TGCCATCTTT CACTTGTGGT TCATCAACTA CTGCATGAAT GATTTGATGT	180

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AATTCTACAC ACATTGGAAA GCTTGTAAATG CTGTCTTACA TACAAATATA TTGATATTTG 300  
 TGCATGCACT CAACCAGGCG GAAATGACCA TACCATGCTA ATTTTCTGGT AnGAAGGCCT 360  
 5 ACATATCTAA A 371

(2) INFORMATION FOR SEQ ID NO: 3050:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3050:

CGCCAAATAA AGATAATACA CGTATTGGTG AAGATATAAC TGTRAACTGCA CATATCTTAA 60  
 20 TTGATGGCGA AACAACGCCG ATTACGAAAA CAGCAACATA TAAAGTAGTA AGAACTGTAC 120  
 CGAAACATGT CTTTGAAACA GCCAGAGGTG TTTTATACCC AGGTGTTTCA GATATGTATG 180  
 ATGCGAAACA nTATGTTAGG CCAGTAAATA ATTCTTGTCG ACAnATGCGC AACATTGAAT 240  
 25 TTCCAATTTG TTGGAnCATA TGGGCTAACA AGGTGTTTAG GCATATCTAC TCGTCTTATT 300  
 GGGTGCATAT GTAATGGCAA GCA 323

(2) INFORMATION FOR SEQ ID NO: 3051:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3051:

CCGnACCAAT CGGTTTACAG TTCATTGGTA AACCATTGCG ATGAAAAAAC GTTATATCGT 60  
 GTCGCTTATC AATATGAAAC ACAATACAAT TTACATGACG TTTATGAAAA ATTATAAGGA 120  
 GTGGAAATCA TGCATTTTGA AACAGTTATA GACTTGnGTT CACGTAGAGT TAAAAACGGA 180  
 45 CTCAAAAATG TTTCTCCATC ACCAGCGCAT TInGAGCAGA ACCTAACTCA AATACGAATG 240  
 GSTATCGCTTA GCATATCCAG TGCTTACCAG TTGTTAATAA GCGTGCGTAG ACGGGCATGC 300  
 GTGCTGCAAT GCCTAAATAG GAACG 325

(2) INFORMATION FOR SEQ ID NO: 3052:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3052:

CTTTTAATCG	CTTGAAACT	ATAGGTAAGA	CAATACAAGT	AGCTACAAAG	CCATATATTA	60
CTGTTAATTG	ACCTATGAAA	AAATATCCGC	TAACGGGTGC	CGTCAATCCT	GCGATAGCAA	120
TACCAATAAA	AAGTACAGTC	CACGAAGGAT	AAACATTTTC	AAGTGAAAAA	TCTTTTAAAT	180
ATTTTATTGA	AAAAATAATC	ATATGCGTCA	TAATCCCAC	AAGGCATAAA	ATCCAAATAG	240
GCGTATTAAG	CTATTGTAAA	GTTTGTTACT	AAAAATGTT	TTAAATAGTG	TnCTAAAAAG	300
CCGGCATGAA	AATGTGTGAC	CTGATGAACT	GAGGCTGTTA	TTGTCTTCAC	TTATTAAATT	360
TGTCTAGTCT	AAAGGTGATC	CAATCAGAAG	CAAGTCCGCA			400

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(2) INFORMATION FOR SEQ ID NO: 3053:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 367 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3053:

AATGAGATGC	GAAGGATGAT	CAGAGAAAAA	GTCTCTCAAT	CAGGTGTGAA	AGTCAGATGG	60
TTATCACAAC	TTTGGCGTAC	GTTTTCGATA	TAATGCACTA	GGTGATTITAA	ATACGAGCAA	120
TATTGTTTCT	TCAAAGAAA	GTTTCGGTAT	TACTGAAGTG	TGAAATCTGT	CTCTATGCAT	180
GCCGGATCGA	CATTAGCATT	ACTAATCCAG	AGAAAGCAAA	AGGTATTGTG	TATACACCAG	240
AACATTGCCA	GCGAAAAGTA	AATGGTCACA	GCTGTAGAnC	AAGGTATTTA	TAATGGGGGC	300
GGTAAAGCAG	AAGGCCCCCTA	TGTAGCATTT	CnTAAAGnTG	GGAAAAGGTA	AAGCAGCATT	360
ATCGGTG						367

45

(2) INFORMATION FOR SEQ ID NO: 3054:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 382 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3054:

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TnATTTATCT nAGCTCATGA CATGATGGCT GTTCACATTG CAAGGCGTTG ATGATnAAAT 120  
 AAGGAAAGGC ATTAGGAAAA AGCCACAGGG AAAACATTTT AGCAGCAGGT TCTTGGAAATC 180  
 5 ATATATTCAA GTTCAACAAG CGAATGCTGT TAAATTGCCC TTTGGATGAC AATCAATTTC 240  
 ATATCGTTTT AAATGAAGCA ATGTTAACAA TGTTACCCAT CGCCATAAAG GAAAAAGCAT 300  
 TACGCGAGTA CTACCGAGTC TAAAGCCTGG GGGTATCTGT TAACACATGA TATTGTCATC 360  
 10 GTTAATGAAT CACATGCCAC AC 382

## (2) INFORMATION FOR SEQ ID NO: 3055:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3055:

CTTAAGATTA GGTGTGCTTA ATTAGTACTG GCTGGGAACG ATAAAGGCAT ATTGCAAAAA 60  
 25 ATAGAACATC CATATCCATT AAATGTATTT ACGCTAAATA TTGnCGACTT ATATTTTTAG 120  
 ACATAGAGAA GAGACAAGAC AATTTTAAAC GATGCAACGA CAGTTAGGCT GAGGCAGTTA 180  
 AAACAAATAT TTGATACACA TGTTGnCAGA TAAAAGTCAG TGTTCCCATC AAATGChAAT 240  
 30 TTTGTACTAC TAAAAGCTCA GCAGCGCAAC AATTAGGACA ATACGTATAT GAACAAGGGA 300  
 TTTAAACCTC GCTTTT 316

## (2) INFORMATION FOR SEQ ID NO: 3056:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3056:

GTTCACCATC CGTTTATTTT AATGAAAAA TCGACAAAAA TGGTCGTGAA AACTATGATG 60  
 CAACAATTAT TCCAAACCGT GGTGCATGGT TAGAATATGA AACAGATGCT AAAGATGTTG 120  
 TATACGTACG TATTGATAGA ACACGTAAAC TACCATTAAC AGTATTGTTA CGTGCATTAG 180  
 50 GGTTCCTCAAG CGACCAAGAA ATTGTTGACC TTAAAGTGAC AATGAATATT ACGTATACTT 240  
 AGAGAAAGAC nGCACTGAAA ACACTGACCA GCGTATTAGA ATCATGACGT TACGTCCAGT 300

CTTAGCAGCG TGGGnCGTAT

380

## (2) INFORMATION FOR SEQ ID NO: 3057:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 327 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3057:

TATGTGATGG ACTTAAAAAA ACGAACTCAA TTAATACAAT GGGCTCAAGA AAAAGAAGAA	60
CGATTTATTA TAGAAGATGA TTATGATTCC GAGTTTAGAT ATTTGGGCAA ACCCATTTCCA	120
GCAATTCAAG GTCTATATTC AAGAGGAGAA AAAGTGATTT ATATCAGTAC ATTTTGCAAA	180
GTCTATTTTT CCTAGCTGTT CGAGTTGGCA TATATGGTGT TACCCTATTC TATnATGGAA	240
AAAATATCAT TTCTnCAAAA TCCACCATTG GAAGGGCAAC ACTGGTAACC TGTTTCATAT	300
GGCAAAACCT TATTGGCAAC GTTTnAT	327

## (2) INFORMATION FOR SEQ ID NO: 3058:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 284 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3058:

CGAAAAAGGA GAATGAAACA TGAGGTAATA CAACATTACA TGCAACAACA ATTTATGCGT	60
GTAAGACATA ATGGAAAGCA GCTATGGCTG GAGATGGGCA AGTAACGCTT GGTTCACAA	120
GTCATCATGA AACAAACGGC AAGAAAAGTG CGACGTTTAT ATGAAGTAAA TGTTAGCTGG	180
TTTCGCAGTA TGTAGCAGAT GCGTTTACTT ATTTGAAAAA TTCGAAACAA nATTACAACA	240
GTTTAGTGGT AACTTAGAAA GAGCnGCTGT TGAATTGGCA CAAG	284

## (2) INFORMATION FOR SEQ ID NO: 3059:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 302 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

AAAGAAGCCG ATGAAGAGCT TTGCATTGAG CTCGACCCAG GTATGGCTTT TGGAACAGGT 60  
 GATCATCCGA CTACAAGTAT GTGTTTGAAG GCAATAGAAA CATATGTATT GCCACAGCAT 120  
 5 TCAGTAATTG ATGTTGGTAC TGGCTCAGGT ATATTAAGTA TTGCAAGTCA TCTAATCGGT 180  
 GTAAACGTA TTAAAGCGTT GGATATTGAT GnaATGGCAG TGAGTGTAGC TAGAAGAAA 240  
 CTTCAGAAGA natCATTGTG AACGTTGAAT TGGAAGCTGT TCCAGGTAA CATATTGGAA 300  
 10 AG 302

## (2) INFORMATION FOR SEQ ID NO: 3060:

(i) SEQUENCE CHARACTERISTICS:  
 15 (A) LENGTH: 330 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3060:

TTTTTAANGA CACATTGnGC TGTGTTTAAT GCATGAAAGG AACCACTGAC ATGCATnAAA 60  
 25 TCTTTGAATG GTTCTTTATC AATTCCTTCC CCCCTCTCAT GTTTTGTATC TTAAATCAA 120  
 TATAATTCAA AAAGGTCGA GGATATGAAA TCACATCTTC GACCCTTTAT TTACTATTTT 180  
 AATTCAGCCA CACGCAAACG GTTATTTGCT CTCTCTAAAG CTCTTTCGGC TCTATGGAAT 240  
 30 ATCAGTATTG TCGTCAATCA TTTTCCAAGT GAGACTCTGC TCTTGCTTTG GCTAATTTAG 300  
 CTCTTTCAAC ATCAATTTCT CTTGCAGTTC 330

## (2) INFORMATION FOR SEQ ID NO: 3061:

(i) SEQUENCE CHARACTERISTICS:  
 35 (A) LENGTH: 301 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 40 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3061:

CGATCAATCA ATATAATTCA CGGCGCAAAA CGTTTATTTA GCATGTTCTT GCAGACTCTG 60  
 AAAGTGGCAT TAAACCTTCC ATTAAGATTT TTACCATTCT AGGCATTAAT ACCATTACTG 120  
 CAGCCATTGA CATTCCTAAA TTAATGATGT CTCCAGGTTT GTAACCTGCT AACACACCAA 180  
 50 TACCTAamCC TAAAATTAAG CCGACAAATA TAGACTCTCC AAATGCGCCA AAACGTTTTT 240  
 GAATTGnTTC AGGATCAGCA TCTAACTnat TCAGACCGGG TACTTTTTGT AACAAATTTAA 300

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## (2) INFORMATION FOR SEQ ID NO: 3062:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3062:

TATAAAATCA ATGATTTTAA CAAATAAAAA CGTACCGCAA ATACTGCAAA TAACAGCAAA 60  
 TACTAGTTTT AATAAAATAT GACCGGTTGG AAAGAACAAT AAAGCAATTA AAATACCTAG 120  
 TTTAGCCCAT TCCATCGTTC CAGCTGTAGT CGGACTAACA AACTTATTTT GCATCATTG 180  
 TTGGCATTAT CAAGCCTGCT GAAAGCCAAC GAACTTCCAG CAATTAAAAT ACTCATCGTC 240  
 CTTGGTATTC GGGCTTGGAG AATAAAATGA TTCCGCTGGT GACTCAGTTG AAATGTAGTG 300  
 AAATCTTTGA ATTGGATAGT TnCACTGCAC ACCTGATGGn AnCAACGGAA 350

## (2) INFORMATION FOR SEQ ID NO: 3063:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3063:

TTAGTGATTT TAACGTGTAT CGGTAATTTT AAATAAATGT TTAATGCTTT TGAAAATACA 60  
 GTTCTAACCG AAGACGTCGG GTACACTGAA TCACCGGAAA CGCCAAGGTC TTTTATTAAA 120  
 CCTTGTTTAC TATATTGCAT ATACTGTGGA TGCTGTCGCA ACACATTGAT TTGATAAGGA 180  
 TGTGTTGGTA ATAAAATAAA ATCTTTGGGT ATCTCTGATA TATCTATGTC TGCTAATTGG 240  
 ATACnACACT TTCTCAACCT GGATCCTTCC TTTTACCTnC CACCATAGCC GCGTGGAnCA 300  
 GGAAACCATC CTGGGATGCA CCAGCCAAAA TAAATGCCAA TT 342

## (2) INFORMATION FOR SEQ ID NO: 3064:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

GTCCAGCTCC AGAACCAAAC TTAACAGTAT TATGGTCAGT ACGTTTACCT GACAACTTCA 60  
 AAACATACTG TGCAAAAATG AGTATTAAAA CAAGTTCTAT CCAATATGAA AATGATGACA 120  
 5 TTATGCGTGA AAGCTATGGC GATGACTATG GTATCGCnTG TTGTGTATCA GCGATGACAA 180  
 TTGGTAAACA AATGCAATTC TTCGGTGCAC GTGCGAACTT AGCnAAAACC TTACTTTACG 240  
 CTATCCATGG TGGTAAGATT GAAAATCTGG TGCACAAGTG GGCCCAACCT CCGAGGGATT 300  
 10 nACCAGCGGA GTAATT 316

## (2) INFORMATION FOR SEQ ID NO: 3065:

(i) SEQUENCE CHARACTERISTICS:  
 15 (A) LENGTH: 322 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3065:

TGATTGCGTG GATCAGCAAC TTCAAAGATT AACAAATAAT ATTACTTGGG CAGATAACCG 60  
 25 CGCTGCAAAA TATGCAACAG TAATAAATGA AGTGCAATGAT GGGCAATGCG ATTTACCAGC 120  
 GnACAAGCAC AnCGGTTTCA TCCTATGTCG CGATTAGCGA AGATTTTTGG ATGAAACATG 180  
 ATGGCCAGAT GTATTTCCAC GTACTGCTAA GTTTGCAGAT ATTAAACAT ACATTTCTAT 240  
 30 CATTATTGAT ACATATATCA TTGATTATTC CATGGCTTCC GChACAGGGA TGTTAATTAG 300  
 AACATAGATT GGAGTGAGGC AT 322

## (2) INFORMATION FOR SEQ ID NO: 3066:

35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 373 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 40 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3066:

45 TATAAAGAAT CCTGCCTTAC CTAAGAACAC TTGTCTTGTC GTTAAGACTG ACTCTAGACT 60  
 CTTATGTTTA TTATCAACCG TTAATAAACT TACCATCAAG AGTGACCTA CCCATACTGA 120  
 CAGTGCAGTA TAGAATGGTG TCATACCTGA ACCATAATCC TTAAGTGGGA AAACATCAAC 180  
 50 AGTCTTCTTA TTAATAGATT GCAATAATAC CCGCTGCTTT TTCAAATCAT TCTANTGGTC 240  
 GATTAATTGT CGACGCATCA TCTTGTCAT TCTTGAAATT TATTCGCTTT TCAACTTTCA 300

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CACGCTGACA TAC

373

## (2) INFORMATION FOR SEQ ID NO: 3067:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 311 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3067:

15	TTCAGAGTTC GGAACATAAG GCGCTACAAT GTTGTGTTGC CAGTAGTTGA CTGAATATGC	60
	GTTTGTAACA AGCTTTTTTC GATTCTAGTC AACAGTAATT AAATTTATGA TATGGGCAAT	120
	ACTTTGTAAT ACTAATATTA AATGGCGACT TTATTTCACT ATGTTATAAG AGTGCCATTT	180
20	GTTGATAAAG GnATACTAAA GGGTATCGTT TGAATTTTA GTAAC TAGAT ATGTTCCGGT	240
	ATAGACCGnA TTGTGGATAC GTAAATTTAA TGcATGAAT TTAAAATGA AAACATGACA	300
	TTAAATGAAT C	311

## (2) INFORMATION FOR SEQ ID NO: 3068:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 275 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3068:

35	TATGATTATC TAGTAAGTAA ATTGCTGACG CGCCGAATAC CGCAAAGAAT ATAAAGCAAA	60
	CTAACGCCGG GACAAAAAGT ACACCTAGGA ATAAATTCTT TAATCGTACG TCCTTTTGAC	120
40	ACACGTGCAA TAANATACCT ACAAATGGGT GCCCAGGnTA TCCACCATGG CCCAGTAAAA	180
	GATTGTCCAA TTTTGTAACC ATTGGGAATT TTTGACCACC TGTCGGAATG CGTAAACTCA	240
45	TACTTAAAGA AATTTGCATT ATAATTACCT AGACC	275

## (2) INFORMATION FOR SEQ ID NO: 3069:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 321 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

AAATGGGTTT TGTGACATTA ACGTCTACAA AAGATGGTTC AGAAGAAACA CACGAGGCTG 60  
 ATGGTGTATT CATCTATATT GGTATGAAAC CATTACAGC GCCATTTAAA GACTTAGGTA 120  
 5 TTACAAATGA TGTGGTTTAT ATTGTAACAA AAGATGATAT GACAACATCA GTACCAGGTA 180  
 TTTTTCAGC AGGAGATGTT CGCGACAAAG GTTTACGCCA AATTGTCACT GCTACTGGCG 240  
 ATGGTAGTAT TGCAGCnCAA GTGCAGGGAA TATATTGACA TTAACGATCA GCCTAAnTCC 300  
 10 GAGCnGATTA GATGTGAGCG G 321

## (2) INFORMATION FOR SEQ ID NO: 3070:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3070:

GTTTGACCTG CATATTTGAC AGTCATAACC TTTGTATCAC CATTATATTA ATATCAAAAT 60  
 25 CTTGGAACGT GTTATTTGAG nTGACATTTA ACTTCGCAGC ATTATCAGCT GTTGAACCTG 120  
 ATGTATACGT TCGCAACCC ATAActATCT GTGTTACAAT GCACCAAACG CACCTCCACC 180  
 30 AGCTACATTA GATGGGCAGC TTCGCCCTTG AGCTGATTGG TTTAGATGAT TGTGATACGA 240  
 TCCAATTTGA AGCCAAATnG TACTTAAGCA CAATCCTACT GCGGACCGTT TAACCCTGTT 300  
 TCACCTATAC ACTGnTGAAA GGCAAACCGT ACCACTCACC ATTTCCATGC CTTCCATATT 360  
 35 TGGTTACCAA ATTTACTTTT CCCnGAAAAA TGAAACTCTT 400

## (2) INFORMATION FOR SEQ ID NO: 3071:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3071:

TGGCCATTG TCATTGCATT TTTACCGTGG GTGTTGATTA TTATTCCTTA CTTACTATTT 60  
 50 AAATCGGATA CACTAAATAT TATTCATACG GGTGATAATA TTGCACGAGG TCTAGGTGTA 120  
 AGGTTAAnCA GAGAACGTTT AATATTATTC TTTATCGCAG TGATGTTATC ATCTGCTGCT 180  
 GTAGCATAGC AGGTTCAATT TCGTTTATCG GATTAATGGG TCCGCATATT GCCAnACGTA 240

## (2) INFORMATION FOR SEQ ID NO: 3072:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3072:

GACTCCCTGC AGGTCGACGT CTAGAGGATC CCCCCACAGC AATTCACCTA TACATGTAAC 60  
 AGTGTGAAAT AATAACGTCA CAACGGCATA ATACACATTG CAACGTCCCA ACAACATATC 120  
 ATAGAATCGT AACGGCATGA CATCAACACC AAACCTGGGC TATAACACCA TAACAGCGCA 180  
 ACGCCACATC ATAGGCACTA CATCAAGTCG CATCGTAGCA CCAGCACATC AAAGTAACAT 240  
 GGGCATCAAC ATCAAACCGG TCTATAACAC CATAACACCG GCAATGCCAC ATTCATAGGC 300  
 ACTACATCAA GTCGGCATC 319

## (2) INFORMATION FOR SEQ ID NO: 3073:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3073:

ATATACGCTT ATCAGCTGGA GCTCAATAGA TGGAGGATGA TTATGGGGCT ACCGGTTCTG 60  
 TCTATAGCAC TGGTCTATCA GCTATGTGGA TTACAATCGG TTTAACATTA GGTGCTTATA 120  
 TAAATTACTT TGTTGTTGCT CCTAGACTTC GTGTTTATAC CGAATTAGCT GGAGATGCAA 180  
 TTACATTACC AGATTTCTTT AAAAATCGTT TAAACGATAA AAATAATGTG TTAAAGATTA 240  
 TTTCTGGATT GATTATCGTA GTATTCTTTA CATTATATAC nn 282

## (2) INFORMATION FOR SEQ ID NO: 3074:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3074:



AATCGAnAAA TCATGGATGT ACTTGAATCA AATGCAAACA GCGAAGTGTh TTGAATTGCA 120  
 TGGTAGCGTT ATAGACGAGC CAGTAGAAAT TCAATCAATT AAAGTATATG TTCCTAACGA 180  
 5 TGATGAAGGT CGTACGACAA CTGTAATTGG TAATGCTTTC CCTGACTCAG AAGTTAAATG 240  
 CATTACACCA GCAGATATCA TkGCTTCAAT GAGTTACTTC TTTAACTTAT TAAGCGGtAT 300  
 TGGGtATACA GATGATATTG GACCATTaGG TAACCGTCGT TTACGTTcTG tAGGkGGaAT 360  
 10 TACTACmAAA CCaATTCCGT ATcGgTTTTAT CCAAGA 396

## (2) INFORMATION FOR SEQ ID NO: 3075:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 376 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3075:

ACCTACATTT GCAGTTGTCG GTGTATAACC GGCTGGTGTT GAAAACTCTA CACTATAAGT 60  
 25 TCCATTGCTT AAACCAAGTGA ACTGATATTT ACCATTTTCA TCTGTTGTCG TACGATCTAA 120  
 TTCTTTACCG TTACTATCTT TAAGAATGAC ATAAACACCT TTAATCCCTT TTTcATTGGC 180  
 ATCTTGTTTA CCATCTTTAT TTGTATCTCC CATAcATAGT CACCTAGATT ATATTChTTT 240  
 30 GGGCGCCATA GCAGTTGATG AGCATTcACA TTGAAAAACT ATTGACCACT ATATTAGTTT 300  
 GCAGTGCTAA GnATAACATT TCCATACGTG ACATACTGAT AGACTGTGAG TGATGTATGC 360  
 35 GCTGnTGCTC ATAACG 376

## (2) INFORMATION FOR SEQ ID NO: 3076:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3076:

TTACATCACC AATTAGACGT TATCCTGATT TAACAGTTCA TCGTTTAATC CGTAAGTATT 60  
 50 TAATTGAGAA ATCAATGGAT AACAAAGAAG TGAAGCGTTG GGAAGACAAA TTGCCTGAGT 120  
 TAGCTGAACA TACTTCTAAA CGTGAACGTC GTGCTATTGA GGCAGAACGT GATACTGATG 180  
 AATTGAAAAA AGCAGAATAT ATGATTCAAC ATATTGGTGA TGAATTTGAA GGTAAATGTCA 240

AAnGChGnGA TATACGTTTG AGGCGCAATG C

331

(2) INFORMATION FOR SEQ ID NO: 3077:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 345 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3077:

AATCATATGC ATCGATTTC	AGCAACAGCA ACCATTCATC	CTATGTCCCA TTAGCAAATT	60
TTTTGGATGA AACATGAATG	GCAAGATGTA TTTCAACGTA	CTGCTAATTT GCAGATATTA	120
AAACATACnT TTCTATCATT	ATTGATACAT ATATCATGAT	TATTCATGGC TTCCGCAACA	180
GGATGTTTAT TTAGAAACAT	TAGATTGGGA TGTTGAGGCA	TAGAACTGCT GGGTATTTCC	240
AAGGAAATGT TGCCGGAATT	ATTCCAACAA CTATTGATGT	AAGTATGAAA GAACGTATGC	300
AACATAATGG GCTAATAAAG	TACACCGTnT GTTAATGGTG	CnATG	345

(2) INFORMATION FOR SEQ ID NO: 3078:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3078:

GATTATCAAG CGATTGATCA	AGTATCATCA TTGTTGAAAG	AAAAATATGG CATTGCACAT	60
TCAACGTTGC AAATTGAAAA	CTTGCAATTG AATCCATTAG	ATGAGCCATA CTTGACAAA	120
TTAACATAAA TAAACATTG	TAGCGCCTAA AACATTAATC	TATGTCATAG GCGCACGTTT	180
CGTTTTATAC TTATGTTGCA	TCATTAAAT GATTTTCGTC	AATTTCTTTG ATGCTATCTA	240
CATCTAACAC GAGGTAACT	TGCGTTGATT TTGATAAAGT	GATCATAGCT TTTAGTACTT	300
GAGGATTTTT ATTGTTGCTG	TTACGAATGT GGTGATGTTT	AATGCGGGAC AGTAATTTAA	360
GTTGTTTTTT TACAATTGAG	AGTGTGATAT TTCGATTCGG		400

(2) INFORMATION FOR SEQ ID NO: 3079:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 319 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3079:

5 AAACGTTTAA TATACACTTT TACACGTCGC CTTCAATTGAA GCGAATTGCC ATAACCTTCA 60  
 CATTATATAT AGTTCTTTCC ATATAAATGT CCAAATTTTT AGAACAACGC AATAATAAC 120  
 CATCCACCTA ACTTATCAAA AATTAAAGTG GATGGTTTTT CATTTCATT TATATTTATA 180  
 10 TTAGTGTTAA TCCAATCATA GATTATCTA TATGCACTGC TCTATACaTT TCCTCaTTTA 240  
 ATTTGcyTTA CTTTCATTTA TATCATTATC AGAACACTTG GCGTGTCATC GntATTATTT 300  
 CGCATCTTTG AnACGTTTA 319

15 (2) INFORMATION FOR SEQ ID NO: 3080:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 285 base pairs  
 (B) TYPE: nucleic acid  
 20 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3080:

TCAAATGCAT CTAGGnCACA TTATTCTATT TGGGCATTCT TAGTGCTGTT CTTATTTGCG 60  
 GCTTTAACGT CATCTATTTT TTTATTAGAA TTAAATGTTT CTAAC TTCAC GAAGAATGAC 120  
 30 AATACAAAAC GTAAAAAAGT CGCAGTGATC GGTAGTATTT TAGTATTTAT CATTAGTATT 180  
 CCAGCAACCT TATCnTTTGG TATCCTAAAA GATGTAAGAT CGGTGCGGGA ACGATTTTTG 240  
 ATAATAAGGA TTCCACCGTT CGAATGTAAT GAAGCCATAA GCGGG 285

35 (2) INFORMATION FOR SEQ ID NO: 3081:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 40 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3081:

ATCATAGCGT TTCTCCTAAA AATTACGATT AATCAAAGTA TGCCATTATT TAACTTTAGT 60  
 TTCTTCAGAA TTATTTGCCC CATTATCATG TTTTCTTCT TTATTAACAG CATTTTTATC 120  
 50 ATTTTAAACA AGATACAATT TACCAATTAA TGGGCGGTGT GCGTGCTGGT ATGGGTTATA 180  
 CTGGTTCACA CGATTTAAGA GAATTACGCG AAGAAGCACA ATTTACACGT ATGGGTCCTG 240

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CATTCTAATT AAGATAAAGG AGAACGACAA ATATGGGAAA TGGCAAAGGA CCAAGAGTTA 360  
 ATCCTTGTCT TAGGACTTTG GTAGGCCATT ACACCCATTA 400

(2) INFORMATION FOR SEQ ID NO: 3082:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 248 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3082:

TGAATTTGCT CCAAATAAAA ATACAATTGC CATTAAAATC ACCAGATATT ACAAGTGGCA 60  
 ACATGTTAGA AACACCGTTC ATTAAGTGTT TATAGAATGC TTTACCTGGG CTTATTTCTT 120  
 GACTGTCATT TGAGTTACCT GGCAACAAAA GGTTTACGAC TTGTATCTAA TGAATACCAT 180  
 CTGCTACTGG TnCTTCTACG ACATTTTAC CATCGAnCG GTCCGTCTCA ACATGTACAT 240  
 CAGCAGCA 248

(2) INFORMATION FOR SEQ ID NO: 3083:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 368 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3083:

TACTAAAGGT TTAAATCAAA AATGGCTAGG TATCGTATTT GCGATTTTAA TTACAATTAC 60  
 ATTTGCATTT GIATTTAACA CAGTGCAATC TAATACAATT GCGGAGTCGT TAAATACGCA 120  
 ATATAATATT AGTCCAGTAA TCACAGGTAT TATTTTAGCA ATCGTAACAG CTATTATTAT 180  
 ATTTGGTGGT GTACGTAGTA TTGCTACGTA TCCTCGTTAA TGTACCGATA TGGCTATCAT 240  
 TACATGGTAT GGTTTAGTAA TAATGCTATT AATTTAGACC AATTGTCCnA TGATAGGACG 300  
 ATATAAAAGG CATTGGnACG ACAAGnACTG GTGCGCTGAG gGCTCGGTCT CCAGGACAAC 360  
 GGGGTATC 368

(2) INFORMATION FOR SEQ ID NO: 3084:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 256 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3084:

5 TTGGACTTTA TAAAGTTACT AAGTTGTAGA TTATCCTGGT AAAGAAGATA TTGCGGTTGT 60  
 ACAAGTTGAA GAAAAATCAA CACAACCAAA AGGTAGAAAA TTCAAAGATT TCACTAGTAA 120  
 ATTTAATATA GCATCAGAAG CTAAAGAAAA TGAACCTATA TCAGTCATTG GTTATCCAAA 180  
 10 TCCTAATGGA ATAAC TACAA ATGTATGAAT CAACTGGTAA AGTATTATCA GTGAATGGGA 240  
 TATAGTGnAT CGGATn 256

## (2) INFORMATION FOR SEQ ID NO: 3085:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 311 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 20 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3085:

25 ATATGCATAT GCTTCTTTAG GTGAACGAAT ATCTGGTTCA GATACGATTT CAATTAGCGG 60  
 TGTACCTTGA CGGTTCAAGT CAACTAATGA ATACTCCACC TTTATGTGTT GACTTACCAG 120  
 CATCTTCTTC CATGTGAAGA CGAGTAATAC CGATTGnTT TGTTCACCG TCGACTTCGA 180  
 30 TATCGATATA TCCCATTTCA CCAATTGGGT TGATCAATTG AGAATTTGAT AGCTTTGGGA 240  
 TATCGGGATA GAATAGTCTA CGGTCAACTA GATCnGGTGC GAnTCCATAT TTAGTGCCAT 300  
 GCAGCACGCA T 311

## (2) INFORMATION FOR SEQ ID NO: 3086:

35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 271 base pairs  
 (B) TYPE: nucleic acid  
 40 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3086:

45 ATGTAAATGA TCATCCTTCA TAATAACAAC GATTACTGAT CTTGATCATG ATTTTGAACA 60  
 ATAACAACTG CTTTATTAAT ACCTTGATA CGCTCGAGnC ATGCCAACCT CTGACAACTC 120  
 50 AATCCTAAAC CCTCGAATCT TAAC TTGTTT GTCCTTTT CGA TATAAATAAT CTATGTTGCC 180  
 ATCGGGTAAC AAACGAACGA TATCACCCT TCCTATACAT CAGCTGATTT ATATTTGAAT 240

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## (2) INFORMATION FOR SEQ ID NO: 3087:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3087:

GTAAAGATTT CAATTCATCA TCTTTAAATA AACTTAATGG TAATTnGTTA TACChAATAA 60  
 AGCCTTCTGG ACACTTCCTT TAGACCGACG ACCGTCTTAG CTAATGTCGA TTTCCCTGAC 120  
 CCTGATTCAC CGACAATGCC TAATGTTTCG CCTTTTCTAA TAGCCAAGTT AATATCATAA 180  
 CTGCTCGGTA TGGGCTGCCC CTCGGTGATG TGTAATCCAC GCTCCACGCG ATCGATTTTA 240  
 ATAAAATATC ATGGTT 256

## (2) INFORMATION FOR SEQ ID NO: 3088:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3088:

AAGGTTATTT GAATGATCAA GGTATCCACA AAAGAGGTGC TGAAATAGAT CGACTCGTTA 60  
 AAGGATGTAC AGGTGTTAAA CGTACAACTG GACAGCATCC AGGGGGTATT ATTGTAGTAC 120  
 CTGATTACAT GGATATTTAT GATTTTACGC CGATACAATA TCCTGCCGAT GATCAAAATT 180  
 CAGCATGGAT GACGACACAT TTGATTTCCC TTCCTnTCAT GATATGTATT AAAACCTGAT 240  
 AAACnTGGAC ACGTGATCCC ACCATGATCG ATGCCTCCAG ATTATCAGGA ATGATCCAAA 300  
 ACCATACCTG AGATGTAAGA GTATCAGTAT TAGACnC 337

## (2) INFORMATION FOR SEQ ID NO: 3089:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3089:

AAACATTACT TTACGCTATC AATGGTGGTA AAGATGAAAA TCTGGTGCAC AAGTTGGTCC 120  
 AAACCTCGAA GGTATTAAACA GCGAAGTATT AGAATATGCC GAAATTCAAG AATTTGATCA 180  
 5 AATGATGGAT TGGCCTAGCA GGTGTTTACA TTAATTCATT AAATGTATnA CTACATGCAC 240  
 GATAATACAG CTATGACGAT TGAATGGATT ACATGTACAG AATTGTCCGn CCATGGCACA 300  
 GGA 303

10 (2) INFORMATION FOR SEQ ID NO: 3090:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 15 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3090:

CTTTCGTTAA AGGGGCATAT TCATATAATG GATGGTCATT AATAATAATT CCTGCCGCAT 60  
 GTGTAGATGT ATGTCTTGGT AAACCTTCTA ACTTTTACA AATACTGAAC CAGCGTTCAT 120  
 25 GTCGATGGTT TCGATGTACA AACTCTTTAA AATCGTCAAT TTGATATGCT TCATCAAGTG 180  
 TAATTCCTAA TKTATGTGGG ATTAACTTG GAAATTTTAT TLAATGTAAC TTCATCAAAC 240  
 CCCATAATTC TTCCAACATC TCTAGCAACT GCTCTTGCAA GCAGATGACC GAAAGTCACA 300  
 30 ATTCCAGATA CATGTAGCTC GCCATATTTT TCTTGGACGT ACTGAATGGA CCCTTTCTCG 360  
 GnGTGTATCT GCAAGGTCAA TTTTCATTnT CAGGCATGGT 400

35 (2) INFORMATION FOR SEQ ID NO: 3091:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 340 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3091:

45 TTGTTTTTTC ACGTTCAATn ATTATCTTCA ACTTGTGACT ACAGATTTTA AAATGGAATT 60  
 TACAAGTATC TTCTTCAATA TTTTGCATCA TGATATCAAA TAATTCATGA CCTTCATTTT 120  
 GATAGTCACG TAATGGATTT TGTGTGTCAT AAGAACGTAA GTGAATACCT TGACGTAATT 180  
 50 GGATCCATGT GTCGATATGG ATCAGTCCAA TGGCTATCAA TAGAACGAGG TAAATCATA 240  
 CGCTCAAACC CCATCCATTG GnTCCTCTAA GATACCTTTT GACCTTGGAT AGCnGCTCAA 300

## (2) INFORMATION FOR SEQ ID NO: 3092:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3092:

CGACACCTCA ATAATCATAT CGTAATGTTT AACTTTTCCT GATTAAATG TAATTTTCATT 60  
 TCCATTGATA GCATTAATTT CCTCATTTAA ACGGTATGGA ATCTCCCGCT TATCTAATTC 120  
 ATCAAGTATA GGTGATTCA GTCGGCATCC ATAATTTATT TATCTTATCA GATCGATGAA 180  
 TAAAGTAGGG TGTAACCAC GTTCATAAA GATTTCAAGG AACTCCAATG GAACATAACC 240  
 TGCACCTACC ACCAATACTT TATCCACTTG GATTGGCTTG GAGGAATGGT CGGATAGGCA 300  
 TCCAGGGCCT CCAAATTCC nAGGGGAAAn GGTAATATCC ACCTTCCAAG GCCAAGGGCC 360  
 AATTGGCACC TGGCCACCCA GGGnCTTAAA AAGGGGTAA 400

## (2) INFORMATION FOR SEQ ID NO: 3093:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3093:

TTATACCCGn CAAATTCATA AATATAGTnC CTTTTCAATA GATTGATATG TATGTCTAAA 60  
 TGTATCGATT AACTTTGCTA ATGCTGCTTC ATCTAATGGT CGGTCTGCTA ATTTTAAAAA 120  
 TGTATTCTTC AATAGGTATT CCCATATAAT GCGTTATTTC TTTAGATGAT GGTTCCGTTA 180  
 AGCCACATGC TTAAATGCA CTTTGTGTG CTACTTCACC ACATTTTTTC GTGTCTGCCA 240  
 ACGTACCATC AA 252

## (2) INFORMATION FOR SEQ ID NO: 3094:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear



AATCTATTAA TAATGAAGAA AAAATTGTAC TAGCACGTAG ACGGTTAATA AAGTTCGATA 60  
 AAGATATCAG TATTCCATAT ATTCTAAAGC AAGCATATTC TAAAGAAAAA AACAGTTATA 120  
 5 TATTCTTGTT AGAATCACAA GATTCTATAT TCTTTTCACA AACACCTGnn CAATTAATAA 180  
 AGGTCAATAA TAAAATCTAT CGACTAAAGC TGTGCAGGTC AATTAAACGG TCACAAGTGA 240  
 GGCCGAGGTA CAAAAAATGT TGAGCATTTT AAAGTATAAA CTTATCGACA CGnTTGTGTG 300  
 10 CAGTTTTTCAT GTTT 314

## (2) INFORMATION FOR SEQ ID NO: 3095:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 332 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3095:

GGTGAGGCGG CATTGAGAAA AAATGCTGAA GTAATCGAAG CTGTATCGCA GTCTTGTTTG 60  
 25 ACAACAGGAT TTTGTTTATG GTGCCAATTA GCTTTTTCAA CGTATTTAGA AAATGCCACG 120  
 CAGCCACATT TAAATAATGA CTTACAACAG CAATTGTTAT CTGGAGAAAT ATTAGGTGCT 180  
 ACCGGATTGT CTAATCCCGA TGAAGTCATT TAATGGATTT AGAAnAAGTT GGACCCTTTG 240  
 30 AAACACCACC TTAATGTTGG ATGGGACCAA TTGGGTGGTC CAGTGGGAnC GTAATGCCCA 300  
 GCTGTAAAGT nATAATCCAA GGAAAGACCC AT 332

35 (2) INFORMATION FOR SEQ ID NO: 3096:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 40 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3096:

45 TTTATGCATA CGCGCACTCA TCACACTACC GACAACAACA TCATCTTTTC GAGCATATCT 60  
 ACTTAACAAC GTCATGACCA CACTCATAAA GAACATAAAA TCAGTAATTT GATGCTTTTC 120  
 TACATACTTT TGAAGTAGCT GTCTCATTTG TTGATTCATG TAAATGACAT CATGCTCCAT 180  
 50 TTGTCGGTTT AATAATTGGT CTAACATAnT CTGTCGGGTA AGCCTAAAAT AGGGTACTTC 240  
 ATCCTTGAAT TGAGGATACC CATATTGGTC CTAAGGTTTCG GTCCATATCC ACGGATGGCG 300

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ATTTAAGGTT GGATAAAGGT GCCGTTAAGG ATCCAATTCC

400

(2) INFORMATION FOR SEQ ID NO: 3097:

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- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 265 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3097:

15

ACTCTGGTCC TTCTGCATAA CTGCCGTAAA TAATTCACCT TCATCACACG CTGTACCTAC 60  
 CAATAATCCC nCAGGATATA CGTGGAATTC GAGGTGTACG GTAGAAATAC TTCACCAATG 120  
 ATGCACTTAC AATTTTAAAT AGATTTTAA GACCTTGTG GTTTTGTACA ATTAATGTGA 180  
 CATGACTAGG TCTTGCACGT TTATATGCAT CTTCACTACT GAGTTTMTTG GTTGATTnC 240  
 GTTATGATTT AATACGGCTA ATTCT 265

(2) INFORMATION FOR SEQ ID NO: 3098:

25

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 321 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3098:

35

CTAATGTATC AGTTTGGCAT GAATCTTTT GCATCTTTCA ATAATTGTTG TGATCTTTTT 60  
 TAGTCACATC ATCAATTTTC TTATCTTCGT ATAATGCTTT TTCAATCTTA TGATATCCTG 120  
 ACCATTCTTT TTCCTTTTTC TCTTCTTTCA TATCTGCAAG CGGGCATCCA ATTTTAGGAT 180  
 CCTAAATCTC CCAAATGCTT CTGAACTGGT CAGAGCGTCA TAATACATAC GACTTTTGGA 240  
 TATACGCTTT TnCTTGGGCA TACATTATTT CAATCGTTTA CAAATTTTTC TGACCTTTTA 300  
 AAATCATTTnA CTGTCAnCAG A 321

45

(2) INFORMATION FOR SEQ ID NO: 3099:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 276 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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ATCCGCAATC TGAGAAACAT CATCTTCGAG TTGTTGGAGG GTTCCAATTT TCAAGTCATA 60  
 AATCAGATGA TGAATGGCGA GAGTTTGGAC TAAATCATTT TGTATTACCT GAAGTTTTAA 120  
 5 TTTCAACTGA TAATAATGGG ACATTTTTAA CTTATACAGT TAAAAGGGAA AGTTTACTG 180  
 TTGAGGCATT GAACGATTTA ATGGATTGTT CAACAATATA TCGGACATAG AGTGGACGAC 240  
 CAATGGGGGA ATACCAGAAT GAGATATTAT AAAACA 276

(2) INFORMATION FOR SEQ ID NO: 3100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3100:

GTCATTTGAT GACAATGGTA TTAGACCAAG TACCAACCGT TCTGTGCCAC nTAAAACGTT 60  
 GTTAATAACT TGCCGGGCTT CACACTAATC AATGGTGGCA AAGTAGGGGT GTTTAGTCAT 120  
 25 GCAAnGTTAA GAACGAGCAT GTTTGATTCA GGAGATAATA AGAACTATCA AGCACAAGGA 180  
 AATGTAATTG CATTAGGTCG TATACATGGA ACTGATACGA ATGACCATGG CGATTTT 237

(2) INFORMATION FOR SEQ ID NO: 3101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3101:

nCGATATAAC AAGTTTGTTA GACTTAAAGG TGGCGATCCA GCGATATTTG GTCGTGTGCA 60  
 AGAAGAAGTC GACATACTAA ATGAACATCA TATTGCGTTT GAAATTGTAC CAGGGGTGAC 120  
 ATCAGCGAGC GChAGTTTGG CTACTATGCA GACAGGTTTG ACAATGCGTA CAGTTGCTAA 180  
 45 AAGTGTGGAC ATTTTCTACA GGTCACTTTT AAAGATTCAG AAGAAAATGA AGTGGGATGG 240  
 TCCATTCCTT AAGT 254

(2) INFORMATION FOR SEQ ID NO: 3102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3102:

5 CAATCACTCA TGTAGTAATT GATACCTAAG AAGTCGTTTA AATCTTTGGC TGCATCTAAA 60  
 ATGGCATAAT CTTCAThTGT AATGTTTAAT TTACCGCCAn TAACAGATAA GATATGTTGC 120  
 ACACCTTCCA TCGTTTCACG AGTAATACTT ACCTAAATAT GTTGCACTCA AGATGAATTT 180  
 10 ATTATGGATG GATATCTTCT AAATTCTGCT GCACGGGACA TCTTCAGGAT TTGGATGGTT 240

## (2) INFORMATION FOR SEQ ID NO: 3103:

## (i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 328 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3103:

20 GTTGTAACCT TCAATTGTTT AAATAAATAA CACATATCAT TGGAGGTGAA TTGATATGCC 60  
 AGATTCAATC ACAATTATAG ATGAAAACAA AGTGGTTGAT GTTGTATTAA TTGCAGGTAG 120  
 25 AATTTTACTT GAATCAGGTG CTGARACATA TCGAGTTGAA GATACAATGA ACCGTATCGC 180  
 ACATAGTTAT GGTCTTCATA ATACATATAG TTTTGTCACT TCAACTGCAA TTATTTTTTC 240  
 ATTAACGAT CGAACAAGTA CAAGATTAAT TCGTTACAAG AGCGTACAAC AGATTTAGGG 300  
 30 AANGTGCGAA TAAGCGGGGn AATTCTTC 328

## (2) INFORMATION FOR SEQ ID NO: 3104:

## (i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 265 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3104:

40 TTTTGCTTTG TCGCTAATA ATCTAATGTT CGTGGAACCG nAACCAGAGA TATTACAAAT 60  
 45 ACATCATCGA CTAATCGCAG GTGTCGTTGA TTCTCCAACA ACATGTGCCT GTTTGCCGAG 120  
 CTGATTTAAG GCGGCATTGC AAACTATTC GCCACGAATC CTGAACGTCC TTTGCCAGCT 180  
 ACAAATATAT GTTCAGCATG TAGTATTTTG GATGCAAAGT TGAAAACCTCA TCCGCTTCAA 240  
 50 CATGTGACAA AGTCACTTTA ATCnA 265

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 243 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3105:

ACTAGTAGAG TATCTAATGG TGATTTAATC ATTATTACTG CTGGTGTACC AACTGGTGAA 60  
 ACTGGAACTA CTAATATGAT GAAAATCCAC CTAnTTGGTG ACGAAATTGC TAATGGTCAA 120  
 nGTATTGGAC GTGGATCACT TGTTGGTACT ACATTATTGC TGAAACTGTT AAAGATTTAG 180  
 AAGGTAAAGA TTTATCTGAC AAATTGATCG TTACTAACTC AATCGATGAA ACGTTTGTGA 240  
 CCT 243

(2) INFORMATION FOR SEQ ID NO: 3106:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 234 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3106:

CTATTGCGTT TGGGTAAATC TAAAGCAGGC GTAnATTATC AAAGTTTGGG ATATGCAACC 60  
 AGCACACTTA TTCTTTATGA TTGCAGCGCC AGAAGTGGnG CCCAAACACA TCTAGATGCT 120  
 TTACTAAGTT GTCTGGTATT TTAATGGATG AAAATGTACG TGAGAAATTA TTACATGCTT 180  
 CATCACCTGG AAGAAGTACT AGCGATCATA GATGAGGCTG GATGATGAAG TGGA 234

(2) INFORMATION FOR SEQ ID NO: 3107:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 227 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3107:

TTTTGAAGCG GCATAATCAT GAAGAATAGG ACTAGGATTA TAACCTTGTA CAGATGATGT 60  
 CGTTGTAATT GACGCACCCG GTTTTAAATA TTCCAATGAC TTTTGAAC GTCCAAAATA 120  
 GCGGnTAGAn ATTCTTTCA AATGTTTCTG TAAATGCCTC AGTTGTAAAT CCATGAATAT 180

## (2) INFORMATION FOR SEQ ID NO: 3108:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3108:

CTTTAAGTTA CGTTCGGCTT TGATTAAAGT AAAACGTGGT ACTGTTTCCT ATGACAAGAG 60  
 TCTAATTGGA TACAAATGTAA ACAAATGGT GATTGTAT TATAGATAAT AAACATTCGn 120  
 TATACATTCA ACATATCGAT GACCACTTGG ATTAAGCAAC GTAATATCAT TCGTACTGCT 180  
 CAAGAAATGA CAAACGAAAT ACGAGAAAAT TTTGAGTCAT ACACGTCATT TAGAATGAAT 240  
 AGTATTATGC AAGTACT 257

## (2) INFORMATION FOR SEQ ID NO: 3109:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3109:

CTTAAAGCCA AGTCGATCTG CTAATTTTGC AAGTGTCACT GAATCTTGCA ATGCCTTTTG 60  
 TGCATCCTTA CCTTCATCTA TTAAGGCATA GTCTAATACG CTTAATTTAA CCAATCCGTC 120  
 ATCTCCAAAC TTATCCTGTC ATGTCAAACC GACATAACAT TTGTAGCGTT CTTAATACCA 180  
 TTCCCTCTGC ATATACCCAC GTATATGATA ACGTnTTTCA nTTAACT 227

## (2) INFORMATION FOR SEQ ID NO: 3110:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3110:

TTTCTTCATC GTTTGTGAGA AAGAGGTATT TTAAATTGGG AAAnCAGGTA AAAAGGATGG 60  
 AAGTACATAA AAAGAGCAAT GCTTGGGCAT TATTCCnCTT GTTATTATTT GTGGCGTTGT 120

GATAACGTAA TTGTGCGTTA TTAATGAATC GAAAAGAATC ATTGCTAAAA AGTGAGTCTC 240  
 CGAAAGGCGG CCTTCAACTG TTAAGAGTGA TTTATTGCAG GCTTCAATCG CGAAATGGTG 300  
 5 CnAAGCGCGT ATTAGCACTA GCCGAA 326

## (2) INFORMATION FOR SEQ ID NO: 3111:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3111:

CTACGGCGCC TTGCATCTTT CCCAACAATT AACCCCAACT CTATTAGCAC AGATTTATCA 60  
 20 ATTGATTCAT AAGCTTCATC AAAGGGTGAA CTAACATGCA TTAACGCTTC TTTAATATCA 120  
 ATTAAGTCGG CATGTTCAAC ACCAATTTTC CCTTTTTTAT TTTTAGCTTT TTCTCTATCA 180  
 ATATACGCAT GTTTAACACC TTTGACATGT TCAGTAAATT GTGACTTCCT NAATTTTTTA 240  
 25 TCCTCCCTTG GTGnnGGGGG GGGGGGGGGG GGGGGGGGGG GGGGGGGGGG GGGGGGGGGG 300

## (2) INFORMATION FOR SEQ ID NO: 3112:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3112:

TTATTGTTAA CACAAGGnTT CGAACAAGGT TGGTTTAGTA CATTTTCAAT CATTTGTCTG 60  
 40 AGCATTTTTA TCATCACTAC GTTGATATTC ATCATCATCG AACGTCGACA TGAAGTACCT 120  
 TTTATTGATT TCTCAGTATT ACGCAACCGT CCGTTCATTG GTGCATTTTT AAATAACTTT 180  
 GTTTTAAATA GCGGTCTAGC GTAACAGGGT CTTTCATATA TGCTCAACAC ACCTGGTTTTA 240  
 45 TCGCGCGCAA TCGGACTGTT ACATGCCAAT GCCATGGGCG TTCGAGATCG TTAGTGAAAG 300  
 CACATAGTTC GGGCAATGAG CCACATGGTC GTGTCCGTCA CGCACACATA TAGCAGCT 358

## (2) INFORMATION FOR SEQ ID NO: 3113:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3113:

TCGGTCTTGA AAACCGACAG GGGACTTAAC GGCTCGCGGG GGTTCGAATC CCTCTTCCTC 60  
 5 CGCCATCAAT ATTTATATTA AATTCTATAT ATAATGAAGG TAAGTGCTCA AATTTTGAGT 120  
 ATTTACCTTT TTTATTTGTC TTTGAATGGC TCGTAATTTT TGATAATAGA AATGATAAGG 180  
 CATTGAGATT GGAAGGGCAT TTGGCTTGTG CAATATACAT AGCAAAATGT CGTTGTTGTT 240  
 10 TTGTGATAGA T 251

## (2) INFORMATION FOR SEQ ID NO: 3114:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6591 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3114:

TTTAAGTGAA TTnCTTTGGG TTACAGAAWT TTCAACAACT TTAAAGCACG TATAATGATG 60  
 25 ATTTTCAGCT TGTACAAAGG AGAAAAAAG AAGACAACCA AGCCCAATAA TGGACTGGCC 120  
 GCCTAATAAT AAAAActCTA AAAGTTGTAT TTTAAAAATA GTTCTTTAAA TTATATACCC 180  
 ACCACATTTG GTGGAGaACC GTTAAACAAT GCATAGTTGC TTAACCTCCA ATATTGAACT 240  
 30 CATCATTACA ATTTGACATA GAGTCTATTA AAGCGTGTGC CATTGAGTC CACTTTTATT 300  
 TGTATTGTAT AGAGAGAAAT AAAAGAAAC CTGTGTTTAC AAGGTTTCTA ATACGTTATG 360  
 TTATGTAAAT AACAGTTAAT TATACCGGTG GTCGGGGTCG AACCGACACT CCACAAGTGG 420  
 35 AACGgGATTT TGAGTCCCGC GCGTCTGCCA ATTCCGCCAC ACCGGCTTAA TGGTAAACAA 480  
 AAAACTTCCC TTTGGAAGCA ATTATGGAGC GGAAGATAGG ATTTACACCT ATACCTCGTT 540  
 CCGGGAAGGA ACGTGtTCTA AAAGTTGAAC TACTCCCGCA AATATTAAAT TATGGAGCGG 600  
 40 AAGATAGGAT TTACACCTAT ACCTCATTCC AGGAAGGAAT GTATTCTAAG AGTTGAAATA 660  
 CTCCCGCATT ATTATTAAAT TATGGAGCGG AAGATAGGAT TTGCACCTAT ACCTCGTTCC 720  
 45 GGGGAAGGAAC GTGTTCTAAA AGTTGAACTA CTCCCGCATA AACCTGGAGG CGGCAACCGG 780  
 ATTTGAACCG GTGATAAAGG TTTTGCAGAC CTCTGCCTTA CCACTTGGCT ATGCCGCCAA 840  
 TAACTGGGCT AGCTGGATTG GAACCAACGA GTGACGGAGT CAAAGTCCGT TGCCTTACCG 900  
 50 CTTGGCTATA GCCCATTAAAT AATAAGGGCG GCTGAAGGGG ATCGAACCCT CGAATGTCCG 960



	CGAACCCACA CCAAAGGTTT TGGAGACCTC TATTCTACCG TTGAACTATG CCCCTATTAA	1080
	AAATAATAAA TGGAGGGGGG CAGATTCGAA CTGCCGAACC CGAAGGAGCG GATTTACAGT	1140
5	CCGCCGCGTT TAGCCACTTC GCTACCCCTC CATAAATGGT GCCGGCCAGA GGACTTGAAC	1200
	CCCCAACCTA CTGATTACAA GTCAGTTGCT CTACCAATTG AGCTAGGCCG GCTAAGAAAT	1260
	GGTTCAGGAC AGAGTCGAAC TGCCGACACA TGGAGCTTCA ATCCATTGCT CTACCAACTG	1320
10	AGCTACTGAA CCATAATAAA AATGTAATGA TGGCGGTCTC GACGGGAATC GAACCCGCGA	1380
	TCTCCTGCGT GACAGGCAGG CGTGTTAACC GCTACACTAC GAGACCTATA AAATATTGCG	1440
15	GGAGGCGGAT TTGAACCACC GACCTTCGGG TTATGAGCCC GACGAGCTAC CGAACTGCTC	1500
	CATCCCGCGA TAATAAAAAA TAATGGCGGA GGAAGAGGGA TTCGAACCCC CGCGGCCCGT	1560
	TAAGGCCCTG TCGGTTTTCA AGACCGATCC CTTGAGCCGG ACTTGCGTAT TCCTCCATTA	1620
20	TTATAGGTAA ATCGCTATTA ATTATAAAAT TAAATGGCGG TCTCGACGGG AATCGAACCC	1680
	GCGATCTCCT GCGTGACAGG CAGGCGTGTT AACCCTACA CTACGAGACC ATTAGTAAAA	1740
	CGGAGGAAGA GGGATTCGAA CCCCCGCGAG CCGTTAAGCC CCTGTCGGTT TTCAAGACCG	1800
25	ATCCCTTCAG CCGGACTTGG GTATTCTCTC AAAATTATAT GgAaCTGCAG GACTCGAACC	1860
	TGCGACCGAA CGGTTATGAG CCGTTAGCTC TAACCAACTG AGCTAAAGGT CCTAAATATA	1920
	ATTTTACAAC TAATAAATAG TGGCGGTGGA GGGGATCGAA CCCCCGACCT CACGGGTATG	1980
30	AACCGTACGC TCTAGCCAGC TGAGCTACAC CGCCTTATAT AGTTTGTAAG TAATATGGTG	2040
	GAGACTAGCG GGATCGAACC GCTGACCTCC TGCGTGCAA GCAGGCGCTC TCCCAGCTGA	2100
35	GCTAAGCCCC CATAATAATT ACAGTATATC GGAAGACAG GATTGGAACC TGCGACCCCT	2160
	TGGTCCCAA CCAAGTGCTC TACCAAGCTG AGCTACTTCC CGTATAATTA ACGCGCCCGA	2220
	TAGGAGTCGA ACCCATAACC TCTTGATCCG TAGTCAAACG CTCTATCCAA TTGAGCTACG	2280
40	GGCGCATATG TTTTATTGA AAATGGTGCC GAGGACCGGA ATCGAACCGG TACGgTGATC	2340
	ACTCACCGCA GGATTTTAAG TCCTGTGCGT CTGCCAGTTC CGCCACCCCG GCACTATAAA	2400
	AATGGAGCAG AAGACGGGAT TCGAACCCGC GACCCCAACC TTGGCAAGGT TGTATTCTAC	2460
45	CGCTGAACCTA CTTCTGCATA TGCGGGTGAA GGGAGTCGAA CCCCCACgCC GTAAGGCGCT	2520
	aGATCCTAAG TCTAGTGCGT CTGCCAATTC CGCCACACCC GCAAATGGTG AGCCATAGAG	2580
	GATTGGAACC TCTGACCCTC TGATTAAAAG TCAGATGCTC TACCAACTGA GCTAATGGCT	2640
50	CTTCCATGGT GCCGGCCAGA GGAATTGAAC CCCCCAACCTA CTGATTACAA GTCAGTTGCT	2700
	CTACCAATTG AGCTAGGCCG GCAATATGTA AGAATAAATG GTGGAGAATG ACGGGTTCGA	2760
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	AAACTGCCTG	GCAACGTTCT	ACTCTAGCGG	AACGTAAGTT	CGACTACCAT	CGACGCTAAG	2880
	GAGCTTAACT	TCTGTGTTCC	GCATGGGAAC	AGGTGTGACC	TCCTTGCTAT	AGTCACCAGA	2940
5	CATATGAATG	TAATTTATAC	ATTCAAAACT	AGATAGTAAG	TAAAAGtGnA	TTTTgctCGC	3000
	AAAACATTTA	TTTTGATTAA	GTCTTCGATC	GATTAGTATT	CGTCAGCTCC	aCATGTCACC	3060
	ATGCTTCCAC	CTCGAACCTA	TTAACCTCAT	CATCTTTGAG	GGATCTTATA	ACCGAAGTTG	3120
10	GGAAATCTCA	TCTTGAGGGG	GGCTTCATGC	TtnAgGATtT	TCAGCACTTA	TCCCGTCCAC	3180
	ACATAGCTAC	CCAGCTTATG	CnTTGGCACG	ACAACtGGTA	CACCAGAGGT	ATGTCCATCC	3240
	CGGTCTCTC	GTAATAAGGA	CAGCTCCTCT	CAAATTTCT	ACGCCCACGA	CGGATAGGGA	3300
15	cCGAACTTcT	aCGACGTTCT	GAACCCAGnC	sTGTACCGCT	TtaATGGGCG	AACAGCCCAA	3360
	CCCTTGGGAC	CGACTACAGC	CCCAGGATGC	GATGAGCCGA	CATCGAGGTG	CCAAACCTCC	3420
20	CCGTCGATGT	GAACCTTGG	GGGAGATAAG	CCTGTTATCC	CCGGGGTAGC	TTTTATCCGT	3480
	TGAGCGATGG	CCCTTCCATG	CGGAACCACC	GGATCACTAA	GTCCGTCTTT	CGACCCTGCT	3540
	CGACTTGTAG	GTCTCGCAGT	CAAGCTCCCT	TATGCCTTTA	CACTCTATGA	ATGATTTCCA	3600
25	ACCATTCTGA	GGGAACCTTT	GAGCGCCTCC	GTTACCTTTT	AGGAGGCGAC	CGCCCCAGTC	3660
	AAACTGCCCG	CCTGACACTG	TCTCCCACCA	CGATAAGTGG	TGCGGGTTAG	AAAGCCAACA	3720
	CAGCTAGGGT	AGTATCCAC	CAGCGCCTCC	ACGTAAGcTA	GCGCTCACGT	TTCAAAGGCT	3780
30	CCTACCTATC	CTGTACAAGC	TGTGCCGAAT	TTCAATATCA	GGCTACAGTA	AAGCTCCACG	3840
	GGGTCTTTCC	GTCCTGTCGC	GGGTAACCTG	CATCTTCACA	GGTACTATGA	TTTCACCGAG	3900
35	TCTCTCGTTG	AGACAGTGCC	CAAATCGTTA	CGCCTTTCTG	GCGGGTCGGA	ACTTACCCGA	3960
	CAAGGAATTT	CGCTACCTTA	GGACCGTTAT	AGTTACGGCC	GCCGTTTACT	GGGGCTTCGA	4020
	TTCGTAGCTT	CGCAGAAncT	ArCcACTCCT	CTTAACCTTC	CAGCACCGGG	CAGGCGTCag	4080
40	cCctATACAT	CACCTTACGG	TTTAGCAGAG	ACCTGTGTTT	TTGATAAACA	GTCGCTTGGG	4140
	CCTATTCACT	GCGGCTCTTC	TGGGCGTTAA	CCCTAAAGAG	CACCCCTTCT	CCCGAAGTTA	4200
	CGGGGTCATT	TTGCCGAGTT	CCTTAACGAG	AGTTCGCTCG	CTCACCTTAG	AATTCTCATC	4260
45	TTGACTACCT	GTGTCGGTTT	GCGGTACGGG	CACCTATTTT	CTATCTAGAG	GCTTTTCTCG	4320
	GCAGTGTGAA	ATCAACGACT	CGAAGACACA	ATGTCTTCTC	CCCATCACAG	CTCAGCCTTA	4380
50	ACGAGTACCG	GATTTGCCTA	ATACTCAGCC	TTACTGCTTA	GACGTGCAAT	CCAATCGCAC	4440
	GCTTCGCCTA	TCCTACTGCG	TCCCCCATC	GATTAAAACG	ATTATAGGTG	GTACAGGAAT	4500
	ATCAACCTGT	TATCCATCGC	CTACGCCTGT	CGGCCTCAGC	TTAGGACCCG	ACTAACCCAG	4560

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	TTCGCTACTC ACACCGGCAT TCTCACTTCT AAGCGCTCCA CATGTCCTTA CGATCATGCT	4680
	TCAACGCCCT TAGAACGCTC TCCTACCATT GTCCAAAGGA CAATCCACAG CTTCGGTAAT	4740
5	ATGTTTAGCC CCGGTACATT TTCGGCGCag TGtCACTCGA CTAGTGAGCT ATTACGCACT	4800
	CTTTAAATGA TGGCTGCTTC TAAGCCAACA TCCTAGTTGT CTGGGCAACG CCACATCCTT	4860
	TTCCACTTAA CATATATTTT GGGACCTTAG CTGGTGGTCT GGGCTGTTTC CCTTTCGAAC	4920
10	ACGGACCTTA TCACCCATGT TCTGACTCCC AAGTTAAATT AATTGGCATT CGGAGTTTGT	4980
	CTGAATTCGG TAACCCGAGA GGGGCCCCCTC GTCCAAACAG TGCTCTACCT CCAATAATCA	5040
15	TCACTTGAGG CTAGCCCTAA AGCTATTTTCG GAGAGAACCA GCTATyTCCA GGTTTCGATTG	5100
	GAATTTCTCC GCTACCCTCA GTTCATCCGC TCACTTTTCa ACGTAAGTCG GTTCGGTCTT	5160
	CCATTCAGTG TTACCTGAAC TTCAACCTGA CCAAGGGTAG ATCACCTGGT TTCGGGTCTA	5220
20	CGACCAAATA CTAAACGCCC TATTCAGACT CGCTTTCGCT ACGGCTCCAC ATTTACTGCT	5280
	TAACCTTGCA TCAAATCGTA ACTCGCCGGT TCATTCTACA AAAGGCACGC CATCACCCAT	5340
	TAACGGGCTC TGACTACTTG TAAGCACACG GTTTCAGGTT CTATTTCACT CCCCTTCCGG	5400
25	GGTGCTTTTC ACCTTTCCTT CACGGTACTG GTTCACTATC GGTCACTAGA GAGTATTTAG	5460
	CCTTAGGAGA TGGTCCTCCC AGATTCCGAC GGAATTCAC GTGCTCCGTC GtACTCAGGA	5520
	TCCACTCAAG AGAGACAACA TTTTCGACTA CAGGATTATT ACCTTCTTTG ATTcATCTTT	5580
30	CCAGATGATT CGTCTAATGT CGTCCTTTGT AACTCCGTAT AGAGTGTCTT ACAACCCCAA	5640
	CAAGCAAGCT TGTTGGTTTG GGCTCTTCCC GTTTCGCTCG CCGCTACTAA GGGAAATCGAA	5700
35	TTTTCTTTCT CTTCCTCCGG GTACTAAGAT GTTTCAGTTC TCCGGGTGTG CCTTCTGATA	5760
	TGCTATGTAT TCACATATCG ATAACATGAC ATAACTCATG CTGGGTTTCC CCATTCCGAA	5820
	ATCTCTGGAT CAAAGCTTAC TTACAGCTCC CCAAAGCATA TCGTCGTTAG TAACGTCTT	5880
40	CATCGGCTTC TAGTGCCAAG GCATCCACCG TGCGCCCTTA ATAActTAAT CTATGTTTCC	5940
	ATCCTACAGG AAACGCGTTA TTAATCTTGT gaGTGTTCTT TCGAACACTA GCGATTATTT	6000
	CTTATGAATT CAAGCTTATT TAAAACTCTT TATTCACCTG GTTTTGCTTG GTAAATCTA	6060
45	TATTTTACTT ACTTATCTAG TTTTCAATGT ACAATTTCTT TTTAGTCAAG CGCTCGCATA	6120
	AGCAATATCA CTTTAACCAA AAAATATTTG AATGTTAAAT AAACATTCAA AACTGAATAC	6180
	AATATGTCAC ATTATTCGCG ATCTTCTGAA GAAGATGTTT CGAATATATC CTTAGAAAGG	6240
50	AGTGATCCA GCCGCACCTT CCGATACGGC TACCTTGTTA CGACTTCACC CCAATCATTT	6300
	GTCCACCTT CGACGGCTAG CTCCTAAAAG GTTACTCCAC CGGCTTCGGG TGTTACAAAC	6360
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ATCTACGATT ACTAGCGATT CCAGCTTCAT GTAGTCGAGT TGCAGACTAC AATCCGAACT 6480  
 GAGAACAACCT TTATGGGATT TGCTTGaCCT CGCgGGTTCG cTkGCCTTTG TAATGTCCAA 6540  
 5 TGTAGCACGT GTGTAGCCAA ATCCATAAGG GGCATTATGA TTTGACGCAT C 6591

## (2) INFORMATION FOR SEQ ID NO: 3115:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3115:

GGTGCCAAGC AATAAATATG ACTATGCTCA AACTGAATTA ATGGTGGGTG TGTCGCCATC 60  
 20 GTAATTGGAT CGTCTGAAGG CGCATATAAA TGATAGTGCT CTTCGAATAA AGGTAGCATA 120  
 TGTAAATTGTT TGTGTTTACG TATTCTGGT GTAAGTTCCG TGAAACCAAT GTCTATATTC 180  
 CCATTAATAC GCTATTATAA TGTGTCAGGT CCAATAAGCC CCGGATGACA TGTGTATCCA 240  
 25 TTTGGAAATG GAACCGTTGG GAAAGTGGGA ATAACATGGG GGAACGTCAn TCCCCnCCAA 300  
 GCCCATnGAG GTACCTTTAA TTTTA 325

## (2) INFORMATION FOR SEQ ID NO: 3116:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3116:

CCGnTTGAGT TCGGTGGCGA CATGATTGAT TTTGTAAGTA AGTATGATGC AACATGGGCT 60  
 40 GnTTTACCTA CTAAATTTGA GGCGGGTACT CCATTAATTG CTCAAGCATT GGGCTTGTCA 120  
 GAAGCTATTC GCTATTTAGA ACGCATAGGT TTTGATGCAA TTCATAAATA TGAACAAGAA 180  
 45 TTAACGATAT ATGCTTATGA GCAAATGTCT G 211

## (2) INFORMATION FOR SEQ ID NO: 3117:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3117:

AACGTTTTTT GAAATGATTG CGGCGATGTT GGCGACAGTT AAAGTAGGTG GCATCTTATA 60  
 5 TACCTATCGA TATTGATTTT CCGAATAAAC GACAAGGTGC AATTTTGGAG GATGCTAAAG 120  
 TAACTGCAGT CATGTCTTAC GGC GTTgNAA TTGAAACGAC ATTACCAGTC ATTCAATTGG 180  
 10 AAAATGCTAA AGGCTTTGTT GAATCAAAGG 210

## (2) INFORMATION FOR SEQ ID NO: 3118:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 225 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3118:

TTAATTGATC CTAGCTTGGT TTGCCTCTGT CACTTTATCA TTGATATTTT GGACAGTTGG 60  
 GTTGCCATTC AACACTTGAT TAATTTCACT TAACTTTGA CGCGCTGCTT GTAATTTTGG 120  
 25 GGTGTACGCA TTAAACGAAC GGnCGTCATA CCTGTTGTAT CCGTTGGTTG ATTAATGCTT 180  
 GTTCTAAATT GCGTTTCCAA GTTThAAGCG GCGCTTATCT GGTGT 225

## (2) INFORMATION FOR SEQ ID NO: 3119:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 222 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3119:

CCAACATGAT GCTAGTTTGA TTAAGTTTCT TCTAAACAGA CTTCAAACGG CATGGTTTAG 60  
 CATATCCTAT TAAGGTTGAA TCGCGTTAAC AGCACATAGG AAATGCTGTT AGGCGATGCA 120  
 GAGTGCAGATT AGGCAGCTAC TGGAAAATTA TTGTTTGATT TGCCAGTTAT TATAAACTGT 180  
 45 GTGTGTTGAT GnCGAnCACA ACCCCTCCGA ACACGCTTAA TG 222

## (2) INFORMATION FOR SEQ ID NO: 3120:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 246 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3120:

CGGCGATTAT ATTAAAAAGC CAATTACAGA ATGTAGTGGT AATGAAATAT GCCAAGAATG 60  
 5 GCTGTATCAC TTAGGTGTAT CAACTGACAA AATTGAAGAC TTAGCAAAAC ATGCATCTAA 120  
 TACGATTTCCT GTTTATATGC CATATATCAC ATCTTATTTT ATGGACGCGT GCTATCGGCG 180  
 TACAGACCTT TTAGTCGTGC CCGGCATGCA ATCTnCAGGA ACTTAGGCAT TTATTGGTGA 240  
 10 ACTTTG 246

## (2) INFORMATION FOR SEQ ID NO: 3121:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3121:

CAAATACCTT CTCAACnTTG TACTTTTTTGC CTAATTGAGC TGCACGAATT GCTGCAACGT 60  
 25 ATCCACCAGG ACCTGCTCCG ATTACTATAG aTCTGTTTCA ATTGGGAAAT CTCCAACCTAC 120  
 CATGTTTTAC CCCTCCAITA ATAATAATTC TGGATTATTT AATAAACGTT TAATGTGATT 180  
 CATTGCATTT TGGCCAGTTG CACCATCAAT TTGTCTGTGG TCAAAGCTTA ATGAKrtGct 240  
 30 AATACTGGTG CTGCAACAAT TTCTCCATCT TTAACGATAG GTTTTTGAGC AATACGGCCA 300  
 ATTCCTAAGA TTGCTACTTC TGGGGTGATT GATAACTGGA GTGAACCATT GTCCACCAGC 360  
 35 TGAACCGATA TTA CTGATTG TGCATnnGCA CCTTnCAT 399

## (2) INFORMATION FOR SEQ ID NO: 3122:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 301 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3122:

CAGACAAACC TTGAATTATT CTACCTATAA TTAAAAATGC TGGCAAAGGT GTAATGATGA 60  
 TGAGTAATGA ACCTACAACA TTTAATATCA ATCCTACATA AGTAATTTTG ACGCGACCAA 120  
 50 ATTTATCAGC AACATCACCA GCACCTACGT AAACCAACCA GCCAATAAGG CAGATAAGCT 180  
 AACAGCGTAT TATCGTTCCC ACGTCACTAC TATATGTGGA TGTATGGGAC ACAGTTTACC 240

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301

## (2) INFORMATION FOR SEQ ID NO: 3123:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 378 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3123:

15	GGAGCAAATT TATCATCTGC AACTAGACAC AACATCACTG TTATTAGTAC CGGGTTATAT	60
	AGTAGCAGTC ATTGTTGGTG CACTAAGTGG TAAATCGGC GAATATCTGA ATTCAAAC	120
	AGCGATTATC ACAGCAATTA TTTAATAGCA CTGAGCTTGA TTTACCTGCA TTGCAGTAGG	180
20	TAATCACATT CAATCTCGTC ATTCTATGAT ATCTTGCACT AGCTTGCTTA ATGATGCACT	240
	TACTACGAGC ATAAACATGT CTATATGCAG GTGCATGTTA TATTATATAT GGCGACGAGA	300
	TCGTnGGCCn ACGTTAACTA ATTCnGCATG TCTAGCCTCG AATTATATAG TAGGAGCGTA	360
25	GTACGCCAAC TGCCACGA	378

## (2) INFORMATION FOR SEQ ID NO: 3124:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 251 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3124:

	TATTGCAAGA AATGAACTGC TGATTTTTAT AGTTTTAGTG GTCATAAAAT GCTTGGACCA	60
40	ACAGGTATTG GCGTATTATT TGGTAAACGT GAGTTACTAC AAAAAATGGA ACCGATTGAG	120
	TTCGGTGGCG ACATGATTGA TTTTGTAAGT AAGTATGATG CAACATGGGn CTGATTTACC	180
	TACTAAATTT GCAGGTCGGG TTA CTCCCAT TGAATTGGCT CCAAGCCAAT TGGGGCTTGG	240
45	CnAGGAAGCC T	251

## (2) INFORMATION FOR SEQ ID NO: 3125:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 233 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3125:

5 CGGTTAAGTA ATACAGGATG TTCTCTAATT ACTTCTTCCA ATACGTCCCA AACTTCATCA 60  
 TCCATACGTT CGATTTTACT CTTGCGATTT TTAATGTTAG TTGCAATTTT CAGTTGAACT 120  
 AATTCTTTCA TTACGAATGG TTAAATAGT TCAAGTGCCA TTTCTTTTGG TAAACCACAT 180  
 TGGTACCATT TCCAGCTTG GACCCnACGG CAATTACCTG AACGGTCCCG GAA 233

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## (2) INFORMATION FOR SEQ ID NO: 3126:

## (i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 413 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3126:

AATAGATTCC CGGGATTCAA AAGCATGGAT GTTGACCTT GTTGnCTCC ATTGGCAATG 60  
 TACTACCTGA TGTCAAGATG AATTATCCAT CACTTTGTTG ACGTGCTTTA TTTTACAGCA 120  
 25 TCAATTTGAT CCAATCGAAA TACCAGATAA CTTAGACTGT GTCCCAGTAA AATAACGATC 180  
 AATCACATCA TGAGACAAGC CAATCGCTTC AAATATTTGT GCCCCITGAT AACTTTGCAC 240  
 TGTGAAATT CCCATCTTAG CCATTACTTT AATGACACCT TCTGACAATA CATCCGTATA 300  
 30 TGTCTTAACA TTATCGACAA CGGTGCCTTG TAACCCCTTCT GTCAATGTCA GTTGTTCAAC 360  
 TGTACGTTGC GCTAGGTATG GCACAATTGa TTCGCGCCAT ATGCGAGTAA ACA 413

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## (2) INFORMATION FOR SEQ ID NO: 3127:

## (i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 209 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3127:

45 GTCGTAAATA CTGAACAAA ATCACGGCAT ACTGTGCAAA TTTnTGAAGA AGCTCAAAAA 60  
 CTATTACAAG CACATCATGC GATTGTAGAA GGATATATCG AATCAGCTTT AGAGCGTGCG 120  
 50 TANATCATCT TCTACATACA TAGGTAATTT TATGSCGATT CCTCATGGAG CATCCTGTAA 180  
 AAAGTTTTAC AATCACATGT GCTTATTTT 209

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## (2) INFORMATION FOR SEQ ID NO: 3128:



(A) LENGTH: 204 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3128:

10 TAAATTAATG GAGTTTGGTA CACGTCGTCG CAAGAAATTG ATGCAGTGGG GCGCTAGAGC 60  
 TGCTTACATC GGGGGCTTTG ATTCTACAAG TAATGTTAGG GCGGGGAAAT TATTTGGTAT 120  
 ACCTGTGTCT GGTACACATG CACATGCATT TGTCCAAACT TATGGAGACC AATATGTTTG 180  
 15 CCTTCnAAAA ATATGCTGAA AGnC 204

(2) INFORMATION FOR SEQ ID NO: 3129:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 239 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3129:

GAAATACCAT TAATATAATA GTCGGTAAAT TAAGAAACGT GGTGCGCGAT TCACAACAGA 60  
 30 AATCTTAACT TATCGAAGTA TCCTGTTTTT TCTGCAACAC CAATACCAAT CATCACTGCT 120  
 AGTACTAAGC CTAATGCGGG AACTCTGAGA AATTTTTAAT CGTATTCTTC TTATCATCGT 180  
 AAATCCATCT GGCTATTATA TTTTAATATA AnGGTTTGAG CTACCGGATG CTAACGnAC 239

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(2) INFORMATION FOR SEQ ID NO: 3130:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 259 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3130:

ATCACAATAA ACATTTTAAA ATTCTTGTTA TCATAATCAT TAAAAGGTAT TAACCTTAAT 60  
 AATATATTCT CTnGTCTCAA CCTTAATCGT ATACTTCAGA CGTCTGTTTG TAGACAATAA 120  
 50 AGTCATTCAC GTCTTCATAT GTCATCAnAT GTTTATCATG ATATGATGAT ATATAATCGG 180  
 TATATACTGT AGATATTACA CATAAGAGAG GATATAATAT GAAAAGGTCA TTAAGATGTG 240  
 CTGAGAGCTG TGTATCAGT 259

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- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 227 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3131:

TGTGCCTGCC ATTTTGCAAT ATCTTCATCT TCACGTGGTA ATGCACAAAA ATGTTTACCA 60  
 TGTGCATTCA CAACTTCAAA AATATGTTGA CATGTGATGT TACTTGATCA TCACGCGTTG 120  
 CCATGGTATG CAAGTGCTGC GATAAATCTG CGGCACCTTC GACTATCATG CTAACCTTCG 180  
 CTTGTnATA TCGCAATGGC ATACCCCTTC AACATCTTCT ATCATGG 227

(2) INFORMATION FOR SEQ ID NO: 3132:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 203 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3132:

ATCGCAGTGA TGnATCATC TGCTGCTGTA GcnTAGCAGG TTCAATTTCA TTTATCGGAT 60  
 TAATGGGTCC GCATATTGCC AAACGTATCG TTGGACCACG TCACCAAGTTG TATTAACCAA 120  
 TTGCCATTTT AGTAGGGGCA TGTATACTTG TAATAGCTGA TACAATTGGC CAAAATTGTA 180  
 TTACAACCAG GTGGGGTTCC AGC 203

(2) INFORMATION FOR SEQ ID NO: 3133:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 201 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3133:

AGCATTTAGT TTAGCGGCAG TAGCTGCAGA TGCACCGGTA GCTGGCACAG ATATTACGAA 60  
 TCAnTTGACG AATGTCACAG TTGGTATTGA CTCTGGTACG ACTGTGTATC CGGACCAAGC 120  
 AGGTTATGTC AAAGTGAATT ATGTTTTTcn AGTGCTAATT CTGCTGTAA GGTGACACAT 180  
 TCAAAATACT GTACCTAAGG A 201

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 207 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3134:

CATTTGTAAC TGTTATTGTT TATAACTTCT GTGTGAAGCG CAATATTACA ATTAAAATGC 60  
 CGAAAGAGGT ACCGnCGAAT ATTTCAAG TATTTAGGAC TTAATTCCAT TTTCAGCGGT 120  
 AATCATCATT CTTTATGCAT TAGGATTnG TCAATCGCAA CCAGCTTTAA ATCAAAATGT 180  
 AGCGGAGGTA TTTTAAATTT ATTCGGT 207

(2) INFORMATION FOR SEQ ID NO: 3135:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 203 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3135:

AACACCTTTA GGTCGTGCAG GTCAACCTGT TGAGTTATGT GGTACTTATG TGCTATTAGC 60  
 GTCAGAAGGA ATCAAGTTAT ACAACCGGAC AAGTnTTCGG TGTTAGCGGT GGAGTGCAAn 120  
 TAGGTTAGGT TTGTATGAGC TTTTAATTGA GCACCATAAT GTTAATTTAG TTACTTCAAT 180  
 CCATTAAATT AAATGAATTG GTG 203

(2) INFORMATION FOR SEQ ID NO: 3136:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 211 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3136:

CACATCCAAT GCANTCTACT AAATCAGACA CACCACAATC TCCAACCATA AnACAAGCAC 60  
 AAACAGATAT GACTCCTAAA TATGAGGTTT AAGAGCGTAT TATACAAAAC CGAGTTTTGA 120  
 ATTTGAAAGC AGTTTGGATT TATGCTCAAA CCATGGACGA CGGTTAGGTT TATGATGTTA 180  
 TTCCAATAGG TTCACTATAA ATAGCTTAGT T 211

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 260 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3137:

ATTGGGAAAT GTTCCCCAC CACCTACAAT TTGTGAATAC AAACAATACG TATTGCAATG 60  
 GACTTTACCT GGGCTTACCA AGTGAATGTA TACGTCACGT ATGATACGAT TGTAATTGnA 120  
 AAATAATGCG AACAGAAAAT CGTTATAAGT ACAAATAATA CAGGTGACTC AACTCCTGCT 180  
 TTTAGATTAA CAAATCTCCA ACCGATACAA TGAGTGCTTG CAACATACCA AGCATTATAA 240  
 AGAATCCTGC CTTACCTAAG 260

(2) INFORMATION FOR SEQ ID NO: 3138:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 212 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3138:

CATAAGCAAT TAATGACTTC GTTAATTGCG AAAGTGTATC TTTTGTGATTA TCATTGCTT 60  
 TTGCATCTTC AAGCTTTCTC ACATCTGATT TGACAGCATT ACTTTCATA TTATCTTCAA 120  
 GCGATAATTT CTTAACTGCA CTTACCATT GCTCAATTGC TTCTGCTAT TGTCATTGCA 180  
 TATCGGAGTA GTAGGAAGTG CnGAATTCGG CA 212

(2) INFORMATION FOR SEQ ID NO: 3139:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 373 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3139:

TATTGGTTTT TATGCGAATA TGGATAATAA AAGGTCTCAC GACATCATTG ATAAATCGCT 60  
 TGAATGTTG CGACGCTTAG ATCAGAGGGG CGGGGTCGGC GCAGATGGCA TCACTGGTGA 120  
 TGGCGCAGGT ATTATGACTG AAATACCTTT TGCATTTTTC AAACAACATG TAACGGAGGA 180

GCACCTGTTA GAAAAGAAGG GAAATTACCT CGTGAAGTCA TTCGTTATGA GTATGACCTA 300  
 GAATATGGTA CAAATGTTTT AACAAATGGCA CAAAGATGCA ATTGAAACCA GGTnCAACGT 360  
 5 GTGTTAnTAC AGG 373

## (2) INFORMATION FOR SEQ ID NO: 3140:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3140:

AGCCTTATAA TAAAGTGCCT TTCATAGCAA TAAGTTGTGT CCATTGACCT ATTACATTTT 60  
 20 TCGTTTTGTA CATTAAATAT AAGAAATACG GTGCACCAAT AATTGCTACG ACAATACCTG 120  
 CTGGAACCCC CACCTGGTTG TAATACCATT TTGGCCATTT GTATCAGCTA TAACCAAGTA 180  
 ACCnTGCCCC AACTAAATG GCATTGGGTA AAACCAnTG 220

## (2) INFORMATION FOR SEQ ID NO: 3141:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3141:

GAGGAGCAGC ACAACCAAAT ACACAACCAG CTGGACAAGG TGATCAAGCT GATCCGAATA 60  
 ACGCTGCACA ACACAACCTG GAAATCAAGC AACACCGGCA AACCAAGCAG GTCAAGGnAA 120  
 40 TAACCAAGCA ACACCTAATA ATAATGCAAC ACCGGCAAAT CAAACACAGC CAGCGAT 177

## (2) INFORMATION FOR SEQ ID NO: 3142:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3142:

CTTTTTTAGC ATTTGGTTTA ACAACnGGT GTTGCAATAT CCCCACTTAA GGTCTGTATA 60

ATTTCATTTT TATGTTCTTC GATAACTTGT ATTGCTGCTT GTTTTCCTCC ATCTGTCAAT 180  
 CCATCATTTG ATTGAGAGAA nCAG 204

(2) INFORMATION FOR SEQ ID NO: 3143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3143:

GTGATGCCAT ATAAATTGGC AATAATGGCA CAAGTACTGT CAGTCCAGCA ATCGCTATAA 60  
 ACTGACTGAG CCATAAAATG CGAAAGTTAC TCGGCCATAT AGACTGATTA ATCATATGTC 120  
 ACCATTGGAT TTGGTACGGT AGTTAAACCT GAAGGCATAC TACCCTCCAC CCACTTATTC 180  
 AACGTTGGAT nATAGGCAAT GGGTAATTAA AAATTTTGT TTTGAAATGG GCCCACGGGC 240  
 TTGTTTTAAT CAAAATTAAA AAATTGTGGT nCTTGGACC 279

(2) INFORMATION FOR SEQ ID NO: 3144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 514 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3144:

TGACTTAATC AAAGCATTTG ATCAAAACAC CAGAATACCA TTATTCTTTA ATATGTTGTA 60  
 CAGTAAACTC TnTATTATTT GTTGCTGTTG GATCCATTGT TCGTCTTTCA ACAAAAACnT 120  
 GACCCAGAAT GAAGTCCGAT AGAGTCAACA AAGCLATAGT ATTTGTAACC ATCTTTTAGT 180  
 TGATaAATGC CACGCGCATC TGTTATTGCG TCATTTTtag GTAcAAATG AATTTkGAGA 240  
 TTTCTCaCaT TATCAGGTAC TTTAAATAAA CGCAAAGTTG GACCGnCTTC AACAGTCTTT 300  
 TCAGCAATCG TATCATTAGT ATCAGCATT TtGATAATAA CATTtGTTGC GCCTTGACCG 360  
 TTTTtagTAG TCATTGTATT AAATCAAGGT TAATTcAGAA TTCGGATTtA CTGTTAATGC 420  
 TTTCTCGATA CCATTAAAAAT CGCCATGGTC ATTcGTATCA GTTCCAGTAT ACGGCCTAAT 480  
 GCAATACATT TGCCTGTGcn TGATAGTnCT TATT 514

(2) INFORMATION FOR SEQ ID NO: 3145:

(A) LENGTH: 302 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3145:

10 ATTCAGACTT TGCATGTGGA ATGGCCACGT TCATGCCAAT AGCTGTCGTA CTCCCATTTC 60  
 ACGTTCTAGT ATTGCATTTT TTAAATGCGA TGTGTGCTCT ACATAACGGC AAATTTTAAG 120  
 TTTTATGAAT CAACATATCC AATGGCTTCG GTTTCGAGAC ATGTCCGTGG ATTCAGTAAT 180  
 15 TAACCATAGT TTGGTTGGAT CCAAACCAT GAGnAGGGTT TAATGGAGGA TGTnGAATGG 240  
 TTCnCCGGTG GTTAATCCTA CATGGTCCAC CCTCTGGTA ACCATGGTGG TGGTAATAAC 300  
 CC 302

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(2) INFORMATION FOR SEQ ID NO: 3146:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 332 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3146:

30

CAGGAATAGG ATCATTGCA TCCATAGCTT CACTTATTTT TTCAGAAGCT AGCGTACAAT 60  
 CATTTAAATC TACGCCACCT TCTTTATCAA TAGAGATTCT AAGAAAATGA TCTCTACCTT 120  
 35 CTTTGACCAT ATTCAACGTC TACAAGTTCC AAAATTCAAG GTCTTCCCAT AATTGGGTTT 180  
 AACCAATCCA CTTTCTACCT GGTTCGGT AAATTTTAC CTCCATACCA GGGnCTCCC 240  
 CCTTTTTTGG GCCAAAATAG GAAAAAGAG GCGGGGAAA TCCTCCCCC AATTCCnTTC 300  
 40 CTGGCCCTGG AGGTTTCCAC CTAAATTTT TT 332

40

(2) INFORMATION FOR SEQ ID NO: 3147:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 204 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3147:

50

GAGAGTGGTT AACAAGCAAA TAGAAATAAT TAAAAATGCA GATGCAGATG CATCGGCGAA 60

55

CnCCAAACAAA TGCAGAAGTT GCTGAATTCC AAATGTAACG ATACCTGCCC ATGAGCGATG 180  
 TGCTCAGAAT GATCAGAGCT AATG 204

(2) INFORMATION FOR SEQ ID NO: 3148:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 217 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3148:

CAACCGGGAC AGGTGGGGTT ATTGGACGTT ATTTTGGCC TTGGATTTT AAGATATTGG 60  
 TCGAAAAGAG ATTACATAAA ATTGTGGCCA AATGCGGATT GCATATTATT GTAACGCCGn 120  
 CTATTGCATT GTTGATTGTT AGGnCTATTA ACTATCTGGA TCTGTATGCC ATTAGCCAGG 180  
 TTTTGTTCa GACAGTTTAG TTTCAGTAGT TAACGGA 217

(2) INFORMATION FOR SEQ ID NO: 3149:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 174 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3149:

CTATTATTAT ATTCCGCGGT GTACGTATAT GTGCTACGTT ATCTTCGTTA ATTGTACCGA 60  
 TTATGGCTAT CATTACATT GGTATGGTTT TAGTAATATT GCTATTTAAT TTAGATCAAA 120  
 TTGTTCTAT GATAGGTCAC GATTATTAAa AGTGCATTTG GTCATCGAAC AAGT 174

(2) INFORMATION FOR SEQ ID NO: 3150:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 181 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3150:

GGGACCGAAT TGACTTCAGC ATTACCAGCA AATTGATTAA TnTTGTGGGC TGGTATTGGC 60  
 TCTGGCGGTA CCATTACAG GTACCGCACG TTATTAAAGC AACATCACGG GCAATGTTAT 120



A

181

## (2) INFORMATION FOR SEQ ID NO: 3151:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3151:

GTTTTAATTG AGCGACATAC TCTTCTGTTA GCTCTGCTAC TTTTAAAT AGAGCGATTG 60  
 ACATCAAACA TAACTGCTAA ACGCTCAACG TCTGCCTTCG TAATGGCTTT TGTAGAAATT 120  
 CTAATAAAT AATTCGAAT GCTATCATTG GTTGTTTCAA CAGCTTGATG CT 172

## (2) INFORMATION FOR SEQ ID NO: 3152:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3152:

ATGGACGTTG AGACATTTAT AAGCGATATA GATTTGCGAT GTTGCATTTA TTAAACCTAA 60  
 TAATGGTAAA CGACAAGTGT GACTGTTACT GGACTTTAAT GAAGGTAGTA ATCAGAATGG 120  
 AAATCAACCA AAAGTAGGTA TTTGAATnTT GGAATAATG AGACATAGCG AGAGTGTATA 180  
 TGCAATACGA CAGTACTnTA AATTAAGAG 209

## (2) INFORMATION FOR SEQ ID NO: 3153:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3153:

TTCTCACAAA GCGCTCAGTT GAAGTAAATC CACCTGGACA ATCCAAATGT ACCTGCTTCA 60  
 TTGCCTAAAG GTTCAATCGT TAnACCTTCC AATAAATTTG CTGTTGCTGG ATAAGGAGAA 120  
 ATTATTGGTA TATTGTCTTA AATTACTATG ATGCCAATTT AAGGTCTGGA TGAT 174

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 267 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3154:

GGATCACATC GTTCATTTAC ACAATCTATT AATATTCAAT GGCACAATAT AGTGTTTATG 60  
 GCATTACGGA TATGATTTAG TAGCnCACCA TTATTAACCG ATCTCTATCT GTTAAAAGGA 120  
 ACTTAAGAGC AATGTTTGCG CATCATCATT TTATGTTGCG TCTTTGCACG AGTTTTCGGA 180  
 AACTTTACAA TATTTGTTGC GGATGATTAT TTAACTTTTC GAGAATGTTG ATGGCACAGT 240  
 CCACTATAnC AATCAGTATC GCAATGG 267

(2) INFORMATION FOR SEQ ID NO: 3155:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 490 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3155:

AATTAAAAAT CAAGCAACTG CTGCAAAAAT GCAAGATCAA ACTGTTCTCTC AAGAAGCAAA 60  
 TTCTCAAGTA GATAATAAAA CAACGAATGA TGCTAATAGC ATAGCAACAA ACAGTGAGCT 120  
 TAAAAATTCT CAAACATTAG ATTTACCACA ATCATCACCA CAAACGATTT CCAATGCGCA 180  
 AGGAACTAGT AAACCAAGTG TTAGAACGAG AGCTGTACGT GTTtAGCTGT TGCTGAACCG 240  
 GTAGTAAATG CTGCTGATGC TAAAGGTACA AATGTAAATG ATAAAGTTAC GGCAAGTAAT 300  
 TTCAAGTTAG AAAAGACTAC ATTTGACCCT AATCAAAGTG GTAACACATT TATGGCGGCA 360  
 AATTTTACAG TGACAGATAA gTGAAAYCAG GGgATTATTT TmCacGAgTT ACCAGATatT 420  
 TACTGGTAAT GGAGACGTGG GATTATTCTA ATTCAnATAA TACGATGCCA ATTGCAGACA 480  
 TTTAAAAGTAC 490

(2) INFORMATION FOR SEQ ID NO: 3156:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 262 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3156:

CCTTCAGTAC CTTGTAATAG TTAnTTAAAT GTTCCGATCA TCGTGTAGTG TGATTCATCA 60  
 5 TACCGGCCTT TTCAATTGAA TACGATCTAA ACCGTTTCGT CAGGTGCTAG TAAGTTACCT 120  
 TCGCCACCTA AATAAGAAGT TCACTCGTTA CGATTMTTTC AGATAGCATC ATTGGTGGAT 180  
 10 TCGTAACTTG TGCAACAGCT GTTTAAGTAT TAATAGTGAT TCGGTCGTCT TCACATGCAT 240  
 TGGCGCACAA TCCnTGCAAC GT 262

## (2) INFORMATION FOR SEQ ID NO: 3157:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 170 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3157:

ATGGTAAAAA TTGCACTATC TGCTCGGGAA ACGATTTTGC ATAACCTATT GTTAATTTTT 60  
 25 TACCTGTTGA TTTAGCTGTA TCTGnCCATT TTTGAGCTT CTGCTGTCGT TTTAGCCATT 120  
 GGGTTTTTCAC ACATCACATG TTTACCAGCA TGCAACCCTG GCTACAGTAA 170

## (2) INFORMATION FOR SEQ ID NO: 3158:

30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 312 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 35 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3158:

40 CCAGGCAGAG GAGCAGCACA CCAATACACA ACCAGCTGGA CAAGTGATCA GCTGATCCGA 60  
 ATAACGTGCA CAAGACAACC TGGAATCAAG CAACACCGGC AACCAAGCAG GTCAAGGAAT 120  
 ACCAAGCAAC ACTAATATAA TGCACACCGG CAAATCAACA CAGCAGCGAA TGTCCAGCAG 180  
 45 CAGCGAACCA GCAGCACTGT AGCAGCAACG ACAACTCAGn CCAATGTAGC ATATGGTGAG 240  
 GCAGTTTATA GACATACATT GTGnCTTGCA TTCACAGTGG ATAGCAGGTC CACTGTACTG 300  
 TACAGTAAGT An 312

## (2) INFORMATION FOR SEQ ID NO: 3159:

50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 171 base pairs

55

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3159:

AATCACATCA AAAACTTCAA TTGTTTACGT TGGCAACTAA CTTTATGTTA GAACGCACAC 60  
AATATCTAAT GTTTAAATC TATCGTCGCA AGATGCTTCC TGTAAATTAT CAGTGCCATT 120  
TTCGATTGGG TTATACAATC TAGTAATCGC ATGATAATTT AATGCTACAA G 171

(2) INFORMATION FOR SEQ ID NO: 3160:

15

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 211 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3160:

CTTGTTTCATT TAATCCATAT AGTATACGAC GATGTACTGG TTTTAAACCG TCACGAACAT 60  
CTGGCAATGC ACGAGCAACG ATAACACTCA TCGCATAATC TAAAAATGAT TCACGCATTT 120  
CACTGGTAAT ATTTTCGTTCA TTAATCTGA TTGAGGGAAT TCCGCCCATC CAGAGTCCC 180  
CCCTCCAAAG TTCAGTTCCA CAGGGGCTAG A 211

30

(2) INFORMATION FOR SEQ ID NO: 3161:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 321 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3161:

GCACAGGTAG CGGTAGTGGC GGTCTATGA TGACTTTGGT AATCTAAAGC AAAATGTACG 60  
ATAATAATAA ACGTCGTTTC GTTCTCTGA TGTAGCAGGG GCAGTGAAGA AACAAGATTA 120  
TTGAATTGTT GATTTCTTGA AGATATAAAA ATTCAAGAAT GGTCTAGGA TTCCTAAGGT 180  
GTCTTCTTTT GGGCTCAGTA CGTAAACATA TTGTAGAGCG TGCAGTGAGT GGCGCACCAT 240  
CTCTTTTGGG TCAGTTTGG AGTTTGTGTT GTCGGCTGTC GGATTnTCGT ATGTAGGAAC 300  
GGCTGTTTAC TThCGTGGAT G 321

50

(2) INFORMATION FOR SEQ ID NO: 3162:

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- (A) LENGTH: 159 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3162:

10

AACATTTGAG CAATATCAAG AAACATTAGA GTATATTTTA TCCCATCATG TAACTCGTAA 60  
 TACAGCAATT ATTGCTTTGG GTGGTGGTGC ACTGGTGATT TTGCTGGGTT TATTGCGGCG 120  
 ACACTTTTAC GAGGCGTGCA CTTTATACAA GTGCCanCG 159

15

(2) INFORMATION FOR SEQ ID NO: 3163:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 157 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3163:

25

GTCAGTTATG GCAAGTGCAT CAACATTTTC AGACACAGAC AAGTCTTACG GCATCTTCTA 60  
 TTTTAAAGCT TGAATTTAA CAAATCATAA GCCGTATGAA TATTTAAATA TGCCACCATG 120  
 ATTGAATGGC CCCTTTCTAT TAGTTanGTT TTGTGCG 157

30

(2) INFORMATION FOR SEQ ID NO: 3164:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 216 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3164:

40

TATAAAAATA TAACGCGGAC AAAAAAGTGA GTTATTACTG ACAAAGTATn TGAGATTGTA 60  
 ACAGGATATA TGAAGCAATA TCAGTTGATC CAACTGTCTAT AGGTATTTCA TCAGCAGGnG 120  
 TTGTTGATGA ACAAAAAGCG AAATTGTATA GCAGGCCAAC ATTCCGATTA TAAAGGTATA 180  
 ATTTTAAGGA TTATTAAAT CATGTCTCTT ATGTCA 216

(2) INFORMATION FOR SEQ ID NO: 3165:

50

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 175 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3165:

5 AGAAACACTT CTATTGAATC GTCTTACTGC TGTTCCTCTAT TTATAACACT TCGTATTGAA 60  
TGAATTCATT ATGCCTATTT GACACATTAT TGAAGTTTTTCTAATGCCTG GATCCTTTAT 120  
ACGTTACGGC TTCGTGCTAT GTTTTGGTAC ATAAAGCTTT GACATATCGA nATTC 175

10 (2) INFORMATION FOR SEQ ID NO: 3166:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 160 base pairs  
(B) TYPE: nucleic acid  
15 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3166:

ACTGTTACAA CAAATTAAAA ATACAACAAG CGAGATATAG TTATTGTTGC TGGAnTGTAC 60  
CAAGTAGTAT TCCAAGCGAT GCTATGGCAA ATTGCACAAA TTACAGCACA GACAGGTGCT 120  
25 AAATTAGTAG TCGACGCTGA AAAAGAATTG GGCTGAAAGT 160

(2) INFORMATION FOR SEQ ID NO: 3167:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 156 base pairs  
30 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3167:

TGTGGGGGAA ACCTGCACAG CAAAACTAA AGCTTATCGA TACATCTAAA CATTGTATTA 60  
40 TAAAATCAGT GCATCCTAGT CCACTGTCTG CATATAGAGG ATTCTTTGGA TCAAAACCGT 120  
ATTCCAAAGC GAATGCCTAT TTAGCGTCAG TAGGnA 156

(2) INFORMATION FOR SEQ ID NO: 3168:

45 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 174 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3168:

55

GTGGCGAGAA ATACCGCAAG CATAAAGATA TCTTTGATCC AACTTACCAA CAGATCAACG 120  
 GAAAAGTACC AGGTAACCAG GAATCAAGAT CCAGACACAG GAAAAGTGAT CGAG 174

(2) INFORMATION FOR SEQ ID NO: 3169:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 213 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3169:

TCAAACGGGG TCAATTTCAA ATGGAAAAAT TATACCGCAT CTTCTCCTGA TAACTACGTG 60  
 ACCTTATCTT CTTTATATTT GCAGACCACG AACATTCAAA CTGCATGCTT GCTCGATTGG 120  
 CAATGTCATA TAACTAGTAA CATGATCATC nCATCAAATT TAGTATGTCA AATGTCCCAA 180  
 TCANTAAATTT GATCGGTGTT GCTCAATTGA TTA 213

(2) INFORMATION FOR SEQ ID NO: 3170:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 380 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3170:

AAAGCACCTT TTCCTAATGA AAGTTGTGCT ACTGGTATCT GTGTTTGATT TACAAAATCT 60  
 TCTAATTCCTT GATGGAGGTG AAAACTGTTA ATTTTCATGTC CAGTAATGAT GATAGGCTGC 120  
 TTGCGTTGAT GCAGTTTAGT TGCTAATAAC TCTATATATG TTGATGCATC CGTATATTTA 180  
 GTTGCCGTCA CTTCAAATGG TGTCGGTATC TCAATTTTCAG AGATTGCGAC ATCGATTGGT 240  
 AAATGTAAAT GAACTGGGCG TCTTTCGGCG ATTGCTGTAT TAATTAAACG TGGTATTTTCG 300  
 GTTGTTGCAT TTTTCAGGTGT GATATAACCT GTGCACGnTT ATATGTGCAA ACATTTTTCG 360  
 ATAGTCGTCA AATGTACnn 380

(2) INFORMATION FOR SEQ ID NO: 3171:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 401 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3171:

5 TAGAAGGTAA GAAGGATCCT ATCGGTGCAA TGGGATATGA TCGCCAATT GCAGTGTGGA 60  
 ACGAGCGACC AGAATCACTA TTTAATTACT TTAAACAGCT GTTGCACAA GTTACGAATC 120  
 CACCAATTGA TCGGTATCGT GAAAAAATCG TAACGwGTGA ACTTTCTTAT TTAGGTGGCG 180  
 10 AAGGTAACCTT ACTAGCACCT GACGAAACGG TTTTAGATCG TATTCAATTG AAAAGGCCGG 240  
 TATTGAATGA ATCACACTTA GCAGCGATTG ATCAGGAACA TTTTAAATT AACTTATTTA 300  
 TCAACGGTAT ATGAAGGGGG ATTTGGGAAG ATGCGTTAGA AGCATTAGGC CGAGAAGCAG 360  
 15 TGGAAATGCTG TTAAGCAAGG GCGCTCCAAA TTCCTAGTGG T 401

## (2) INFORMATION FOR SEQ ID NO: 3172:

(i) SEQUENCE CHARACTERISTICS:  
 20 (A) LENGTH: 166 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3172:

ACATAATTTA AAATAATATT ACATTGTAA TGGnCACCAA GTAACGTTTC GGTTGCTTGG 60  
 30 TGTTTTTTGG TATGAATTAC TTTCTGTTAC AAAACAATCT AAAGCGTTCT GTTATGTTTT 120  
 ATTAAGATTT AATTACAAAC GGAACTAAA TGTAATAGAA TAAACT 166

## (2) INFORMATION FOR SEQ ID NO: 3173:

35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 160 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3173:

45 ATAATGAGAn TGTGTACGT TATGGTGGTG GAAGTGCTGA TGGTGATTCA GCAGTAAATC 60  
 CGAAAGACCC AACTCCAGGG ACCGCCGGTT GACCCAGAAC CAAGTCCAGA CCCAGAACCA 120  
 GAACCAACGA CCAGATACCA GAACCAAGTA CCAGACCCAG 160

## 50 (2) INFORMATION FOR SEQ ID NO: 3174:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 158 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

55



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3174:

5 CTTTATATAA AGAAGGAATT ACTAAACATA CAGTTAGATT ACTTCATGCA ATCGAATTAG 60  
 AACGTTTGAA TTTAAGCCGT AGATTAGGTT TTGAATTATC AACAGCnAAA GAATCACGTA 120  
 TTGAACGGGG GTTATTTAGA ACGTGATAAA GAAGGATG 158

## (2) INFORMATION FOR SEQ ID NO: 3175:

## (i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 154 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3175:

20 TATTTGAAGA TGGCTGTGTA CAAAAATCGG TGTTACGTGA TCATGATACT GTCAGAATTT 60  
 ATAAACCATG GCTAACAGCA CATCAGCTTT CATTGCCChA GTATGTCGTC AGAGAAGATA 120  
 CACCTAATCG CTAATTAATG AGGTTTGGAA ACAT 154

## (2) INFORMATION FOR SEQ ID NO: 3176:

## (i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 472 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3176:

35 AGAAGGTATT TTAGCTCAAT CTCCAGGTCT AAAGGTTGTT ATTCCTTCAG CCCATACGnT 60  
 GCGAAAGGTT TATTAATTC TTCTATTAGA AGTAATGACC CAGTCGTATA CTTAGAGCAT 120  
 40 ATGAAATTGT ATCGTTCATT CCGTGAAGAA GTACCTGAAG AAGAATATAC AATTGACATT 180  
 GGTAAGGCTA ATGTGAAAAA AGAAGGTAAT GACATTTCAA TCATCACATA CGGTGCAATG 240  
 GTTCAAGAAT CAATGAAAGC TGCAGAAGAA CTTGAAAAAG ATGTTTATTC TGTGGAAGTA 300  
 45 ATTGACTTAC GTACTGTTCA ACCAATCGAT GTTGACACAA TTGTAGCTTC AGTTGAAAAA 360  
 CTGGTCGTGC AGTTGTAGTC AAGAAGCACA CGTCAAGCTG GTGTTGGTGC ACAGTTGTAG 420  
 50 CTGAATTAGT GACGTGCATC CCTTCATTAG AAnnCCTATG GAAGAGTGCA CA 472

## (2) INFORMATION FOR SEQ ID NO: 3177:

55

- (A) LENGTH: 150 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3177:

10 TGAAAGCTGG CGAATACAGT GATTGTCATG ATGCGGATCT AnTTGTCATC TGTGCTGGTG 60  
 CTGCACAAAA ACCTGAGAGA AACACGTTTA GATTTAGTAT CTAAAACTT GAAAATATTC 120  
 AAATCAATTG TTGGTGAAGT AATGGCATCA 150

15 (2) INFORMATION FOR SEQ ID NO: 3178:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 166 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3178:

25 TTACTCTATC TTGATTTGAC GAAATACTAT TAnGCTAATA TCGATATTTT AAAAACGAGA 60  
 TGATGTTCCA AAGCAAGCCA TTTCGATGGA CTGCTAATAT TCTTCAGCCA AACGTATCAT 120  
 30 TTTACTCGCA TTTGGTGAAA AGAAACGGCT GCTATTACAC ATTTAT 166

(2) INFORMATION FOR SEQ ID NO: 3179:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 170 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3179:

40 CTTCGACTCT AGAGGATCCC CGCGCTCAAA TTCTAGTGTT AGATGATAGT GGATTAGTTG 60  
 ATAGCAATGG CTTTGCAATG CCGATGTTAC TCGCAATAAG TCATGTGCAT CAATTACTTA 120  
 45 TTAAAGCAGA TTTACGTATG TCTACAAGTT TAnTTGCTA AATCTGGTGA 170

(2) INFORMATION FOR SEQ ID NO: 3180:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 297 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3180:

AGCTAAGGTT GCChTGGGCG TTGCCCCAnT TGGTTAGTCC AGGTGGTCGC GGTGGCCATC 60  
 5 GGTGTATTCG CCAGGTCCTT CAGCCAGGGT TTTTACTATT ATATCCAGTT GTAGCATTCA 120  
 TGATTGGGGC GATTTCGAGAT AGATTCATCA ATGAAATTAA TTTCTGGATT TTATTCGTTG 180  
 GTATTTATTT GGGTATACAT AAGTATGGTA CATGATAGGC AGATATACAA CATTACAACA 240  
 10 TTCATTCTAC TATGCTGGAA ATAACATGAC AGTGATGACA CTACTATCCC CGTCGCA 297

## (2) INFORMATION FOR SEQ ID NO: 3181:

## (i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 349 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3181:

CACTAGGTAC CCCAAAACGC CAGAGGAACT TGGTTAAATC GCACTTACTT GGTGGCTCCA 60  
 25 ATCAACTGGT ACTTCATAAC GTTTGGCATC TTCGCCACTT CACCACTATT ACTCTTTCCA 120  
 CCTAATTGGT TCATGGCTTG TGCTAACGTT TCATGTGCTT CCGCTGAAAT CGATCCATAA 180  
 CTCATCGCCC CTGTATTAAA GCGTTTGACA ATGTCACTTA CCGGTTCAAC TTGGTCGATG 240  
 30 TCAATCGgTG TACATGCTTT AAATTCAAGT AAATGTCTAA TGTGaTCTGT TCTATTTTGT 300  
 TThCACCGnT ThCAGAGTAT GCTTTAAATT GCGCCATAGT CCATTTTCT 349

## (2) INFORMATION FOR SEQ ID NO: 3182:

## (i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 149 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 40 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3182:

45 TACCAACACG TACACCTTCT AAAATAACTG CATTTGCACC GTnTTAATAC ATCATCCTCG 60  
 TTTATAACCG GTGTAAGCAC TAGGGGGTTC AATCACACCT GCTAATACTG CGCCAGCCCT 120  
 ACATGTACAT TTTTACCACT TGTAGCACG 149

## (2) INFORMATION FOR SEQ ID NO: 3183:

## (i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 147 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3183:

10

GCGGTGCCGG TGTTGCAATT GCGCAGTGG TGTTGGTAGC ATGTGGTCTT TCAATCAATG 60  
TTCAATACAC CAGGAGATCC GGAAAAGATG CGTATGAATT TTATGGTAAG TGCACCAGGC 120  
ATTACCACAC CACGCAAnAA CATGCAT 147

(2) INFORMATION FOR SEQ ID NO: 3184:

15

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 180 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3184:

25

CAGCGATATG TTGGCGTTGA AAATCTGCAA TTTGTTTATA ATTCTCTGTT AAAGAACGAC 60  
TTAAATTGAT AAAAATGGAT ACGATCTCTT GGTAAACAGT GACATTTTCT CAATCGGCGT 120  
ATGATGTTTG TGGCACCGAC CATCGAGAAC ATGAAAATCT CATGTCCCAC GCTAGTCGnC 180

30

(2) INFORMATION FOR SEQ ID NO: 3185:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 150 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3185:

40

GGTAAATACG TATTAATCAG ATTAAGATCT GGTGAAGTTC GTATGATCTT ATCTACTTGG 60  
CCGTGCTACA ATCGGGnCAA GTTGGTAACC TACAACACGG GTTAGTTAAC GTTGGTAAAG 120  
CCGGCACGTT CAAGATGGGA AAGGTATCCG 150

45

(2) INFORMATION FOR SEQ ID NO: 3186:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 146 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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GAATTTTrAGG TGAATCAGAA GATTAACGCT GTTGCCTCCT AAGCTAACAG ATACTGGTTC 60  
 GTCAGTTGTC GTTGAAAAAG CGAATGAACA ATTTAATAAA ACCGTAACTC GAGCATTATT 120  
 5 AGAGGAAGCT AACCAAAGCA GGTTTA 146

(2) INFORMATION FOR SEQ ID NO: 3187:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 165 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3187:

AAATTGGCGA GTATGTTGTT ATTGGGTCAG TACTCTGAAA TTAACAATAG nTACGATTGA 60  
 20 AAATGGTGTC ATGTATTCAA CAGTCTGTTG TTAATGTATG CTAGTCGTGG TGCGAATACT 120  
 AAGGTCGGAC CGTTTGCGCA ATTGAGACCA GGCGCGCAAT TAGGG 165

(2) INFORMATION FOR SEQ ID NO: 3188:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 166 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3188:

CAGTTTAGTG GAGACGAATC TAAACGAAAC AAAGCGATTG GACGTGCATC AGTTGTACCA 60  
 35 ACATTCTTTG GTGTAAACGn AACCAATTTT ATTGGTGCC ACCACTAGTT ATTGGAATCC 120  
 TGTGTTCTTT ATTCCATTG TATTAGCACC AATTGTTAAC GTATGG 166

(2) INFORMATION FOR SEQ ID NO: 3189:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 146 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3189:

AACCCTTTAT CTAATCCATT TTCAGTTAAG CGATGACCGC CTGCTAAAAT TTGTGCATCT 60  
 50 GATTCTTTTG CTGCATCAAT ATATGATTGA ATTTTATCTA ATTGATCCTT ACCAGTTTGA 120

## (2) INFORMATION FOR SEQ ID NO: 3190:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3190:

TCCCCCAAAG GGTTTAAGGG GTTAACCCGG GTTGGGAAA AATTTTTTAA CCCCCCTTAA 60  
 AATTCCCCGG AAAAAGGAAA CCCGGGTTTT TAAAAAAAC CCGGGGTTCC CAAAAATTTT 120  
 TTGGGAAAGG GAAAGGAAAA AAGGGTTAAA AAATTTTTGG GAAAAACCCG GGCCCAAAAA 180  
 AAAGGGTTTT TTTCCCCTTA AAAAAAATTT AA 212

## (2) INFORMATION FOR SEQ ID NO: 3191:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3191:

CTTCACTGAC TTTAGCAATT TCATCACCTT TTGCCCTAC AACGATAGCT AATGATTTAT 60  
 ATTGTAAACT CAAATGACCT TGTGAATAC CTCTGACAC AAGCGCGCGA CATGCTGCAA 120  
 AGTTTTGCGC TAAACCAACG GCAGCAAC 148

## (2) INFORMATION FOR SEQ ID NO: 3192:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3192:

CTGCTAATCC GAAATCTTTT TGGAGTTTTA TTAAACCAGC TGCTTCTAAT AGTTTAAGTG 60  
 CACGTGCTTG GTTTGACACA TCATTTGGAA TGACAACTTT AGCnCCATCT TTAACCTTTT 120  
 TGACATCTTT AATTTTATCT GCAGAAATAA ATCCATCAGG GATGGCTCTT AAATATATGT 180  
 TACGTGATAA TTTCTCGAaA AATGGCTTCC CT 212

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3193:

TCGTGCAGTG GTCTTCTGTT AATTGGTGAA TTGGATACT GGTATATTC AGCTGCACCG 60  
 CAAGCAACTT CTATTGATGG CCnAACTGCC TTTTACCTC AAGCAATGGG TATGGTAGTT 120  
 GTTGCAGTCA TTTATGGCTT T 141

## (2) INFORMATION FOR SEQ ID NO: 3194:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1290 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3194:

AATAACGTTT TGAAAAACGA AGATGTTTTA AATGCCTATA TCCGCGGTCG TGGCGGAATG 60  
 GCAGACGCGC TAGGTTGAGG GCCTAGTGGG AGAAATCCCG TGGAGGTTCA AGTCCTCTCG 120  
 GCCGCATCAA AATTCTTAAT TTAAATAAGC GGGTGTAGTT TAATGGCAA ACCTCAGCCT 180  
 TCCAAGCTGA TGTGTGGGT TCGATTCCCA TCACCCGCTC CATAGATAAT TTTAATGAAC 240  
 ATTGAAAAC GAATGACAAT ATGTCAACGT TAATTCCAAA AACGTAAC TAAGTTACAA 300  
 ACATTATTTA GTATTTATGA GCTAATCAA CATCATAATT TTTATGGAGA GTTTGATCCT 360  
 GGCTCAGGAT GAACGCTGGC GGCCTGCCTA ATACATGCAA GTCGAGCGAA CGGACGAGAA 420  
 GCTTGCTTCT CTGaTGTTAG CGGCGGACGG GTGAGTAACA CGTGGaTAAC CTACCTATAA 480  
 GACTGGGATA ACTTCGGGAA ACCGGAGCTA ATACCGGATA ATATTTTGAA CCGCATGGTT 540  
 CAAAAGTGAA AGACGGTCTT GCTGTCACTT ATAGATGGAT CCGCGCTGCA TTAGCTAGTT 600  
 GGTAAGGTAA CGGCTTACCA AGGCAACGAT GCATAGCCGA CCTGAGAGGG TGATCGGCCA 660  
 CACTGGAAC GAGACACGGT CCAGACTCcT ACGGGAGGCA GCAGTAGGGA ATCTTCCGCA 720  
 ATGGGCGAAA GCcTGACGGA GCAACGCCGC GTGAGTGATG AAGGTCTTCG GATCGTAAAA 780  
 CTCTGTTATT AGGGAAGAAC ATATGTGTAA GTAAGTGTGC ACATCTTGAC GGTACCTAAT 840  
 CAGAAAGCCA CGGCTAAcAC GTGCCAGCAG CCGCGGTAAT ACGTAGGTGG CAAGCGTTAT 900

CGGCTCAACC GTGGAGGGTC ATTGGAAACT GGAAACTTG AGTGCAGAAG AGGAAAGTGG 1020  
 AATTCCATGT GTAGCGGTGA AATGCCGAGA GATATGGAGG AACACCAGTG GCGAAGGCGA 1080  
 5 CTTTCTGGTC TGTAAGTGAC GCTGATGTGC GAAAGCGTGG GGATCAAACA GGATTAGATA 1140  
 CCCTGGTAGT CCACGCCGTA AACGATGAGT GCTAAGTGTT AGGGGGTTTC CGCCCCTTAG 1200  
 TGCTGGCATA ACGCATTAAAG CACTCCGCCT GGGGAGTACG ACCGCAAGGT TGAAACTCAA 1260  
 10 AGGAATTGAC GGGGACCCGC ACAAGCGGTG 1290

## (2) INFORMATION FOR SEQ ID NO: 3195:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3195:

TGGTACAGAG TTATCGCTGG TGGTCCTGTT CGTGCCGTAC TTGAATTATC AGGTATCACT 60  
 25 GATATCTTAA GTAAATCATT AGGATCAAAC ACACCAATCA ACATGGTTCG TGCTAACAAT 120  
 CGATGGTTTA CnAAACCTTA 140

## (2) INFORMATION FOR SEQ ID NO: 3196:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3196:

CTATTGGATC AGGAGGCAAC TACGCTTAAG CGCAGACTGC CCATTGAAAC GCCATGCATC 60  
 GCATTTGTCTG CCTGAAGAAA TGGCATATGA GAGCTTGAAA GTAGCGGCTG ATATTTGTGT 120  
 45 CTTTACCAAC GntAATATTG TTGTC 145

## (2) INFORMATION FOR SEQ ID NO: 3197:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear



TGTCGAGTTG GAATTGGACG ATTGAATATC CCATCTCCAT CACTATCAAA GSTATGGGAAT 60  
 TGAATTGTTT CTAATTCGTA TCCACCTTCT GTCATTGATA ATGTAGGGTT AATTTTAGAA 120  
 5 CCATCTkCTG TTTCTAGTTT TAAGTTCCAC TTCTTACCTT CTTCCCAACG TTGACCCATT 180  
 GTGCCATTAG GTACTACTAA ACTATCGCTG ATTGCATCAT GAATAACTGG CTTCCATTCh 240  
 CCTTGCTCTG TTGTTTGACC TAAGTCACTC GCGCTnAAAA ATCGACCCGC TTTATATCCA 300  
 10 TnTTCAGCTG 310

## (2) INFORMATION FOR SEQ ID NO: 3198:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 140 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3198:

TGCTTTATTA ATGCATTGGC TAATAATCCA CTTGTACCAC CACCGGCACA AAGTACTAAG 60  
 25 AGGTTTGTTT TGTGATATTT GAAGCTTTAG TGCATCGTCT GATACACCAC TTGCCGCTAA 120  
 AATTGAATCA GCTTTTnTCG 140

## (2) INFORMATION FOR SEQ ID NO: 3199:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 184 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3199:

TGGTGATTTC AAATCATGAG ACTGGGACAA AATGATGTTT TCATAAAAT TATTTGTTG 60  
 40 TTCCACTCTC ATGATTTTTT TGATGAACAT AATTACATGA TTGATTGCAT CATTGTGTTAA 120  
 AACCAGTGAT TGCAACCTGC CATTCAcAnG GAAAATTACC TAATAAGTGG CGTATTTACC 180  
 45 AGTC 184

## (2) INFORMATION FOR SEQ ID NO: 3200:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 163 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3200:

TTGAGAAGCG TTTAGGAAGT AACGTTTAAC GACGACAGTC GTTCAATGCG ATCAAAATGT 60  
 5 TTTAACACAT GAATCGCTCT CGTACTATTC GTGTGTGACA CATGTTCTTC CAGCATTTC 120  
 TTAATGAATG CTTTTTCTTC TTGGTnTTTA ATCTTTGTAA ACG 163

## (2) INFORMATION FOR SEQ ID NO: 3201:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3201:

GTTATGTTTG AGACTATAAT GAATAAATAT TTAGAAATAT GACTCCGATT GTTCGATGCT 60  
 20 TAATTCAGTT AGAAGCATCA TAAGAATGCA TGATTACTGG TGTAAGATA CGTAATGTnT 120  
 TGTATTGACT GGATGTCTTT GGATAGAGT 149

## (2) INFORMATION FOR SEQ ID NO: 3202:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3202:

CAAGTGACTG AGATTACTGA AGTAAACCCG TTACCGCCAC ACTATATTTG TCCGAAGTGT 60  
 35 AAAACGAGTG AATTTTTC AA TGATGGTTCA GTAGGATCAG ATTGATTTAC CTGATAAACG 120  
 40 TGTGAAnTTG TGGAGGCCAC TATTAAAGAA GACAGAATCC GTTGAACATT TAGATAAGGG 180  
 AAAGTCCGAT TC 192

## (2) INFORMATION FOR SEQ ID NO: 3203:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3203:

CGCCATCTAA CGTTTTTGT ATTGGTTGTT GCTGAGCTAG TTGTAAGTGC CnCATTAAGC 120  
 ATCTTATAGC GTGATAGCCA TCGCCAACG TACAAATCTG CTCCGTATTG TACGCACCAC 180  
 5 TAAGCAGTAC ACACCAGTAA CATTGATAG CGTTATAGCG CAATATACAG TACA 234

(2) INFORMATION FOR SEQ ID NO: 3204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3204:

AACGCCATAA GCTACATGTA TGCTTCTTGC ATGGTTATCA TCCTCTCTTA ATGACTATCT 60  
 20 TTTAATTACG NAATGGCTTA CCAGTTTTTA ACATATGTGC AATTCTTTCA TATGATTTTT 120  
 AGATTTAGTA GCATAAGCAA TTTCTCCACG TTGATGTACG TGATGTAATG ATTCTGGG 178

(2) INFORMATION FOR SEQ ID NO: 3205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3205:

TATTAATCAC GTTGTGTGTC GTTCGTGTTT TCGCAGTATT GATTTGTTGT TCGCATTAT 60  
 35 GCATTGCATT ATTGTACTGC GTAATTGTAC CTGGCTTTTT ACC TTCAGTG CTTACTGGnT 120  
 CATCTAAATG ATTTT TAGCT GTGATTA 147

(2) INFORMATION FOR SEQ ID NO: 3206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3206:

CAGCTGTACT AGTTGAGCGT ATTATCCAAA ACATTTTACG TGATGGCATT GATGTCGATC 60  
 50 GACTTTCAGT CGTAACGTTT ACAAAC TTAA GCGCACGTCA NATGAAGCAT CGTGTAGACC 120

## (2) INFORMATION FOR SEQ ID NO: 3207:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3207:

TAGGGACTTT GAAGCGGAGA GTCTAATGCA TATGGGCAGC ATTATGATCA GCAACTGCTG 60  
 AGAAAAATCC AGTTCTAGCT TGGGATTTAA ATGTGGAGTG GntTAATGAA TGCATTAAGA 120  
 AGCTGCAAGA ACTTATAAGT GTGCA 145

## (2) INFORMATION FOR SEQ ID NO: 3208:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3208:

AAACGGTTTT AGATCGTATT CAATTGAAAA GGACCGGTAT TGAATGnaAT CACACTTAGC 60  
 AGCGATTGAT CAGaACATTT TAAATTAAC TATTTATCAA CGGTATATGA AGGGGATTG 120  
 GAAGATGCGT T 131

## (2) INFORMATION FOR SEQ ID NO: 3209:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3209:

ATAAATTAT CTATAATCTG TTGCTTGTTT TnCTGTTCTA CAAGTATTTT CACATTAGGT 60  
 CCCGCATCCA TTGTAAAATA ACACGGATAC CCCGCTTCTC GGCATTCTGT AACAGCGCCA 120  
 TGACATCATA ACTTTCTGCA CAGTAGGAAC GGGGGTG 157

## (2) INFORMATION FOR SEQ ID NO: 3210:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3210:

AACGTAATAG ATATGGTACT TACTACATGG GAGAGAGTGC TAGATTCACA AACGGCAATC 60  
10 AACCAATCAC AGTAAGAGAA GTGGGGCCAT TCTTATCTnG TCCAGTGGGT TATCAGTTCC 120  
AACCTGGTGG GTATTGTGAT TAT 143

(2) INFORMATION FOR SEQ ID NO: 3211:

15

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 137 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3211:

ATGCATACTG TATGTGTTC AGCATATACA ATTTTGnCCA TCTTTAATGA CAACTGTACC 60  
25 ATTTTTCACA ACATTTAATT CATCTAATTC CTTACCCTTC AAAGTTTATC TGTTGATCTC 120  
GGTAAATAA ATTCTGC 137

30 (2) INFORMATION FOR SEQ ID NO: 3212:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 239 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3212:

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ATTACGCTT TAAAGGACGT AAATACACGA CTAGGCTGTT TACCTTTAGA TCTAAATCAG 60  
AACAAATTTT TTACCATGGT GTTCCCCTTG AATTAGGAAT TTTATATAAA AATAAGCGGG 120  
45 AAGCGTTGTG CCCCCTTAC TCATAAGCTT TAATTAATGC TAAATAGTCT GACACTAGCG 180  
ATTGATAAA ACTATACTAA AATTATTTAG AAGTCACTAA GATGCTAATG ACGACnAnT 239

(2) INFORMATION FOR SEQ ID NO: 3213:

50

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 150 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3213:

CATCCTCAGA GTAGGAATAG CCATACCATC GAATAATTCA CGTACTGTTT CGAATTGAGG 60  
 5 TTCAAATTCT TGAGTTGTAT AGAGCTCGAA AATnTTTGCC CATTAGCATA ATCAGACTTT 120  
 TCAAAAGTCT TGATATTTGA TACCCACGCT 150

## (2) INFORMATION FOR SEQ ID NO: 3214:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3214:

CTAAGCATTG GTTTAACTA ATGTTTCTAGAG CTTTnTGTGG TTTGTAAAnA CAAGTATATT 60  
 nCGAGAACAC GTTTTTGTAT AGAGTCTCAA TTATAAAAGT TAGAATAGTT GACAACAGTG 120  
 TTACGATATT ATTAAACAAC TGTcTATCAT TAACGAAAGC AATTAACAAG AGTACTTGTT 180  
 25 GTGAAATCAT CGTTTAATAG TCAAAGATGA TCATCGTAGG gTAGACAACA TATCaTTGAC 240  
 TtAAGGAAGG GGAATGACCG ATGGGATTAA AAGATCAAGC TGTTACCTGG AGAAGGTATT 300  
 TTCATCAATT TCCAGAACTA TCCGATAAAG AATTTAAGAC TACACAAAAA ATTAAAGATA 360  
 30 TTTTAACAGA ACATCATATT AGAATATTAG ACTTACCAC 399

## (2) INFORMATION FOR SEQ ID NO: 3215:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 386 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3215:

CAGGTGAAAG CACAAGAGGA TTTGCTGTTT ATTTCTCTCC TGAAATTAAG AAATTCATTG 60  
 45 CAGATAATTT AGATAAATAA TTAAACTTA GACATTCACC CAATCCTGAC AAAATATACT 120  
 ATAACAAACA TTTATTAATA TATATTGCAT TATTTAATAT GCATCAAAGC CAATCAACGr 180  
 50 TTGATTTTCA CCAACTCAAT TGTTGATTGG TTTTATTTAT GTATGAATGA ACAACTTTTT 240  
 GACATCATTA AGAATATAAA TGC GTTTGAA AGCATTTGAA AGCnACAACA TTTCTATAAA 300  
 ATTTTTCaAT AACaATTGCG CCACTAAAC TCAAAATTTc CACCACCAAC ATCCAAATTA 360

## (2) INFORMATION FOR SEQ ID NO: 3216:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3216:

AGTTGCATCA ACTGAATCCA ACGCTACGCA ATACGAATTA TTCCAATCTG GCATGCGTGT 60  
 TGGTAGAGAA ATTTTAGCGA CATCTCGAGC ACGGTTTACC TTGCCTTTnT TGGTGGCCAA 120  
 CTTGCTTTAT GCTATGGGTT TTTCAAACCTT AAA 153

## (2) INFORMATION FOR SEQ ID NO: 3217:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3217:

CTTTGCATAT TCTGGTTTGT AGTATTCATG GTCCGTCAT TGTAGACCCA TCAATTGCAG 60  
 CCATTACATA TGCGGAATAT CGAAGCGAAC TTCAAGTTGC TTCAAGCTGG TAGAACACGC 120  
 AnATAAAATT ATTACATC 138

## (2) INFORMATION FOR SEQ ID NO: 3218:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3218:

CACTCCAAAC CAAGGATTTA CGTGCTTTAT ATnGAGGTAA AGCACATCAT GTkGTTaATT 60  
 TTATGcmTTT TaTTGcmCma GraTTAaGAG AAATTTTAGC nTCTTTAGGT TTGAAACGTG 120  
 TAGAAGACTT AGTTGGAAGA ACTGATTTAT TACAACGATC aTCAACATTA AAAGCGAATA 180  
 GCAAAGCGGC TAGTATTGAT GTTGAAAAAC TGTTATGTCC TTTCGATGGG CCAAACACAA 240  
 AAGAAATTCA ACAAATCAT AATCTTGAGC ATGGATTTGA TTAAACAAAT TTATATGAAG 300

AACAACGTGA TGTAGGGGTT ATTACAGGTA GTGAGATTTT GAAACAATAT GGAGAAGCAG 420  
 GACTTCCTGA AAATACAATT AATGTTTATA CGAATGGTCA TGCTGGTCAA AGTTTGACAG 480  
 5 ATATGCA 487

## (2) INFORMATION FOR SEQ ID NO: 3219:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 176 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3219:

ACCAACTCGG AATCATGCAA TGAACACCAT GGTGAAATA AGTGAATTGC ATAAGTATCC 60  
 20 TGGCCTGGCA ATGCTGGTAT AACCTAAAAC CTTGTTGCAC GAAATGTATT CGCTACAATT 120  
 AATGTACCTG CAAAACCGTT TAATAAGAAG TTCGAAATCG TTGCACCTGT ATATGG 176

## (2) INFORMATION FOR SEQ ID NO: 3220:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 203 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3220:

CTGATTTAGG TAATCTTTGC GCAATTGTTT TTTTACAGTT TCGGCAAATG GGTGCCCnGG 60  
 35 CAAATAAATA TTGGCTATGC TCAAACCTGA ATTAATGGTG GGTGTGTCCG CCATCGTAAT 120  
 TGGGnCCGCC TGAAGGGCCG CATATAAATG ATAGTGCTCT TCCGAATAAA AGGTAGGCCA 180  
 40 TATGTAATTG TTTTGTGGTT ACG 203

## (2) INFORMATION FOR SEQ ID NO: 3221:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3221:

AGCTAAATCT TGCCAATATG GTATCAACTT TTCATTCCAC TGATAATCAT AAATTTGAGA 60



GCAATGCCAG AAATGTATTA ACAACTGGCA CGTCTAATAG ATTGCTAACG GATTGTTTAC 180  
 GTACGTTTCAT CGGCTTCTTT CGCTTCTATC GGATCTGGAG AATTGGGATG TTATGACCAC 240  
 5 TGAACCACTT ATTTGTAAGC TCTGTCGTGA TTGACTTCAT AATGCTTGCG CTTGnCCTCA 300  
 TTTCTAACAA CTCATCCTAC TTACnAAATT ACCCnGGGG TACACCTGGT CCACTTCATC 360  
 A 361

10

## (2) INFORMATION FOR SEQ ID NO: 3222:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 152 base pairs  
 15 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3222:

GGGGCTCCGn GGAGGCAAGG GTAGAAAATG ATGTAAACGC TGCATTACTA GGCGAATTGA 60  
 AATTACATCA ATATCAAGCA GAACGGATCT TTTGTATGAC GCTTGGTACA GGCATTGGGG 120  
 25 GTGCGTACAA GAATTAATCA AGGTTTCATGT TG 152

## (2) INFORMATION FOR SEQ ID NO: 3223:

(i) SEQUENCE CHARACTERISTICS:  
 30 (A) LENGTH: 123 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3223:

TTTGTTAAAT ATAGGCCCTG CAATGAGTGT ACTGGAATGG CAATAATCAT ACCATACAGT 60  
 40 AATACATCTC CAACATTTGC CTTnAATTCT TTTCCCATGA CTACCGGTCC TGGGATGTGG 120  
 TGG 123

## (2) INFORMATION FOR SEQ ID NO: 3224:

45

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 145 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 50 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3224:

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TGGTTGGTAA CCGTAAATTA ATGCCTGACA ATGATATTAG CTnCTAAGC ATATTTCTGA 120

TGATTTAACA CATTATGAAA CGAGA 145

(2) INFORMATION FOR SEQ ID NO: 3225:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 129 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3225:

GGTATTGTCT AGTCAATTAC TAACACCATT TAATTGTGGn AAGCAAAAGC TAAAGGTTAT 60

CGTGCGCTAT TGCAGGCATT GATGCTTCCA ACAAAGTCGA GTATTCAGTT GCATCAAAAG 120

TTTGCTTTT 129

(2) INFORMATION FOR SEQ ID NO: 3226:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 170 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3226:

GACACTACCG TTCCACGTA GCATCAATCG TCTCAGTCGC ATCGTAGTCA TCTGTATGTG 60

TTCCAGCATA TACAATTTTG CCATCTTTAA TGACAACGTA CCATTTTCAC AACATTTATT 120

CATCTANTCC TACCCTCAAA GTTATCGTTG ATCTCGTAAA TAGTCGGCAA 170

(2) INFORMATION FOR SEQ ID NO: 3227:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 140 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3227:

TTACTGCTTT ACGTTTATCA TTTTCTAATT CanAAATTCG TCATTCAGTT TCAACTTTAT 60

CGACAGCTGG ACTTTGCGCA GATAAATGTG CTGCTGTAAT ATCTAACACA TCGATTGCTC 120

TTATCTGGCA ATAATCGTTG 140

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear.

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3228:

GCGCCTATAA TTGCGCTACT TGATTTAATT GAGTAGATAA ATCTAATCCG AATAAATCCG 60  
 TGACTTGCTT GATAAATAGC AACAAATGCTn CAACTAAACC AGTTAGTACT GCTTTGTTTT 120

## (2) INFORMATION FOR SEQ ID NO: 3229:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3229:

GGCTATACAC CGACTACAGT AACATCTGGT AGCGACATTG AAAAAGACTC TAATGGTTTA 60  
 ACAACAACAG GTGTTATTAA TGGTGCTGAT AACATGTACA TTAGATAGTG GntTCTACA 119

## (2) INFORMATION FOR SEQ ID NO: 3230:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3230:

TGGGAATAGC AACCAACAAT GCGACAACAA AGCCCGCTAC AAATCTCCAT nAACTAATTG 60  
 CTAAATGTTG GAAAAATTTT TCCAGTCAAC AATGAAAGGC CATATGACTT TTTCTACAA 120  
 GAGCAGGG 128

## (2) INFORMATION FOR SEQ ID NO: 3231:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

AATGCAGCTA TTACTTTTCA CAGATTCCAT ATCGTTCAAC ATTTAAATAG AGAACTTAAT 60  
 AAGTATCGTG TACAAGTTAT GAATGANTAC CGTAATAAAA AAGGACCTGA TTATACAATT 120  
 TTC 123

## (2) INFORMATION FOR SEQ ID NO: 3232:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1656 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3232:

GCCTCAAAGA ACATGCTGAA CAGTCATCGC aTTCATATAG TTTGAAGTCT CGTTTAAAAC 60  
 CATATCTATC ATTACGGTAT GCATATCTTT TAAAACCTAT TCTTTTGTTA TTAGGACATA 120  
 TAAATTCATC ATTAAGTTTCG TCATATTTCC AATTTTGAGT GTCGAAAATG TCACTTTTAA 180  
 ACTTTCTAGT TTTATCTTTA ATAAACATGC CATACGTAAT AAGTGGCGTT TTATTAAAAT 240  
 CATCTATAAT GGCCATATAG TTTTGCTCAC TACCATAACC TGCATCAGCT ACAATAAACC 300  
 GAAGLATTTT GAATCATTGT TAAAAATGGA ATTAAAGTTC TAGTATCTGT CGGGTTTTGA 360  
 AATAGGTCAT AGGATAAAAC AAATTGAGAA TTTGTCGCTA TTTGTAAATT GTATCCTGGC 420  
 TTAAGTTGGC CATTTTTTCAT ATGGTCTTCC TTCATTCTCA TAAAAGTTGC ATCATGATCA 480  
 GTTTTAGAAA AACTATTTCT ATCTTTAAGA ATCGATTTTT GTTCTTCATA TTTATTTTTT 540  
 CTTTCGGAAT AATCATCAAA TTTmTTTTTG AACTTCTTAA TCTTAGTTCT TTTTtaCGGG 600  
 TCTGTTTTCT AATTTGAGTA CTATCTTCGT TCTCAATAGA ATGATTTAAA yCTTCGATTT 660  
 CTTTATCTAA ATGACTACCA ATTAAATCTA TTTCTTCTAT TGTTAAATCG CTATCTCCAT 720  
 CTTCTTTTAT CTCTGGTATT ATTTTTTCTT CAACTAAGTC ACGATATAAT GTTTTTGAAT 780  
 TTTGTTCAA TTTGATTTCG TGATTTTGAA TACTTTTCTT CCACACAAAT GTATACCTAT 840  
 TGGCATTAGC TTCTACTTTT GTACCATCAA TAAGATTTTG CTTTAAACAT TGACTATGAA 900  
 ACTGGATAAA TAAAGATTCA ATTAACGCAT CAGTATTAGG ATTCACTCTA ATACGATTAA 960  
 TAGTTTTATA AGAAGGTGTT TGATTTTGAG CTAACCACAT CATTCGAATA CTGTCATGAA 1020  
 GTAATTTCTC TATTCTACGA CCAGAAAATA CAGATTGAGT ATATGCATAT AAGGTGATTT 1080  
 TTAACATCAT TTTTGGATGA TAGGATGTTG CGCCACGATG ATGTCTGAAT TTATCGAATT 1140  
 CGCTATCAGG TATCGTTTCA ACAATTTTCAT TAACATATCG CGAAATATCA ATTTGAGGAA 1200

GGCACTTCAT TAATTTAGTT TAGTGGTATT TATTAAATTA TACGAAGGGA CCCAACACAG 1320  
 AAAATTCAAA TTATTGAATT AAACATTTAT GTGCAAGTTT GGCAAAGTGT CTTATTTTTT 1380  
 5 AAAAGTATGT AAAAGTAAAA TTACATGTTA ATACGTAGTA TTAATGGCGA GACTCCTGAG 1440  
 GGAGCAGTGC CAGTCGAAGc CGAGGCTGAG ACGGCACCCT AGGAAAGCGA rCCATTCAAT 1500  
 ACGAaGTATT GTATAAATAG AGAACAGCAG TAAGATATTT tCTAATTGAA AATTATCTTA 1560  
 10 CTGCTGTTTT TTTAGGGATT TATGTCCCAG CCTGTTTTTT GTGATTTTTTA ATAATTTGAA 1620  
 TATGGrAAAT GTATTaWTct CTCATTTGTA TAGATT 1656

## (2) INFORMATION FOR SEQ ID NO: 3233:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3233:

TTGCTCATAA ATCTTTTCTT GGCGCTCTGA ACACTATCTT CTATTCTGTC GGAATTTTTT 60  
 AAACATAGTC TTATCATTTn CTTCTAATCG CGTTAAACGC CAATCTTGTT CATGTCGTTT 120  
 GGTAATCCA 130

## (2) INFORMATION FOR SEQ ID NO: 3234:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3234:

GCCACGATAA AGAAGTAAGA ACAACACATG GTGTTACTGG TACAGGCTCA TGTTCCTGGG 60  
 AAAGTTATTT GTGnAAAATG GTGTGAATTA CCTGGGGAAA AATCAACAAA CTGACTATCC 120  
 45 AA 122

## (2) INFORMATION FOR SEQ ID NO: 3235:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3235:

5 AACCAGGATA TGAAATCTGT GACTTATTGC GTTAGATCGT TTTGTAAC TG CTACTATTGA 60  
 AGAAGCAGAC CAATATAAAG GTACCATTCA TTGCAAAGC ATTACATGCA TGAACCCAGT 120  
 TGACATTTAG TTAGAGATGG AAGATAGTAT TGTGCATTG CAGnTTCCAC ATG 173

10 (2) INFORMATION FOR SEQ ID NO: 3236:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 122 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3236:

20 GCGGTGTGCA TTTGAAATG TTATCAAGAA TATTGAGTTA ATTCGCAACG ACATTATACC 60  
 AGCGATTANA AAGCATTAT CAAAATACGA GGGGCGTCAT CATGAATATT GTATTATTGT 120  
 CA 122

## (2) INFORMATION FOR SEQ ID NO: 3237:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 182 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3237:

35 TTTTTTGCCC AAAATTTTTG GGTTTTTTTT GGGTTAAAGG AAAAAAATT TTAAAGGGG 60  
 GGGGGGGGTC CCCC AAAAT TTTTTCCCT TCCCTTTGGT TTGGTTTTTT GGGGGGGGGG 120  
 40 CCCCCCCCCT TTGAAAACC CCTTAAAAAA ATTTAAAGGT TAAATTGGAA AAAAAAATT 180  
 AA 182

## (2) INFORMATION FOR SEQ ID NO: 3238:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 111 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3238:

GATGANGTTC GACAACGTAT TGTGGCAGAT GTTGCACTTG ACTTTGAAGA A

111

(2) INFORMATION FOR SEQ ID NO: 3239:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 120 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3239:

AGTTGATCGT ATTTTCCAGA AGAGACAGAA TTAATTGATT ATCGTGTTAG TTCTGTCACT 60  
GAAGGTACTG ATGCCCAAGC AGnAGTACAT GTAAGTTTAT TGATTGAGGT AAGACTGTCA 120

(2) INFORMATION FOR SEQ ID NO: 3240:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 127 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3240:

TACACATCTn TCTACGATTG TAGTTTATCG ATAGGTTTCG CATCATGAAA CGTGATAAAC 60  
AACCAACATG ATGCTAGTTT GATTAAGTTT CTTCTAAACA GACTTCAAAC GGCAGTGTTT 120  
AGCATAT 127

(2) INFORMATION FOR SEQ ID NO: 3241:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 124 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3241:

GACTAAAATA CATGTTGGAA TACTTGGTCC CATGGGAAAA TATTGGACTG GGTAACCCAA 60  
TCACGGCTTC TGAAGTAGTT CTTTnTCTTC TATTAAAATA GCGACGGAAT CACACCTTCT 120  
GCGG 124

(2) INFORMATION FOR SEQ ID NO: 3242:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 122 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3242:

10

TACGTGTATA CACCGTTATC TTTATGGCTT TGAATTTCCA TAATAAATAC ATACGGnTTT 60  
TGTGCAGAGC TCAGCACATA ATCATCTTTA ACTATAGTTT CTGGGAATCA CTTCATAGTT 120  
TT 122

(2) INFORMATION FOR SEQ ID NO: 3243:

15

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 221 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3243:

25

AACCTTTTCT GCAACCATAC GCCATAGgTA TGtTTTCTTT TTACAATTAA AGaGCCAACC 60  
GTTGTTATAG TCTAACAATG GTTGGCTCCT CTTtTTTTAT GTGCTAAAAA TTTATAGGCA 120  
ATTTTATTAC AACAAATGTAC ATTTAAGGTG ACCTTCATGC CAAAATCGCA TCACTCATT 180  
AATGGAAGCA GCACGTCTTC ATACAAAGTC ACGATCCTAA T 221

30

(2) INFORMATION FOR SEQ ID NO: 3244:

35

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 224 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3244:

45

TTGCATTTTG ATTGTCTGGT GACCTTGGCA ATGACAATTC CCGCTTGCAA TCGGTATCTT 60  
CAATATTATA ATCAGGTCTT GCCTTAGATT TTCGCTAAGT ACCGGTGATT CTCTACCATC 120  
ATACTCACCT CATGnGCTAT TTTTCTAGAG TGCTTCTTTT CACACTTTAT CTTATAAAAG 180  
GCTAGCTACT ATTACCGATT TATCATTATT AGTGGTTTTT ACCn 224

50

(2) INFORMATION FOR SEQ ID NO: 3245:

55

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 117 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3245:

5 GAAAGAGATT AGTGACAAGT TGGTTGTACT ATTACGTAA AATTTGGAGA TTATGTGTGG 60  
TGTTCAGTA TCGGTTCAAT AATTGATATT GCGGCACCGT ATAACCATGT CAAAGTA 117

(2) INFORMATION FOR SEQ ID NO: 3246:

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3246:

CTACAGGCTT TCGTACCACA GGATCAAAAC TACGCACTGT GCCTTGTTACA TACGCATGAT 60  
20 CAGCAATGAC ATTCCAAGTA TTACCACATG ATATTGnCC AATTGTTACT ACCGTTC 117

(2) INFORMATION FOR SEQ ID NO: 3247:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3247:

TACACAnCTT TCTACGTGTG TAGTTTATCG ATAGGTTTCG CATCATGAAA AGTGATAAAC 60  
35 AGCCAACATG ATGCTAGTTT GATTAAGTTT CTTCTAAACA GACTTCAAAC GGCATGT 117

(2) INFORMATION FOR SEQ ID NO: 3248:

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3248:

CCCGTCCTTT GGTGGAACCG TTTTGTAGAA TTAAATAATA TTACAGAGCC GCTAGCAGTA 60  
ACGATCCAAA CGAATTTACC ACCATCACGT GGATTAGGAT CGAGTGCACT GTCGCGGTTG 120  
50 CnTTTGGTCC TGCCA 135

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 106 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3249:

AAAAGCCAAC CCATGnAATG TTGGATTGGC TTTTACATG CCATCTGAAT CTCTAATTTT 60  
AAAAAATAT GGAATATAAA TAAGACAGTA AAAATTAAAT TTCAGT 106

(2) INFORMATION FOR SEQ ID NO: 3250:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 122 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3250:

AACGCTGAAG CAGATAAAAA ACGTCGTGAT AGAAGTAGAC TTAAGAAACG AGTCTGACAn 60  
TCTAGTATTC CAAGTTGAAA AAACTTTTAA CTGTATTTAG GCGAAAATAT CGGTGAAGAA 120  
GA 122

(2) INFORMATION FOR SEQ ID NO: 3251:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 132 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3251:

GAACGTTGAG ATGTCACAAA CTGGTGAAAG TGCACGTTCA ATGCCAATGA CTGATAAAAC 60  
CAAATTCATC AATCACAAAT ACTCCGAAAG CnGGTACAGG TCACTCAGTA AGTAGTAATC 120  
CCAGTACATT AA 132

(2) INFORMATION FOR SEQ ID NO: 3252:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 115 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3252:

GGAAAATCTT CAAATTCTGC AAATTGCCAA TTTACCTAAT AACCAAACAT CTAAGGCATG 60  
 5 TGTAAATGCTG CTACnTCCGC TTCGTCAATCA GCTACAATGA CAAATACAGG TGCCA 115

## (2) INFORMATION FOR SEQ ID NO: 3253:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3253:

TTTCGTCAAA TTATGGGAAT AAAATAATCA TATTTAAGAT AGTAAATATT GAATAAGTTG 60  
 20 CTTTGAAATT TATAAAATGA AAGTATAGTG TCATGGGnAG TATAATAGTC AGATATATAT 120  
 GTAACGGCAC TATATTGAAA 140

## (2) INFORMATION FOR SEQ ID NO: 3254:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3254:

AAATCTCCTA CTTTTTCTAC CCATAAATAA TTGGCTAACT TTTTCATCTT ATCTTCATCC 60  
 35 TTTCTCTTCT ATTTAAAATG CTACAAATAA ATTTCCGCGA GTAATTTTAA TGTTTTACAA 120  
 CGCTGTTCAA TACCTGGAAT AAGCGGTGCT ACTAACACCT CATCAACTTC AaACGTAGCA 180  
 40 ATGAAATCAT CTAATTGTGC TTTAACCTWT TCTTGTGTAC CTGcaATGAT GCGTGCTTGg 240  
 ATGTGCTTGA ATCATCTCTT TGTCTCGATC ATTAAGCTTA TACTTTTGTG CTGTGTCTAC 300  
 TGAAGGAAAA TCTTCAAATT CTGCAAATGT AATTTACCa ATAACCAAAC ATCTAAGGCA 360  
 45 GTTGTAAGCG GChACTTCCG CTTGTTATC AGChACAAG 399

## (2) INFORMATION FOR SEQ ID NO: 3255:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3255:

ACCATTGTC AAAATATTCC AACACGCATT TAGGTGTGCA AGGTATCGGT ACCTAACAAAC 60  
5 GAAGCTATCG TCTCACTAnC CTAAAAGAT TTTAGAACAA CAGCTGCACT CATCAT 116

(2) INFORMATION FOR SEQ ID NO: 3256:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 106 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3256:

AAAGACCTAA GGTTATGTAA TTGGCCTAAA TTTATTAATC GTTTAAATTC AGTTAGTAAA 60  
20 AAGTCTGTGA GTAAGGGTGT ATGGAACTG GTTAAATATT ATAGAG 106

(2) INFORMATION FOR SEQ ID NO: 3257:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 114 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3257:

AACGTCCATC GTAATACCTT TTGTGTCTAA TGTAAGTGT ACATCGTCTA ATAATAAGTT 60  
35 GACGATATCT TGACAATGCA TCTTTATCTA GATGTAAGAn TTCAACGGAT GCCG 114

(2) INFORMATION FOR SEQ ID NO: 3258:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 117 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3258:

TTAAAGCAGT TAATCCACAG GGAAAGTGGT TAATACAGTT GGGCTCTGGT GGATAGTACA 60  
50 GTTGCAGGCA TGGTGGGCTG GGAATTGCTT CAGGGTTTAA CGAnTGGGAA AAGCCTT 117

(2) INFORMATION FOR SEQ ID NO: 3259:

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 124 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3259:

GGACCGCCAT ATCGTTGGCA ATCATCGCAC CTATAATCAT CGCAAGTATA ATAATATTAG 60  
10 CACCTTGCACT ACTTTTAAAC CAGGTTGTTA ATGCCTCAAA AATATTAGAA ATTGGTGCCC 120  
GnTT 124

(2) INFORMATION FOR SEQ ID NO: 3260:

15

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 130 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3260:

TACCAATGTA TATCCATATA CTTTATCAT AATCATTTCA GCCGACTTTA GTTTGATGTT 60  
25 TTTGCTTGAT TAAAACTTT CGGCGATCTT CAGCTTGATG TTTTCGTTTG ATTAAATTGG 120  
TACAATAAT 130

(2) INFORMATION FOR SEQ ID NO: 3261:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3261:

GGCCTTTTTG GGCCGGGGTT GGAAATTGGG GTTGCTTAA TTTTTTAATT AAATTTTGA 60  
ATTAAAAAAG GAAAAAATCC AAAGGTTAAT TTTAAAAAA GCCCAAGGTT TTAAAAATTC 120  
CCCCAACCAA AAAGGGGGGG AAAAAGGTT GGGGGTTTTA AAAATTAnCC AAGGTTTTTG 180  
45 GGGCCCTCCC TTGGGGGTTG GGAATTAAAG GTTAACCAAG GTTTTTGGCC AAGGGGCCCA 240  
ATTGGGGGTT GGGGCCCTGG GGGAAAATT TTGCCCTTC CCAAGGGGTT TTTTAAACC 300  
CGGATTTTTG GAAAAAATA AGCCCATTTT CCCCCCAACC CnAAAGCCCA GTTCCCGCCC 360  
50 ATTTTCCCGG GGTAAACCCTG CCCCCACCGG GGCCATTTTT 400

(2) INFORMATION FOR SEQ ID NO: 3262:

55

(A) LENGTH: 134 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3262:

10 TGGTTCAATG GAAACGTGTA CCGCAAATnC CGTTAAATGT TGTGGATGT TGAGAGACGT 60  
 GGCTGAACTG GCACATTTGG GCAATGACCA ATGGAACAAG CTAATGGGCA AGCGATTATT 120  
 GCGACGGCTG ATGG 134

(2) INFORMATION FOR SEQ ID NO: 3263:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 105 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3263:

25 TTTTTTCTG TTGGTACTTG TTTTGTGGTT GGCGATTGTG GTGTGTCTGA nTTAGTAGAT 60  
 TGCATTGGTT GTGGCGTGTT TGCTTGATGG AGGTGTTGTC ACTTT 105

(2) INFORMATION FOR SEQ ID NO: 3264:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 107 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3264:

40 GTTCCATCAT TCCCACnAT ATCCAACATG TGGGCTACTG CAATGCTTTA GCGGTCAATG 60  
 CCTCATCATC ATCAGCGC CAGTAAATGC GTATAATTAA ATTAATT 107

(2) INFORMATION FOR SEQ ID NO: 3265:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 109 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3265:

GTCGTAACAA TGGTTCGTTA CCAAAGCATA nTTCGCCTTC TTGGCATCG

109

(2) INFORMATION FOR SEQ ID NO: 3266:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 104 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3266:

TTACCTTTAA AATAANGTTC TCCACTAGTT GGGCTAAACA AATTACATAT TTTGCTTTTG

60

GAAATGTACT TTTTACCACT ACCTGATGGA CCTATAATGG GCAA

104

(2) INFORMATION FOR SEQ ID NO: 3267:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 117 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3267:

TAAGCCATCA GAAACAAATG CATATAACGn AACAAACAT GCAAATGGTT CAAGTATCAT

60

ACGGTGCTCG TCCGACATAC AAGAAGCCAA GCGAGAACGA ATGCATACAA TGTAACA

117

(2) INFORMATION FOR SEQ ID NO: 3268:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 101 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3268:

GCTGCACAAG CACAACCTGG AATCAGCAAC ACCGGCAAAC CAnCAGGTCA AGGAATAACC

60

AAGCAGCACC TCATAATAAT GCAACACCGG CAATCAAACA C

101

(2) INFORMATION FOR SEQ ID NO: 3269:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 207 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3269:

5 CATACCCTAT TTTAGATATT ACCTTATTAC AAAATATTTT TACATTAATG TCAGCTGCAG 60  
 GTTAGTATTG TTTTCCAAAA TTTACCGGTC ATCTTTGCCA ATTGGGTGTC GCCAATCGGG 120  
 ATTTATCCTA GGAAGCCGAT TAAAAGGGTA CTGCCAGGT TTTAGCCTGC nGCTGCCTCG 180  
 GGGTTTTCTT TAAATTAATG nAACCGC 207

(2) INFORMATION FOR SEQ ID NO: 3270:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 107 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3270:

20 ATATTGCGAC CACCATAAAC ATAGATGGTG TTTTGTCTT CTGCATTAC AGTGATAAAA 60  
 GGGCTTGGnC CCGTTTTTGC TTCAGCTGTT TTGAATAATA TATGATG 107

(2) INFORMATION FOR SEQ ID NO: 3271:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 122 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3271:

35 TTGGTTACAC TTCTGCTAGT TTTAGTAACG ATGGTCCAAG ATTGTATGAG CCTATTCATG 60  
 GATCAGCACC AGATATTGCA GGTAAAAACG TTGCCAATCC ATTTGGGATG GTTCTnATGC 120  
 TT 122

(2) INFORMATION FOR SEQ ID NO: 3272:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 360 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3272:

50 GAAGGATGAT GATTCCGAGC AnCTTCTTGC AGAAGAnGCG GnaATAACGT GACATATTGT 60



TGCGAGCGCT TGACAATCTA TTCITTTTAA AGAAAGCGGT TGTTAGACAA TGCATTAAGA 180  
 GAAATTAAAG CGGmGTTTAC TTTTGTAAT GAGCATTTGA TTTTtTGAAA ATAAAGCAGT 240  
 5 ATGCAGGCGC TTGACTAAAA AGAAATTGTA CATTGACAAC TAGATAAGTA AAGTGAAAAT 300  
 ATAGATTTTA CCCAAGCAAA ACCGAGTGAA TAAAGAGTTT TAAATAAGCT TGGATTCATA 360

(2) INFORMATION FOR SEQ ID NO: 3273:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 112 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3273:

20 TCAATTTTAA CTGCAAATAA TAAAGCTGCA TGATTTACTT TGTACATTAT TGTAATTTCA 60  
 GTAATACGAG GCAATGTCAG TnGCAGTGTT TAATAAATTT TGTTCGCTAT TT 112

(2) INFORMATION FOR SEQ ID NO: 3274:

- 25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 336 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3274:

35 TACATTTTATG CAATCAACGT TACATTCAAT CGTTGGAGAA AATTGGCTTT ATTGACTTAC 60  
 TAAAATCTAA AAAATCATAT GAAAGAATTG CACATATGTT AAAAACtGGT AAGCCATTAC 120  
 GTAATTAAAA GATAGTCATT AAGAGAGGAT GATAACCATG CAAGAAAGCA TACATTGTAG 180  
 40 CTTATGGGCG TTCAGCGCAG CGAAAGCAAA GCAAGGCGCA TTATTCCACG AAAAGACCTG 240  
 nTGATGTGCG AGCCAAAGTA ATTACAAGGC GTATTTGAAA ACGTATTGAC GGGAnAAATT 300  
 CCAATAAGGA TTATGGATTG nAAGATGGTC CATTTG 336

45 (2) INFORMATION FOR SEQ ID NO: 3275:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 138 base pairs  
 50 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

CAAATGCTTT TGCCACCCCA GATGCAATGG TACCAACACC TGTTTTCGAA ACTAATTTTA 60  
 CCGGCGATAT CTGGCATCTT TTATTTTCGGC ATTTTTTCAA ATCATGGTTA TTCCAGTTTG 120  
 5 GCGGCTTAAA AATTCnTT 138

## (2) INFORMATION FOR SEQ ID NO: 3276:

- (i) SEQUENCE CHARACTERISTICS:  
 10 (A) LENGTH: 101 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3276:

CATTATACGA GnATAAGTAA AATTGATGAT GTGACTAAAA AAGATGCACA ACAATTATTG 60  
 20 AAGATGCAAA AGAATTGCAT GCCAAGCTGA TACATTAGAT A 101

## (2) INFORMATION FOR SEQ ID NO: 3277:

- (i) SEQUENCE CHARACTERISTICS:  
 25 (A) LENGTH: 124 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3277:

TGGTTATTCTG TTCCTGATCG TTGTTGGTAT CTCACTATTC AAnATTATC GTGTGGCATT 60  
 35 ACTTTAGTTA CACCAGGTAC ATTTGAACCT GGCACATTGTT GCGAGTATTT CCGGTCTCGT 120  
 CATT 124

## (2) INFORMATION FOR SEQ ID NO: 3278:

- (i) SEQUENCE CHARACTERISTICS:  
 40 (A) LENGTH: 110 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3278:

GACTTTTTGA CCAGTTGTAG CACGACCACC GAGAGTAGCA TTGCATATGC AATCATTGTA 60  
 50 CCTTCGCCAA CGACTGnGCC AATATTAATT GTTGCGCCCA TCATAACGAC 110

## (2) INFORMATION FOR SEQ ID NO: 3279:

(A) LENGTH: 113 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3279:

10 TTGGTATATA GAGGGCAACC GCACCTGATA AAATGTGnCA CAGTTTTTAC AAGAGGTTAA 60  
 GGAATGAGTT TGGAGGCATA CGAGCATCAA GATACCATTC GATGTTAGTA ATT 113

(2) INFORMATION FOR SEQ ID NO: 3280:

15

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 101 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3280:

25 TTACCGTCAC CGTAATCAGT CCATACTTTA TCAGCTATAC CGGCTTTAAC AGCATAAATG 60  
 TTCGTTCCCTG TAGGCATACC AAAGnCGATA CCATAGTGAC G 101

(2) INFORMATION FOR SEQ ID NO: 3281:

30

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 116 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3281:

40 ACTATGTTTG AAAAAATCGA CAGAATCAGA AGCACAGTCT GAGAACGCAA GAAAAAATTT 60  
 ATGACAAGTT AGATAGAAAT TTCGACGAAC TAAGGGCGTG ACCAAGAAGA AGATGA 116

(2) INFORMATION FOR SEQ ID NO: 3282:

45

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 148 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3282:

55 ACTTGGTTAG ATAATATAGC GTCGATTGTA TCACGAGTGT CTGTTCCAGT CATTATAAAA 60

CGTCGTTCTG ATGCTTTTCC TGAATCAT

148

## (2) INFORMATION FOR SEQ ID NO: 3283:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 100 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
10 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3283:

15 AAATGACGAT AGAGTCAGGT ATTAACATCAT TTTnCAATAG TATCAGGAAG ACTACCAAGC 60  
TTATGTTGAA GGGCATCTTT TGGCGTTACC GGGTTGGGCA 100

## (2) INFORMATION FOR SEQ ID NO: 3284:

- 20 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 101 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
25 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3284:

30 TTAAGAAACC GAGCAGCGCA TAAncCTGCA GTACCTTATC GCTTCTAGAT AATCCGATTG 60  
CGACACCATT GCAAGATGAC CGGTAATTTT GGAACATATA C 101

## (2) INFORMATION FOR SEQ ID NO: 3285:

- 35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 106 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
40 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3285:

45 TAAATATTT CGCATCCCTA CACGCTAAAA TAATACATTA CACTTAAAC GGCTGTTTnTA 60  
AAGCATCCTC CCATAACAT CATCTAGTTG ATAATAGGGG GGGGGn 106

## (2) INFORMATION FOR SEQ ID NO: 3286:

- 50 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 95 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
55 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3286:

TTTAACAATA CCTCAGAACA TACTATGGAA ATTGCTGCAA AGTTAATTGG GCATGCATAT 60  
 5 TGATCATAAT GCGCTTTTAA ATAAAATGGT GGAGA 95

## (2) INFORMATION FOR SEQ ID NO: 3287:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3287:

TCGAAATAAT ATCTACGCAC ACTGATAACA TAAAAATGCC TGGTAGAATA CTAATGAAAT 60  
 20 AAGTGCATAC ATGACCACAT GAATGCTAAT AACATGcAG AACCCATTTT TTGAATATTT 120  
 CACCACTCGA ATCATCAATA C 141

## (2) INFORMATION FOR SEQ ID NO: 3288:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3288:

TAGCTGGACC AGAACACGGT TCGACGTTGC AGGAAGTCTT GAACAGTCGC TGAACGCCAA 60  
 35 GCGGATACTT GGGTTATCCA TGGTGAAAGn AATGGATTGG TGGTGCA 107

## (2) INFORMATION FOR SEQ ID NO: 3289:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3289:

GCTTTGCAAT GCCGATGTTA CTCGCAATAA TCATGTCGCA TCAATTACTT ATGGAAAGCA 60  
 50 GATTTACGTA TGTCTACAAG TTTAGGCGC 89

## (2) INFORMATION FOR SEQ ID NO: 3290:

(A) LENGTH: 108 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3290:

10 TGTACGCCA ACAACAAATC CTACGTCGAC AACTATTTT AAGCGATGAT TGCAATTAGA 60  
 CAGAAATCCA ATCATTTTTG CATTCCATCC AGTGCACAGA ATnTCGAG 108

(2) INFORMATION FOR SEQ ID NO: 3291:

15

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 109 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3291:

25 GATCAAGnCC TGAGAATTTA ATTTAATTTA TTTTATATT GGAGATGGTT AAAATGCTAA 60  
 AACTCAACAT GAGTAACCAA AATATTGCC TTA AAAATGC TGATCATTG 109

(2) INFORMATION FOR SEQ ID NO: 3292:

30

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 121 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3292:

TTGATAATTT TGATATAGAA AGTTATTTAA AATTCGAATA AAAATAATAA CTCATCGACG 60  
 40 TTTAATGGCT AGGTTCCAAT CAACTATGnG ACATAAATTC AAATTCGATC ACGTAACGAA 120  
 A 121

(2) INFORMATION FOR SEQ ID NO: 3293:

45

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 107 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3293:

55

GCGCGTAATA CCTGCACTAC CTCTATCGCT TCTAGATAAT GCGGTTG

107

## (2) INFORMATION FOR SEQ ID NO: 3294:

5

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3294:

15

AAAATGTTAA ACCAAAAAGT TTGGTGAGTT ATAATATGGA ATATTAAATC TGTAGAAGAT

60

AAAGCGAATA TAAAGTGATT AACTTTGGTA ATAAAGAATT AACAGCGAAA n

111

## (2) INFORMATION FOR SEQ ID NO: 3295:

20

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3295:

30

CCCCGACTAA ATCGAACGCT TTAATGTAAT GATTGTCCG AATCCCCATC CTGCACCTGA

60

TAATAAGGCG AATAGCAAGT TGGTCCCGT nGGGAAGCCA CTTGA

105

## (2) INFORMATION FOR SEQ ID NO: 3296:

35

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3296:

45

ATTTATTCAA AACCCGCCAC ATGGGGCAAC GGTGCCATG GCATGATAGT CCAGATACAT

60

GGAAAGGAAT ACAGTCCGGT TAACACTCCA TTAAAAACCT GCGGGTTGGT TAAACCATTT

120

AACCTAAATG GGTTCOAAGG GTTAACGCGG TTAAATGTT TGGAAAGGTT TnCCCAGTTT

180

CCAAAAAGTT TTTnATTCCC C

201

50

## (2) INFORMATION FOR SEQ ID NO: 3297:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 415 base pairs

55

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3297:

TTTAGACTTT CATCAGTGTT GAATATTTCT CCTTTAACGG TTATAGGTAA TATTTCTCTGA 60  
10 GAAATATTTT CATTCCTTTAC ATTTTCCGCT GTCAATTGAT GACTTCGATA AGCAAATTCA 120  
TCTTGTAATT CTCTTGAAAC ATCATACATC TkGGCCACAT TTTCAGCACC TkGAATCATT 180  
GATGGGTCGC TCATTTTCAGG TGCAAATGAT GCACGCTCAT AAAACTCAGG TAATGCTGTT 240  
15 TCGTACACAG AATGCGGTCTG TTTGATTTTC CAAGGTGCTC GACTTGTTACT TTCAACACCA 300  
CCTGCAATAT ATACCTTGCC AGCTCCGGCT TGGATCATGC GACATGCATA TTGaACACTT 360  
TCAAGTCCAG ACCCACATTG cCGATCGTT GTGaGCCAG TATTGAAGCT TAAGC 415

20

(2) INFORMATION FOR SEQ ID NO: 3298:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 164 base pairs  
(B) TYPE: nucleic acid  
25 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3298:

TTAATTGCAG CAGAGCGACT AGCTGATTCA GAGGTGTTAG TTTGTACGGT AATAGGATTC 60  
CCATTTAGGT GCATCGACCA ACTGCCCGAC GAAAAGCCAT TTTGAAAACC AGAAGATGC 120  
35 CGATTCAAAA ATGGGTGCCA AGATTGAAAA TTTGGACCAA TGGG 164

(2) INFORMATION FOR SEQ ID NO: 3299:

40

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 106 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3299:

GTAGATGCCA TTTTCACGTT TCTTAGTTAT TGGCATTTTT TAAATGCGAT GTGTGGCTTC 60  
TACATAACGG GAAATTTTAA GTTTTATGAA TcACATATC AATTGC 106

50

(2) INFORMATION FOR SEQ ID NO: 3300:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 102 base pairs

55



(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3300:

AAAAGGTGTT ATGAGATTAG TAAATCANTA GACAAGCAGG TAAATTAAGT GATGTCGCGT 60  
CATTTAAGGA AGCGATTAC AATCGAGAAC ACAAAGTACA AC 102

(2) INFORMATION FOR SEQ ID NO: 3301:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 127 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3301:

TTAAAAGTTT GGAGATTATG GTGTCGTCTT CAAGTATGCG TTCATTAAAT GATATTGGCG 60  
CACCGTATAA CCATGTCAAA GTACCATTTG NAATCAGTCA TTGGCGCAAT GGCTGCCCTA 120  
GCGTTCA 127

(2) INFORMATION FOR SEQ ID NO: 3302:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 137 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3302:

CCAGCTAGAC GATTGCTAAG GTATTGGATG TTGAAACGT CCATGGACCC AATTGATTAA 60  
TTGGnTGTA CTCGGTCAAT GGTATATCC TAAATGCACT GGCCTGCTGG TGTTCTTCTG 120  
GGCGTTGCTT CGGAAAT 137

(2) INFORMATION FOR SEQ ID NO: 3303:

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 399 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3303:

55

ATATAAATTA ACGACGCGTT AATGCAGGCT GATGTGATTT TTATTGGTTT CCCAATTTTC 120  
 AAGCTTCCAT CCCTGGTGCT TTGAAAAATG TGTTTGATCT ACTTCCAGTC AATGCGTTTC 180  
 5 GTGACAAGGT AATAGGACTT GTAGCGACAG CAGGTTCTAG TAAACATTAT TTAATTCCTG 240  
 AAATGCATTT AAAACCAATA TTGAGTTACA TGAAAGCACA TACGATGCAA ACGTATLATT 300  
 TATTGAAGAG AAAGATTTTT CAAATCAACA AATTGTCAAT GATGATGTTG TATTTCCGTT 360  
 10 AAAAGCGTTG GCACAATCCA CAATGCCAAG TGCCAAAGT 399

## (2) INFORMATION FOR SEQ ID NO: 3304:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 102 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3304:

CACCATTATT TACAGGACCT nCGATGACGT GTGGTCCTGT GTTAAGACAT AACATAATAT 60  
 25 TCTACCTTTG TAATCAGTAC GGGTTTATCT ATCACAGTAC GG 102

## (2) INFORMATION FOR SEQ ID NO: 3305:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 202 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3305:

TCAGCGTTAT CAATGAnTGA CTCTAATGCC TTTTACCCTA TTTTGTAAA TGGAACATGG 60  
 AAGCATAGAG ATGCGrAGTC AGCTAGCGAC TTACCTTGAC GTTTTGCGTA TTCATTCCAG 120  
 40 CTTTGTGGr ATGAGCGGAT ATAAGCATCT TTAGATAATG CACCATCAAC TAATGGATAT 180  
 TTATGTCCAG TTGGACGCCA GA 202

## (2) INFORMATION FOR SEQ ID NO: 3306:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 151 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

AAGATAGGGA TTTACACCTA TACCTCGTTC CGGGGAAGGG TCGGTGTTCT GAAAAGTTGG 60  
 AACTACTCCC GACAAATATT AAATTATGGG AGCGGGAAGG ATCAGGGATT TGACACCTAT 120  
 5 GACCTCCATT CCCAGGGAAG GGAATGTGAT T 151

## (2) INFORMATION FOR SEQ ID NO: 3307:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 87 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3307:

AATTTTCGTTA CCTGCGCCTT CTTTTTGCGG TTTTAAATA AGCGAAAATT TCAGGCGGTA 60  
 20 AGACATAACG TCCCAGAATA GCTAGGG 87

## (2) INFORMATION FOR SEQ ID NO: 3308:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 129 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3308:

ATGATGGCAA AGTCACCAA CTGATTGTGC ACACCAATCC ATCCATCTGC GCTGTAAATA 60  
 35 ATGGTTTCGCA ATAATTTTAA AATACCTTCC GCTACATTG ATTTAAAGCT GGTTGCGCAN 120  
 TGGACTAGA 129

## (2) INFORMATION FOR SEQ ID NO: 3309:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 128 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3309:

GTTCCTTTTA TCGTAGTTGG TGGGACTCCT TATCGGCATC GCGGCTGGAC TCTAGGCGGT 60  
 50 GGAAACGGAC ATTCAAAAGG GATTTAGTTC ATCCCAGATG GATTTCAATT TGGGGAATTC 120  
 CATTTGGA 128

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 83 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3310:

GTACGATTCA GCATAAAGTA CACCACATTT GTCACTACGA CATCTGTAGC TGGTATTGAT 60  
CATGCAATCA TGAATAACGC TAA 83

(2) INFORMATION FOR SEQ ID NO: 3311:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 85 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3311:

CTGAGGATAA AGCGTCTCCA AGATAAGTCT AAAGATCATC ATAATGGGCA AAAAAGGTGG 60  
CAGCGATTTCG GTGGCTGGGA ACAAG 85

(2) INFORMATION FOR SEQ ID NO: 3312:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 129 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3312:

ATTTTATGTC TAAATGCTGG ACCAACAGTA TTGGCTATTA TTTGGTAACG TGATTACTAC 60  
AAAAAATGGA CCGTTGAGTT CGTGGCACAT GATTGATTTT GTAAGTAAGT ATGATGCACA 120  
TGGGCTnTT 129

(2) INFORMATION FOR SEQ ID NO: 3313:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 82 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

TCACCTAAAA TTAATCAAGG GACTTAACAT TGGCGAGTCA AGGTATTGAT CAAGCTAATG 60  
GCACAGTTAA ATGATGCCAA AG 82

(2) INFORMATION FOR SEQ ID NO: 3314:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 87 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3314:

ATGTTATGGA AGAATATTGA GTTAATTGGC AACGACATTA TACCGGCGAT TAAAAAGCCT 60  
TTATCAAAAT AGTGAGGGGC GTCATCA 87

(2) INFORMATION FOR SEQ ID NO: 3315:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 136 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3315:

TGAACCCGTC GTTGCCCATTT TGCCGGTTCC CGAAAGCCGG CGCCnACGGT TCTCCCTGCC 60  
TAAATAGGGG ATGGAATATT AAACCATCTG CACCTGGTTT AACACGCTTT GCAATTTGAG 120  
TTAAGACATC ATAAGG 136

(2) INFORMATION FOR SEQ ID NO: 3316:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 108 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3316:

CATTGGCTGT GTCCATTTTT AATCGTTGCG AGTACGTnTA TTAGCAACTT GGAACTGCCA 60  
TTGTTAATTT CAGCTGTCTG TTACATTTCA ACCATAGTCT TTCACAAT 108

(2) INFORMATION FOR SEQ ID NO: 3317:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 142 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3317:

ATCTGAAGCT GGGTTTACTA GAGAAGGTAT GTACGTGACA TGAATTACTA ATGGATTTAT 60  
TCATCGAGTT ACATCTATAG TTTATTAAAT CAGATACGCC AAAATGCnAA TTAGCTTACA 120  
AAGATGATGC ATTAAATGCA CG 142

(2) INFORMATION FOR SEQ ID NO: 3318:

15

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 386 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3318:

AACATTATGT TAATCAACCT AATGAACGtC TTTATAAATT ACGCTAAACA ATATACAGAT 60  
ATGCCGTTTC TTATCATGCT GGATGAAGAT GAAAATGGAT ATAAAGCGGG TCGATTTTTA 120  
AGAGCGAGTG ACTTAGGTCA AACACAGAG CAAGGCCAAT GGAAGCCAGT TATTCATGAT 180  
GCAATCAGCG ATAGTTTAGT ACTACCTAAT GGCACAATGG GTCAACGTTG GGAAGAAGGT 240  
AAGAAGTGGG ACTTAAACT AGAAACAGAA GATGGTTnTA AAATTAnCCC TACATTATCA 300  
ATTACAGAAG GTGGATACGA ATTAGAAACA ATTCAATTCC CATACTTTGA TAGTGATGGA 360  
GATGGGATAT CATCGTCCAA TCCnAC 386

35

(2) INFORMATION FOR SEQ ID NO: 3319:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 123 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3319:

ACAAATGAATG ACATGATTCG AGGTGGACGA CCCCTCCTAT TTTGCATAAA TGCTTTTTGA 60  
ATCGCCGGTC ATAATGTTTC TTGnCCAATT AACTCAATAT TCTTCATGAC ATTTTCAAAT 120  
GGC 123

50

(2) INFORMATION FOR SEQ ID NO: 3320:

55

- (A) LENGTH: 104 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3320:

GGCGAACTGT CAATTGCCCG TATACAACGT ATTTTAAGAG CTGCAGAACA TnCGGGTGTT 60  
 AAACGTGTGG TCAATGACTG CCAACTTTGG TGCAGTTGGT TTTA 104

(2) INFORMATION FOR SEQ ID NO: 3321:

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3321:

GCGCCGGTTT TAACAGGTAA TTTAAACCA AATACTGATA GTAATGCATT AATAGTCAGC 60  
 AAAATACAAG TATT 74

(2) INFORMATION FOR SEQ ID NO: 3322:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3322:

TCACTCAGGG GGAGATGTCA ATGGGTCAAC ATTATTTGAC AAGGTGTGGA CAGACATGTG 60  
 TTATACGGGA AATTGGGCGA CCGCACT 87

(2) INFORMATION FOR SEQ ID NO: 3323:

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3323:

TGCCAAATGT TCCCATAATT TCATTACGAN TCTTAAGTAG GTGGCTATCA TTACGATGCG 60

55

AATGCGGTCG GAAAGATAAA TAGCTTCATC AATGTCATGC GTCATAAAA TAATAGTTGA 180  
 TTGCGTTTTA TGTTTTAGTT GCACTAGTTG ATCCTGAAGT TTATAACGTG TAAATGCATC 240  
 5 TAATGCACCT AATGGCTCAT CCATCAATAT AACGTTAGGC TTATGCACAT GCGCTCGACA 300  
 TAGTGCCAAA CGTTGTTTCA TACCCCGGA CAGTTGCTCG GGAAAATGCT TTCCCCTGTC 360  
 TTCTAAATCA ACTAATTTAA GCTGTGCGTT AATCTCTTCA 400

10 (2) INFORMATION FOR SEQ ID NO: 3324:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 106 base pairs  
 15 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3324:

GAAACCATCG ATTGTAGCAC GAACCATGTT GGATTGGTGT GTTtGnATCC TAATGTATTT 60  
 ACTTAAGATA TCAGTGATAC CTGTCTAATT GCAAGTACGG TCAGGA 106

25 (2) INFORMATION FOR SEQ ID NO: 3325:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 113 base pairs  
 (B) TYPE: nucleic acid  
 30 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3325:

35 TCTGAANTCG CTGTCTGAAT CTGGAATCAC TGTCTGAAAT CCGAAATCGC TAATCTGAAA 60  
 TCCTGAAATC CGCTAATCTG AAACCTGGAA GTCGCTGGTC TGGAAGCCCT GAA 113

40 (2) INFORMATION FOR SEQ ID NO: 3326:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 78 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3326:

50 TGTACGTAC TTGCTGTTCA ACAAATACGT CTTACTGGAC GTGCACCTCA TTCTTCATCA 60  
 TAGCCTTCTT CATTAAACC 78

55



- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 119 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3327:

AATTGAAAAT TATCTTACTG CGGTTTTTAG GGGTTTATGT CCCAGCCTCT TACTCnAATT 60  
ATATTCACTA TCCATTAGAC CAAATGGGCC ATTTCCAATA ATCCCGCGGT GGTTTCCGA 119

(2) INFORMATION FOR SEQ ID NO: 3328:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 71 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3328:

GTGTTAAAAC GTCACGACGT TTGTTTAAAA TGATGCGTCA TAATGTCTAC ACTTTGCTTG 60  
CGATCATTCA T 71

(2) INFORMATION FOR SEQ ID NO: 3329:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 70 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3329:

CTGACGAACC TTGCATCATT TAACTGTCCA TTAGCTTGAT CAATACCTTG ACTCGCAATG 60  
TTAAGTCCTT 70

(2) INFORMATION FOR SEQ ID NO: 3330:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 69 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3330:

CCAATCTCG

69

## (2) INFORMATION FOR SEQ ID NO: 3331:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 70 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3331:

GGACACTAAC ATTAATATGG ACTGGTAATG TTGCTGTAA TAACTCATA CCAAATCCTG  
GGCATCTCTT

## (2) INFORMATION FOR SEQ ID NO: 3332:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 82 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3332:

CCTTGGGCAC CTTCAATTG CATATTACGA CGTTTTCAG CTGGTTCAA TTGGCAATAA  
CTACACCTAG TGCAGTTGA TC

## (2) INFORMATION FOR SEQ ID NO: 3333:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 76 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3333:

ATAAAATAAT TAGAACTCTA ACATTGGTTT AACTAATGTT TAGACTTTTT GTGGTTTGTA  
AAAACAAGTA TATTGA

## (2) INFORMATION FOR SEQ ID NO: 3334:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 74 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3334:

TGGTAAGTTG AATAAAGTAT TGAAATCGTT GCCAATATCT TTATACCGTT GGTTCCCTGGC 60  
5 ATTTATTGGG AGGC 74

(2) INFORMATION FOR SEQ ID NO: 3335:

(i) SEQUENCE CHARACTERISTICS:  
10 (A) LENGTH: 74 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3335:

AGATAGTTAT GCGCAGTTAA AAACGGTGAA ATGTATTTGC AATAATATGC ATATAGGCAC 60  
20 CATACGAGTA AGGC 74

(2) INFORMATION FOR SEQ ID NO: 3336:

(i) SEQUENCE CHARACTERISTICS:  
25 (A) LENGTH: 76 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3336:

TTGAATCATT GTTAAAAATG GAATTAAAGT TGCTAGTATC TGTCGGGTTT TGAAATAGGT 60  
CATAGGAGAA AACAGG 76

35 (2) INFORMATION FOR SEQ ID NO: 3337:

(i) SEQUENCE CHARACTERISTICS:  
40 (A) LENGTH: 72 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3337:

CCAAAGAGGC GTTATTAAGC TATTGATAAA AGTTATGTTA CTAAAAAATG TATTTAAATA 60  
AGTAGTACCT AA 72

50 (2) INFORMATION FOR SEQ ID NO: 3338:

(i) SEQUENCE CHARACTERISTICS:  
55 (A) LENGTH: 75 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3338:

ATAAGTCGTT CTACCGTATA GCCGTCATTA TTAATCACAA ATAATACCGG TTAAATATGC 60

10

TGTCCTGGTCA TAGTT 75

(2) INFORMATION FOR SEQ ID NO: 3339:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 72 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3339:

TTCATCAAAG TATTCCAATG GGAGAAAAAG CACAATAACA TTATCACTGG ATGCTAAATC 60

25

TAAAGGAACC TC 72

(2) INFORMATION FOR SEQ ID NO: 3340:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 77 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3340:

GTAAAAATAT TTAAATGAAT GTCITCACTG GAGAACCATT GACAACCTGG TACAAGTGGG 60

40

ATTATTGGCG TTATTTT 77

(2) INFORMATION FOR SEQ ID NO: 3341:

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 67 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3341:

AACCAAGGAT GGATTGCTAT TTAATCCTT GGTGCTCTT TATTTATTT AAATTGTAGA 60

55

ACCTAGA 67

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3342:

CTGGCAAAAG CACGTTTAC AAGCATCAAT CCATTAAATTA ATAATTCCAT TAAATGTAGA 60  
 TTCACAGGGA TATG 74

## (2) INFORMATION FOR SEQ ID NO: 3343:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 415 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3343:

GTTTGATCAT TAGAGAGATA TAGATATGCC GTAGAAAATA ATATGTCATT TCGCGATATC 60  
 ATGGTTAAAG AAGAAATGGA ATTAAGCGGT AAATCACGTG ATGAAGTGCG AGCGaAATGA 120  
 AACAAAATTT AGATGTCATG CGAGACGCAT AATCAAAGGG ACGACAGGTG ATGGGGTTGA 180  
 AAGTGTAcGG TCTACACTGG TCATGATGCT GCTAAACTAC GTGATTATAA TGAAACACAT 240  
 CATGCTTTGT CTGGGATATG AAATGATTGA CGCACAAGGG TGCCATTGCA ACAAATGAAG 300  
 TCAATGCTGC CGATGGGTAT TATTTGTGCA CGCCAACAGC TGGTTCCTCG GGTACCATTC 360  
 CCGGTGGCAC TTTTAAATTA GAAAAACAC TGGATnGAAC CAGAAGAGCC AATGn 415

## (2) INFORMATION FOR SEQ ID NO: 3344:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3344:

TCCTATACCA CCACCGTCAA CAGCTCCTGC CATCGATCGT ACTTTCAATA AGTCCAATAA 60  
 TCGCAGTGGT AATTTCTAAT ACTA 84

## (2) INFORMATION FOR SEQ ID NO: 3345:

- (A) LENGTH: 474 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3345:

10 CGGGAGGTGT TAANTCTTCA CAAATGCCG TACTATTCTT TGATGnAATC CATCAAATTA 60  
 TCGGTTTCAGG TGCCACAGGA AGTGATTGAG GTAGCnAAGG GTTATCTGAT ATTTTGAAC 120  
 CTGCATTAAG TCGTGGTGAG ATTTCTATTA TTGGTGCaAC AACACAAGAT GAATATCGAA 180  
 15 ACAATATTCT TAAAGATGCT GCATTAACGC GCAGATTTAA TGAAGTGCTT GTTAATGAAC 240  
 CAAGCGCTAA AGATACTGTT GAAATTTTAA AAGGTATTCG CGAAAAATTC GAAGAACACC 300  
 ATCAAGTAAA ATTACCAGAT GACGTATTAA AAGCATGTGT TGACTTATCA ATTCAATATA 360  
 20 TTCCACAACG ATTATTACCA GATAAAGCAA TCGATGTGTT AGATATTACA GCAGCACATT 420  
 TATCnGCGCA AAGnCCAGCT GTCGATAAAG TTGAACTGG AGAACGAATT TCTG 474

25 (2) INFORMATION FOR SEQ ID NO: 3346:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 64 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3346:

35 AAAATTAATA ACTCCTTGGT TATTGATATG CCTAAAGAAG AAGGTACAAT ACAACTAACA 60  
 TTAG 64

40 (2) INFORMATION FOR SEQ ID NO: 3347:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 89 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3347:

50 AGGAATAACT TGATATTGAT GATAAAATCG TCAAACGGCA CTAATATTTA AAAACAAAT 60  
 GTTTTAAGTT GTTGATTAA AATATTAAT 89

55 (2) INFORMATION FOR SEQ ID NO: 3348:

- (A) LENGTH: 107 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3348:

10     ATAACTTGTA CTGCTTCCCA TTAATCACTG TGTCTCTTCA CCAGGAGCTG GCATTTCITT     60  
        AAAGAACAAT TCTGATAAAG GTACAATTTC ACCGGGCATA ACTTCAT     107

(2) INFORMATION FOR SEQ ID NO: 3349:

- 15     (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 74 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3349:

25     CAACGCATCC TGCATTITTA CCTATTCTCG AATCACCGGT AATTAGTACA CCAACACCGT     60  
        AAACATCTAC TAAA     74

(2) INFORMATION FOR SEQ ID NO: 3350:

- 30     (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 62 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3350:

40     AGATGCACCT ACTTCTAACT GTCGCCAACA TCGCCGCAAT CATTTCAAAA CTACGTTCTG     60  
        TA     62

(2) INFORMATION FOR SEQ ID NO: 3351:

- 45     (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 73 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3351:

55     GCTGCAACA ACAAACTATT TTTGATTAAA TTGTGGATAT GATGGTAACC AACCAAGTCT     60

## (2) INFORMATION FOR SEQ ID NO: 3352:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3352:

ATTGAACGCA AGATTTCGAT ATAGAACATC TAGCGACGTC GATTGCAAG GTTGAACCAT 60  
CTACATTAGG TGAGGAA 77

## (2) INFORMATION FOR SEQ ID NO: 3353:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3353:

TAATCAACAC GAGGAGATGC TATTTAATGT CATCTGACAC AAACAGTTTA GCACATACA 59

## (2) INFORMATION FOR SEQ ID NO: 3354:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3354:

TTATGTAACC GACGAATGCT GCGATAGTGC TACGCCATCA CCGCCAGCTA ATCCGATTG 59

## (2) INFORMATION FOR SEQ ID NO: 3355:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3355:

TAACTATACC TTTAGGGTTA CTACCAGCT TAGGTAGGTC ATAACCTTTA ACCACATCT 59



- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 59 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3356:

AATAACGCTA AACCTAAAT GCTAAATAAT CCGCCGAACA ACATGCCGTT GTTTGTTGA

(2) INFORMATION FOR SEQ ID NO: 3357:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 77 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3357:

CCAGAACCAC CCAGCCCTT TGAATATGGG AACTCAAAC GATCTACTGG CTGATGTAAT

TACCCCTGTT TTGATTG

(2) INFORMATION FOR SEQ ID NO: 3358:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 59 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3358:

AAGTTAGGTC TAGGGAACAT CGATAAATTA CCAGTAGTAA ATGCAGTTGA ACAACCAGA

(2) INFORMATION FOR SEQ ID NO: 3359:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 59 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3359:

CATGACCTTT AAATTGCATA TCTTCTGCAT CAGGTGCATC GCTTTTAACA ATAACGTCA

(2) INFORMATION FOR SEQ ID NO: 3360:

- (A) LENGTH: 59 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3360:

10 ACGCGACAAC ACCGCCCTCA ACTAAAGTAG AAGCACCGCA ACAAACAGCA AATGCGACA 59

(2) INFORMATION FOR SEQ ID NO: 3361:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 66 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3361:

GATTTGATCG AATTGAACGA ACATTTGCTT CTCAAACGAT TGCATCTATT AAAGAAGTAT 60

25 GTCTAG 66

(2) INFORMATION FOR SEQ ID NO: 3362:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 58 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3362:

GGTTGCACAT CTTTACTAC AAATTCGCT GGTAAAGATG TTGCAAAAGT ATGTCCGT 58

(2) INFORMATION FOR SEQ ID NO: 3363:

40

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 58 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3363:

50 CCTTGAAACG GCAACATTTT TGGGTCCTTC TCCATCATTT TATTTAAAAG CGCATTAT 58

(2) INFORMATION FOR SEQ ID NO: 3364:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 58 base pairs

55

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3364:

TTGAGAATTT AGGAGGTTAA TCGGTTGATT AAAAGTGGCA AAGCACGTGC ACATACGA

58

10

(2) INFORMATION FOR SEQ ID NO: 3365:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 58 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3365:

20

TTTTTTTTTAT TTTGGATAAA AGGAGCAAAC AAATGGATAT TAACTGGAAA TTGAGATT

58

(2) INFORMATION FOR SEQ ID NO: 3366:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 58 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3366:

ATTCATCGGT AATGACATTA TTTTACTTT GTAATTCAG TAACAGTTGA TCATCATG

58

35

(2) INFORMATION FOR SEQ ID NO: 3367:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 58 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3367:

TAAATTAACA GCCGGATGAA ATGAAAGGTG CTACATGCAC AATCAGTAAT ATCGGTTC

58

(2) INFORMATION FOR SEQ ID NO: 3368:

50

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 58 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3368:

TACCTACTGG TGAGATTGGC GAACTTGCAA TTAAGGCTAA AAATGTCACG CCAGGATA

58

(2) INFORMATION FOR SEQ ID NO: 3369:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 58 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3369:

TTAAACGGAG AAGGCTTTAC TTTACATGTT GAGGAAGGTC AAGAAGTTAA ACAAGGTG

58

(2) INFORMATION FOR SEQ ID NO: 3370:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 68 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3370:

CTGCTAAACT ACGTGATTAT AATGAAACAC ATCATGTCTT TGTCTGGTAT ATGTAAATGA

60

TTGACGGC

68

(2) INFORMATION FOR SEQ ID NO: 3371:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 399 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3371:

ATTACCAACA GCGAAATAT TGAAAAGCTG TAAAAAGCT GGTGCAsmCm TACTTGGATT

60

GAGAATTTAG GAGGTTAATG CGTTGATTAA AAGTGGCAAA GCACGTGCAC ATACGAATAT

120

TGCACTTATA AAATATTGGG GTAAAAAAGA TGAAGCACTA ATCATTCCAA TGAATAATAG

180

CATATCTGTT ACATTAGAAA AATTTTACAC TGAAACGAAA KCACTTTTAA CGACCAGTTA

240

ACACAGGATC AATTTTGGTT GAATGGTGAA AAGGTTAGTG GCAAAGAATT AGAGAAAATT

300

TCAAAATATA TGGATATTGT CAGAAaTAGA GCTGGCATCG ATTGGTATGC AGAAATTGAA

360

## (2) INFORMATION FOR SEQ ID NO: 3372:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3372:

ATTTCAACAA CTTTAAAGCA CGTATAATGA TGATTTTCAG ACTTGTACAA AGGAGAAA

58

## (2) INFORMATION FOR SEQ ID NO: 3373:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3373:

AAACCGAGCA GCGCAGTAAA CCTGCAGTAC CTTTATCGCT TCTAGATAAT CCGATTG

57

## (2) INFORMATION FOR SEQ ID NO: 3374:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3374:

AGTACGAATA TTACCTTTAT TTAATGGGTG AGCTAAGTTA CTTTTCATTT CTTTCGTG

57

## (2) INFORMATION FOR SEQ ID NO: 3375:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3375:

GGTGAAGTAT AACTTTGTAA TGGCAGCGCA CTTAATGACT GCCAATAATT GTGACCAACA

60

ACTAACAGAC

70

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 57 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3376:

TTCCAAACTT CATTAGGTGA TAGCTTTAAT TTCAAGGCTG GCAATCGCCA TAACAAG

57

(2) INFORMATION FOR SEQ ID NO: 3377:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 70 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3377:

TCCTTCAAAG TCAATGGATT TGATCCTCAG AGGACTCAGT GTATCCTCCA AGTGACCTGG

60

CTCGCATCCA

70

(2) INFORMATION FOR SEQ ID NO: 3378:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 56 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3378:

ATGAATCATT AAGCCTTTCG GTGCATATGC TGCAAGACTT TGACCAGCAT GACCAT

56

(2) INFORMATION FOR SEQ ID NO: 3379:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 56 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3379:

CCAACGACTG CGCCAATATT AATTGTTGCG CCCATCATAA CGACAGCACC ATCTTC

56

(2) INFORMATION FOR SEQ ID NO: 3380:

- (A) LENGTH: 57 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3380:

10 ACAAAAGCAT CAAGCTGTTG AAACAATCAA TGATAGCATT CGAGATTATT TAGTTAG 57

(2) INFORMATION FOR SEQ ID NO: 3381:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 56 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3381:

CATATAGTTT TGCTCACTAC CATAACCTGC ATCAGCTACA AATAACCGAA GTATTT 56

(2) INFORMATION FOR SEQ ID NO: 3382:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3382:

35 GAACACACAG GCAACCCAAA GCAGTGACGG CGAAANTTGG ATTGATCTTG CAGCATTGAA 60

GAAGATCGCG ATGACTATAC AATCAATATC GAGTAGAAGA CCGAT 105

(2) INFORMATION FOR SEQ ID NO: 3383:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3383:

50 NGTATGTGAA AACTATTTGG CGATATTTTA GTGATGAGCC TCAGTGATCC TGGTTCCTGG 60

TTATCACCTC TGCTAGTTTA GTACCGATGG TCCAAGATTG ATGAGC 106

(2) INFORMATION FOR SEQ ID NO: 3384:

55

- (A) LENGTH: 57 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3384:

10 TTCTTCGTCA AGATCAATCT CTTCAAGTAC AATCTTTAAT ACCTTCTGCA CCCATTT 57

(2) INFORMATION FOR SEQ ID NO: 3385:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 65 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3385:

CGGGCATCTT AAAGCCGATG TTTATCCTGT AATCCTCCAA AAGGAAACAT GTACCTCAAT 60

25 TAGAG 65

(2) INFORMATION FOR SEQ ID NO: 3386:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 71 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3386:

CATTTTAAAT TATTTCTATT TGCTTTTAA CCACTTCTCT GACTGCTTCC GAATCATTTT 60

TCTTAACTGC A 71

40

(2) INFORMATION FOR SEQ ID NO: 3387:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 55 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

45

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3387:

TTAGAAAATG ATAAACGTAA AGCAGTAAGT GCTGAAGAAT ATAAAAAAGC TGACG 55

(2) INFORMATION FOR SEQ ID NO: 3388:

55



- (A) LENGTH: 56 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3388:

10 TCTTCGACAA CTTTAATAAT ATTAGCCAAC GCAGTGTCCC CGCCAACTTT TGTTCG 56

(2) INFORMATION FOR SEQ ID NO: 3389:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 56 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3389:

ATTATTAAAC GATTAATGAC GCTGGCATGC CAATTCCAGA TGATCATCGT CGTATC 56

(2) INFORMATION FOR SEQ ID NO: 3390:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3390:

35 AAATGCTATG TACCCACTTT AGATGAAATT TTAGTAACGT TATGGCCCGA AATGCCAACT 60

ATTATATTGA 70

(2) INFORMATION FOR SEQ ID NO: 3391:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3391:

50 CAAACGCAAT AGCTGGTGAC TTAAGTGGG GCACTTGGCA TGTGGATGGC AATACTTCG 59

(2) INFORMATION FOR SEQ ID NO: 3392:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs

55

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3392:

GCATCTACTG GGAAACGATT ACAAATTGGT GATTATTAC AAAAGCCAAC TGTAT

55

10

(2) INFORMATION FOR SEQ ID NO: 3393:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 55 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3393:

20

TTTATAAATA TCCAGTCTG AACGCGATTG CCATAACGGA TCAATGGCAG GATTG

55

(2) INFORMATION FOR SEQ ID NO: 3394:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 55 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3394:

TGCTTACGCT CAGTGACATA ATCTAATGTG GCACGTAAAG CGCCACCATA CCACC

55

35

(2) INFORMATION FOR SEQ ID NO: 3395:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 58 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3395:

45

AGTCACCAAT TGTTGGTACA GGTATGGAA CACGTTGCAG CACGTGATTG TGGTGCGG

58

(2) INFORMATION FOR SEQ ID NO: 3396:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 55 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

50

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3396:

CAAATGCATT TAAAACCAAT ATTGAGTTAC ATGAAAGCAC ATACGATGCA AACGT

55

5 (2) INFORMATION FOR SEQ ID NO: 3397:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 54 base pairs  
(B) TYPE: nucleic acid  
10 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3397:

TGTTGATGAG TCGTGTTTTA TCTCAAGATG TGTTACTCAA AAAGTTATAG AAGA

54

(2) INFORMATION FOR SEQ ID NO: 3398:

- 20 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 54 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3398:

CTTCGTCAAG ATCAATCTCT TCAAGTAAAT CTTTAATACC TTCTGCACCC ATTT

54

30

(2) INFORMATION FOR SEQ ID NO: 3399:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 55 base pairs  
(B) TYPE: nucleic acid  
35 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3399:

AATGAAAAGC TAGCTGTAGT TGCAAGAAAA ACTGGCTTAG CGATGGCAGT TGGAT

55

(2) INFORMATION FOR SEQ ID NO: 3400:

- 45 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 54 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3400:

55

(2) INFORMATION FOR SEQ ID NO: 3401:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3401:

TAAAAATCGC GCACTTAAAC CGCTTATGAC AATCATTATT ACCGCAATAT GCTTG

55

(2) INFORMATION FOR SEQ ID NO: 3402:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3402:

GGCACCTCCT TGGATTATTT TTCTTCTACT GTTACTAAGT GCTTAACTTT GTTG

54

(2) INFORMATION FOR SEQ ID NO: 3403:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3403:

GATAAGTCTA ACAAGTGGCA CCCATAATCG ATTAACTAC CGCCACCTTG CAACGTTT

58

(2) INFORMATION FOR SEQ ID NO: 3404:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3404:

TCGTTTTCGT CCCCAAATTC TGCCAACTTA TTCATGAACT TATCTAGCGC TATTGTTCTT

60

TGTCT

65

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3405:

AAATTTTCAGC ACCAATTGTT ATTGGACGAC ACCATTTAGA TGCTGGTTCA GTTGC

55

(2) INFORMATION FOR SEQ ID NO: 3406:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3406:

TCGATTTTCAG CGGAACACAT GTAACGTTAG CACAAGCCAT GAACCAATTA GGTGGC

56

(2) INFORMATION FOR SEQ ID NO: 3407:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3407:

AATTGCTAAT GGTCAAGTAT GGACGTGATC ATTGTTGGTA CTACTTATTG CTGAAACTGT

60

TAAAGATTAG AAGG

74

(2) INFORMATION FOR SEQ ID NO: 3408:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3408:

TGATTTTACA CTTGATAACG GATACTTCGA AGAGATACAT CAGCAGCGTT CAGCTCAGAT

60

AGTGCTCA

68

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 54 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3409:

TATGATTAGA AAAAGGGGAA TTTTATGGA GTATAAGAGT TACTATGATT CGCC

54

(2) INFORMATION FOR SEQ ID NO: 3410:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 54 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3410:

TATCTTTCAT CATTGAAGAA GATCGCGATG ACTATACAAT CAATATCGAG TATA

54

(2) INFORMATION FOR SEQ ID NO: 3411:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 53 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3411:

TTGAAGTGCA CGAATCGAAT TATTGTAAGC AGTAATACTT GCCGGCTTCT TAC

53

(2) INFORMATION FOR SEQ ID NO: 3412:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 63 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3412:

TAGCCGATGG AACCCCATAA CGGTTGCCCT ATAAAAGTAT TGTTTTTGTA TAGTGCTAAA

60

TCA

63

(2) INFORMATION FOR SEQ ID NO: 3413:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3413:

10 ACTACCATTG CTGTTCCGG TTTCACAACT GGTTCAGTAT CATTTACAAC TGC 53

(2) INFORMATION FOR SEQ ID NO: 3414:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 62 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3414:

ATGCTGTTGT AAACGGTAAT ACAACATACC TGCCCAACCC GGTAACGCCA AAAAATGTCC 60

TT 62

25

(2) INFORMATION FOR SEQ ID NO: 3415:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3415:

ACTTAGATCA ATCACATGAT GCCTCACGGA ATCCATTATT TGAAGGTCAT GTTAG 55

(2) INFORMATION FOR SEQ ID NO: 3416:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3416:

TTAGTTCCAG CAATACCTGC TACAGTTGCT GCAGATGCTT CTTTACCCCA TGG 53

50

(2) INFORMATION FOR SEQ ID NO: 3417:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs

55

- (C) STRANDEDNESS: double .
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3417:

TGATTTAGGT GCAAAAATTG TAGGTATCGC TGAGGCTTAC GGTGCATTAC ACGATCCAA

59

10

(2) INFORMATION FOR SEQ ID NO: 3418:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 53 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3418:

20

CGTGATCACC ATCAACAATT GCTCGATCTA ATTCAGTAAT TCAGATTCAT GTT

53

(2) INFORMATION FOR SEQ ID NO: 3419:

25

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 55 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3419:

TGGACCTACT GCAATAACTG AACGTCCTGA ATAGTCAACA CGTTTACCAG TAAGT

55

35

(2) INFORMATION FOR SEQ ID NO: 3420:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 53 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3420:

45

TGTCTCCGGT ACCGTTTGCA CCAGGAATAA AGATGAGCAC GGGTCCTTGT CCG

53

(2) INFORMATION FOR SEQ ID NO: 3421:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 72 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

50

55



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3421:

AAATTAAGAA AATTCATTGC CAGATAATTT AGATAAATRA TAAAACTTA GACCATTCAC 60  
5 CCAATCCCT GA 72

(2) INFORMATION FOR SEQ ID NO: 3422:

(i) SEQUENCE CHARACTERISTICS:  
10 (A) LENGTH: 54 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3422:

CATATGTTAA ATGGACTCGC TAGATTTAAG TCGCAATAGT AGCGGCCGTT TCTT 54

(2) INFORMATION FOR SEQ ID NO: 3423:

(i) SEQUENCE CHARACTERISTICS:  
20 (A) LENGTH: 52 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3423:

CACGTTTCAA ACCTAAAAGA TGCTAAAAAT TTCTCTTAAT TCTTGTGCAA TA 52

(2) INFORMATION FOR SEQ ID NO: 3424:

(i) SEQUENCE CHARACTERISTICS:  
35 (A) LENGTH: 54 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3424:

ATCGCCTAAC CAAGATGCAC CATCGGTGAT TTTATCGCCT GCCGCTTCAA CCAT 54

(2) INFORMATION FOR SEQ ID NO: 3425:

(i) SEQUENCE CHARACTERISTICS:  
50 (A) LENGTH: 59 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
55 (D) TOPOLOGY: linear

AATAGAAAAT GTACGTAGCG GTATGATGAG GATTTCGCAG ACTAGTTTAG GGTCAAGTG

59

(2) INFORMATION FOR SEQ ID NO: 3426:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 52 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3426:

CCAACGCCAG ATCCAGAACC AAGTCCAGAC CCAGAACCGG AACCAAGCCC AG

52

(2) INFORMATION FOR SEQ ID NO: 3427:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 52 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3427:

CCATATTAAT GGTTATGTTT ATGTGAATGC TTGCTTGCTG GACTTGTCTT TT

52

(2) INFORMATION FOR SEQ ID NO: 3428:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 52 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3428:

TAAAACAGAG ATTGATACTG CAGAAGATAA CTGTATCTCT CCATCTACTG TA

52

(2) INFORMATION FOR SEQ ID NO: 3429:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 52 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3429:

TGAAAATCCA CAAGTCGCAC GTACAGTGTT TGAAAAGGT ATTATGGCGG CA

52

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3430:

ATAATTCTTC CAAATATATG AAAATGGATT TGTCTTTTTT TTATAAAAAT CTTATGCTTT 60  
TTAACTAATT GTAAGA 76

## (2) INFORMATION FOR SEQ ID NO: 3431:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3431:

CTGCGGGGGA TAACTGTATC TCTCCATCTA CTGTAAGTC GTATTAGAAC TAAAGCGGCT 60

## (2) INFORMATION FOR SEQ ID NO: 3432:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3432:

GGCTTCAGGC TCATTGATAG GTAAAAGTTG CAAAGCCTGC AAAGCGATTG GG 52

## (2) INFORMATION FOR SEQ ID NO: 3433:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3433:

TCGCACGATA CGCCTCCGAA TGAAGAAGGT TTATTGTGCG ATTCTTTTAT TGTAAATTT 60  
TAAATTTT 69

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 51 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3434:

10

GATCGCTATC CATTAGCTAA ATTAAACGT TCAAACCTCAG GTACATGTTA C

51

(2) INFORMATION FOR SEQ ID NO: 3435:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 51 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

15

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3435:

TATAGCTACT GCTGCAGCTG CGGCCATTGC AGATGCTGAA CCAACTTCAG C

51

25

(2) INFORMATION FOR SEQ ID NO: 3436:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 70 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3436:

35

ATTAAAGCCA ACATTAATTT ATCCACTATT AACAAATACG GCTACAGGCT TATTAATGAT

60

TTATACCTTT

70

40

(2) INFORMATION FOR SEQ ID NO: 3437:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 51 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3437:

50

TTTGTGTTGTT GATTCTTCTC CACCTGTTTC AGGTAGTTCA GATTCTTAG A

51

(2) INFORMATION FOR SEQ ID NO: 3438:

55

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3438:

10

GTGAATTCCG TAATTACATT TTAGGCTTGA TTTTCTATCG CTTCTTATCT G

51

(2) INFORMATION FOR SEQ ID NO: 3439:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3439:

TTAAGACAGG TTCCTTATGG GACTCTAACA ACGTATGGTG CTATTGCCAA A

51

(2) INFORMATION FOR SEQ ID NO: 3440:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3440:

35

CACTAGAAGA AACGGATTCA TCAGCTATTG GTATCGATTA CCATACTGCT GTGGA

55

(2) INFORMATION FOR SEQ ID NO: 3441:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 77 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3441:

CTTCTGGCAA TAGACCGCGA GTTACTGGGG GCAAACCAG TGTGTAAAAC CGGA ACTACT

60

50

ATGAGGGGCA TGAAAGT

77

(2) INFORMATION FOR SEQ ID NO: 3442:

(i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 55 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3442:

GTTCGGTTGT GACAGTCAGT GGACGCGTTA CCAAATGGGC GGGAATTAAA GCAAA

55

10

(2) INFORMATION FOR SEQ ID NO: 3443:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 51 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3443:

20

ATGAACCTTG GGATAAAGGT GATGCCCAA CTTTCCGTAA CTCATGATGA T

51

(2) INFORMATION FOR SEQ ID NO: 3444:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 51 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3444:

CAACGACGA AAGCGGAGTG GCCCTTACC TTCACAGAAT AATGGTCTAA T

51

35

(2) INFORMATION FOR SEQ ID NO: 3445:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3445:

45

ACCGAGCAGC GCACTAAACC TGCAGTACCT TTATCGCTTC TAGATAATCC

50

(2) INFORMATION FOR SEQ ID NO: 3446:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

50

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3446:

CCAATGCAAC GATCCAGTTA TTGTGTTGGC GCAATTGATT AATAGTATTC

50

5

(2) INFORMATION FOR SEQ ID NO: 3447:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3447:

GCGCATCATA TCCCATTGCA CCGATAAGAT CCTTCTTACC TTCTACAAGT

50

15

(2) INFORMATION FOR SEQ ID NO: 3448:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3448:

GTTCTTACTT CTTTATCGTG GCTCCAACGT GCTCTGTACA TTTTTCCTCA TCTCTCTACT

60

30

(2) INFORMATION FOR SEQ ID NO: 3449:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3449:

CAACACCACC GACACCAGAA GTACCAAGCG AGCCGGAAAC ACCAACACCG

50

40

(2) INFORMATION FOR SEQ ID NO: 3450:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3450:

55

TTATCACGGT ATATGAGGGG ATTTGAGG

88

(2) INFORMATION FOR SEQ ID NO: 3451:

5

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 50 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3451:

15

TGCAAAACGT TATGAAGTAC AAGTTGATGG AAGCAACAAA GTAAGTGCGn

50

(2) INFORMATION FOR SEQ ID NO: 3452:

20

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 64 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3452:

CAGTTAAGTC ACCAGCTATT GCGTTTGGTG ATCTTAAGCA GGCCTGGATT ATCAAGTTTG

60

GGTA

64

30

(2) INFORMATION FOR SEQ ID NO: 3453:

35

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 131 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3453:

TCGTAAACAA TATACTATCT CAACATTTAT TCATCCAATG GAGATAACGT ATTGCGCGGT

60

TTACAGGTA ATTTAAACCA AATACGGTAG TAATnATTAA TAGATAGCAA ATCAAGTATA

120

45

AAGAATAAGT A

131

(2) INFORMATION FOR SEQ ID NO: 3454:

50

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 50 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

55



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3454:

TTAAAAATGC AGTTATGGCC TCTAAAATCG TATTAAGCAT ATTAGCGCCC

50

(2) INFORMATION FOR SEQ ID NO: 3455:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3455:

TGCTACATGG CGTTACGGTC AAGATCGTCA ACGATTGATG GGTACAATTG A

51

(2) INFORMATION FOR SEQ ID NO: 3456:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3456:

ACAAACTGCC AACGATTGGT CGTGTGAATC ATCCAGTGA AGAAGCGCAn

50

(2) INFORMATION FOR SEQ ID NO: 3457:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3457:

AATCACGTGA GAAGGATACA GCTATTAGTA TCGGTATCAT CGCATTGATT

50

(2) INFORMATION FOR SEQ ID NO: 3458:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3458:

(2) INFORMATION FOR SEQ ID NO: 3459:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3459:

GGGCCAACAA ATCGGAAACT GCCAATTGGA CGGTTGCCGT CATCAAACCC

(2) INFORMATION FOR SEQ ID NO: 3460:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3460:

TGCTTCCGCT AGAGGATCCG GTATTGCTAG TCAATTACTA CACCATTAA ATTGTGGAAG  
CAAAAGCT

(2) INFORMATION FOR SEQ ID NO: 3461:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3461:

TGGTCTTCGC AATCCACGGA TATACCTTAG TACCAGGTAA TTGACCACCT T

(2) INFORMATION FOR SEQ ID NO: 3462:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3462:

AAGCTATTAA TGTAATTTAT CAATTGATTG TGCAACGGAC ATCATCTACA AGACCG

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3463:

ATACCAAATG TGAGAAACTG GAGCAGCAAn TTCAATGTGA CCCATTCTTT

(2) INFORMATION FOR SEQ ID NO: 3464:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3464:

TCTTTACGGC GTGGTTCTAA TCGCATCTTT TTCAATCTAA GTGCGTTTnT

(2) INFORMATION FOR SEQ ID NO: 3465:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 57 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3465:

AAAGAAGATT GGAACGTGTA TTGACGACTG CACCCAGGTA TGGGTGTTG CCGACA

(2) INFORMATION FOR SEQ ID NO: 3466:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 63 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3466:

ACATCCGAAA GATGACTTGT TTAAAAAGC AGAGCATGAT TTGCTTACTA TGATTACACG  
CGG

(2) INFORMATION FOR SEQ ID NO: 3467:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3467:

10 TACCGATGAT TTCCGAGACA TAGACCGGCC TGTCTGGGGG TCAACTGGAA CTTGGTC 57

(2) INFORMATION FOR SEQ ID NO: 3468:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3468:

TGTTCTTAAT ATTTATGTTG TAAAAATGTA CAATCTAATT AAAGCAATAG TCTTGGGCA 59

25

(2) INFORMATION FOR SEQ ID NO: 3469:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3469:

35

TCCATGATCG TTCAACATTT AAATACACAA CTTAATAAGT ATCGTGTACA AGTTATG 57

(2) INFORMATION FOR SEQ ID NO: 3470:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3470:

50

CCCTGTTTCAG GCTATCCTCT AAAGTGACGA TATAGAATAG CGATTAATAT CGCGATAGT 59

(2) INFORMATION FOR SEQ ID NO: 3471:

(i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3471:

5 TACGCCATCA nCGCCAGCTA ATCCGATTGC GACACCTAAT GCGAAATCAT 50

(2) INFORMATION FOR SEQ ID NO: 3472:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3472:

AACGTCATCA AATGGAAGTA CGTGACGTTT ACTACTCTCA CTATGGCCGT ATGT 54

(2) INFORMATION FOR SEQ ID NO: 3473:

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3473:

30 TAATAGGCAT TCCCATTAGG TGCCTCGACA ACTGCAACGC AAGCATTGTA AACAGA 56

(2) INFORMATION FOR SEQ ID NO: 3474:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3474:

TTTTAAGAAT GTCGCGTTAT CTGCGCCCAT TGGATTGACA TACTTCATAC GTATA 55

45 (2) INFORMATION FOR SEQ ID NO: 3475:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

55

GCCTTTAGGT AAAATGGGCA GAAATGCTAA TCATTTTGGC GGCAGAAATGA AAAA

54

(2) INFORMATION FOR SEQ ID NO: 3476:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3476:

AAAnCATTCTG CAATCGACCA TAATTTTTTA TGTAATTCAG CTTGTTGCTG

50

(2) INFORMATION FOR SEQ ID NO: 3477:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3477:

GGAnGACCAT TAATCGATAT CGGTACACAC GCTTTAGATT TAACGTTATG

50

(2) INFORMATION FOR SEQ ID NO: 3478:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 60 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3478:

TGCCTCCTTA CGCCATGATG CTTATTCAAA GTAAATTGCT TTGCCGGACT TTGCAGACTG

60

(2) INFORMATION FOR SEQ ID NO: 3479:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 77 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3479:

GGTCTTTTCAG CTGCTAACGA GTTCTGTGA CTGTTTCATGT CTATCACTTT GCGTTCCTC

60

## (2) INFORMATION FOR SEQ ID NO: 3480:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3480:

CAAGTATCAT ATGGACGGCT CGCCCAACAC AAAACAAGTC CAAGCAAAAC

## (2) INFORMATION FOR SEQ ID NO: 3481:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 62 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3481:

ATTAACAAC ATAGCTCGGC TAATCCTTTA AAGCTTTTGA GTTTTCTGT TGTAGAACAA

GA

## (2) INFORMATION FOR SEQ ID NO: 3482:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3482:

TGTGGCTAGC TGTTCCTTTT TTAGGTGCTG TGTAGGAGAT GAACTGATCG T

## (2) INFORMATION FOR SEQ ID NO: 3483:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3483:

GCAGTTTATA AGTAGAGAGA CAGCTGATCA TGAGATAAAA ATGGGTAAAT ATTT

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 55 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3484:

TTATCTATCA CAGTACGAAT CCCCCAGAGT ACCGATTGTG ACAGCAACTT CTGCG

(2) INFORMATION FOR SEQ ID NO: 3485:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 52 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3485:

ATCTCTGGTT CGATTCCCGT CGAGACCGGC ATCATTACAT GTTTATTATG GG

(2) INFORMATION FOR SEQ ID NO: 3486:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3486:

TGTGTCACGA TAATAGGCGT AATATCACTC TTTGGCATGA TTGCCGGATG

(2) INFORMATION FOR SEQ ID NO: 3487:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 67 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3487:

TATTTTGTGAT CACACTCAAC GCACAAACGA ATGGCCTTTA CCTTCACAGA ATAATGGTCT  
 AATGTAA

(2) INFORMATION FOR SEQ ID NO: 3488:



- (A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3488:

10

TAGGTGGTCA ATTACCTGGT ACTAGGTATA TCCGTGGATT GCGAGGACAA

50

(2) INFORMATION FOR SEQ ID NO: 3489:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 60 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3489:

CAATTGTACT TCATAACGTT TTGCATTTTCG CCACCTTCAC CACTATATTT TCCCATGGTC

60

25

(2) INFORMATION FOR SEQ ID NO: 3490:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3490:

CTAAACTGAT TGTTTTACGT AACGTTTCAT CGGCTTCTTT CGCTTCTATC

50

(2) INFORMATION FOR SEQ ID NO: 3491:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3491:

TCGATTTACC TTTCATCATT GAAGAAGATC GCCATGACTA TACAATCAAT AT

52

50

(2) INFORMATION FOR SEQ ID NO: 3492:

(i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 52 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3492:

AACCTTTTCA CAAATATCAT ATAACTCTTC TAATGGGATA ATCTCTTCAT GT

52

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(2) INFORMATION FOR SEQ ID NO: 3493:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3493:

GGTTTTAAAC CGTCACGAAC ATCTGGCAAT GCACGAGCAA CGTACATACG TATCTAAAGT

60

TACGCTT

67

20

(2) INFORMATION FOR SEQ ID NO: 3494:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3494:

TACGTTATGT TATGTAAATA ACAGTTAATT ATACCGGTGG TCTGGGTCGA

50

35

(2) INFORMATION FOR SEQ ID NO: 3495:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3495:

CGCTTGTTGT TGTACTTTGG CAGTTCGCGT TGTGGATTGT GCCAGCGCTT TTAAACCGTA

60

45

(2) INFORMATION FOR SEQ ID NO: 3496:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

50

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3496:

GGCACCGGCT TCTCTATTGC TTCTTTAGCA TATCTGCAGC TCTCTCAAGG GACATG

56

(2) INFORMATION FOR SEQ ID NO: 3497:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3497:

CACCTTTAGG ATACGCGTCT AACCACTGTG TCGCGTCTCT ATATATCGCT AAACACGTA

59

(2) INFORMATION FOR SEQ ID NO: 3498:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3498:

AAGTAATATC TGAATGCGTA TATTGTCTAA TTTCAAATTC TACAGACATC GACGT

55

(2) INFORMATION FOR SEQ ID NO: 3499:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3499:

ANTGTACACG TCCATCTTCA CATGACAACA ACGATATTTT GACCATCACA

50

(2) INFORMATION FOR SEQ ID NO: 3500:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3500:

(2) INFORMATION FOR SEQ ID NO: 3501:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 52 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3501:

TGTGTGCCTT TAAGTTGTTG ATGACACGCA TTCACGACAA CAGACATGAC AC 52

(2) INFORMATION FOR SEQ ID NO: 3502:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3502:

CTGGCTTCAA TGGCAACTTC TGTACCTGGT ACCAATGGGC GATGACCGAT 50

(2) INFORMATION FOR SEQ ID NO: 3503:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3503:

TGTCCGACTT GGC GGnATCG TAATTTAGCG CnTGTAATTC TAAAGGGACC 50

(2) INFORMATION FOR SEQ ID NO: 3504:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 64 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3504:

AACCTTCATA TTGCTTCTAA TAAGAAACCG AGCAGCGCAC CAAACCTGGC AGTACCTTTA 60

TCGC 64

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3505:

TATTGATGTT GAAAACTGTT ATGTCCTTTC GATGGGCCAA CACnAAnATA

## (2) INFORMATION FOR SEQ ID NO: 3506:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3506:

GAATATGGTA TCAATGGTAT GCACTAAGGC TTTATGAAAT TCATTTAAAA T

## (2) INFORMATION FOR SEQ ID NO: 3507:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3507:

CGGTTTTAAT CGGTAAATTA AATATGGATG AGTTTGCAAT GGTGTTTACA GAACATCTAT

TTAA

## (2) INFORMATION FOR SEQ ID NO: 3508:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3508:

CAAGGCCTTG TTTTAAAGC AGCTACAGTT GGCAATATGT CCACTCATGT

## (2) INFORMATION FOR SEQ ID NO: 3509:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3509:

10

CAGATGCAAA TTGACATGGT CATCAACATC nGThCATTAA AAGATGGACG

50

(2) INFORMATION FOR SEQ ID NO: 3510:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 94 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3510:

ACAAGAGGGT CACCCAGCTC GGTCGATTCC CACCGCCACA TCATGATATT TATTCATAGA

60

GTTTACGCAC TGTACATGAT TGAATGCGAT AAAG

94

25

(2) INFORMATION FOR SEQ ID NO: 3511:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3511:

ACTCAACAAT GGATATTCTT AACTGAAAA ATGGGTAATG GTGCAAACAT AGTA

54

(2) INFORMATION FOR SEQ ID NO: 3512:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3512:

50

CCGGATGCAC ATTTGATGAC TGAAGTCCGC GATAAAGGGA CAAnAGTCAn

50

(2) INFORMATION FOR SEQ ID NO: 3513:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs

55

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3513:

GCATTAAATT GAAACAATCG GATTTACAAT TTTCTCTTAA TGCTGTCGTC TACACAGC 58

10

(2) INFORMATION FOR SEQ ID NO: 3514:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 66 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3514:

20

GTGTTTCGTGT TCATGCAAGG TGAATGCGAG TGATCTGTTG GTATGGGCTT TATGCATGGC 60  
AATCTG 66

25

(2) INFORMATION FOR SEQ ID NO: 3515:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3515:

35

ATGCCACTGA TAATGChnCT GAACTTATTG ATGACTTCTC ATTAGACTAT 50

(2) INFORMATION FOR SEQ ID NO: 3516:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3516:

45

CGGCGACAAA GAGTAAACAC AGCGGAGGGA CAAAGCCCGC GACTAGCAAC 50

50

(2) INFORMATION FOR SEQ ID NO: 3517:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 51 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3517:

5 ATGCCTATGT AGCACCGAGT ACCGATACCG AACACTTAGC TACGCCAGTT C 51

(2) INFORMATION FOR SEQ ID NO: 3518:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3518:

GAGCATnAAG GTGATTnGA TCGCTATCCG TTAGCTAAAT TTAAACGTT C 50

(2) INFORMATION FOR SEQ ID NO: 3519:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 64 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3519:

30 GATTGGTATT TAGCTTTAAA TTTATGGTTG GAATAGTAGG TGGCATATAT CGCTGTTAGT 60

ATCG 64

(2) INFORMATION FOR SEQ ID NO: 3520:

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3520:

45 TCTTCAATCT CAGGGGCATC TACTAACATA TCATCCAGTC AATATTGCGT CACATTGTTA 60

ATCGGTTCCG ATC 73

(2) INFORMATION FOR SEQ ID NO: 3521:

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 base pairs  
(B) TYPE: nucleic acid  
55 (C) STRANDEDNESS: double



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3521:

5 TCAAATTGGC AATTGGTACG AATGTCGACT GTACTAACAT CATTAGCTCA TGATTGCCAG 60  
GTGATTTTCAT GGATG 75

(2) INFORMATION FOR SEQ ID NO: 3522:

10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 57 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3522:

TTCCAATGGG CTTCTGACTT TGGCGGTTTT AGTGCTTGGG TTGCCGGCGG TTTTGGA 57

20

(2) INFORMATION FOR SEQ ID NO: 3523:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 72 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3523:

30 TGGTGGAGGT TTGTGTTTTT CCGTGTCGGT TTTGTGTTTC GTCTTGGTTC CTTTGTTTTT 60  
TGTGTTCTCT TT 72

35 (2) INFORMATION FOR SEQ ID NO: 3524:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 51 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3524:

45 ATATCACAAT ATACCGGTTT ATATGCTGTC TAATCATAGT TGAATAGTGA C 51

(2) INFORMATION FOR SEQ ID NO: 3525:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 59 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

50

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3525:

TAGACCGTCG TGGATAGTTT TGGGTACGGT AACCAATTTA TTTGAAGAG ACCATCCTC

59

(2) INFORMATION FOR SEQ ID NO: 3526:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3526:

TAATAACGTT GCCCTCCCAT GTATATCCTA CCAACATGAC ATCTTGTA

50

(2) INFORMATION FOR SEQ ID NO: 3527:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3527:

TTCCCAACGA GCAGTCGCAT GCGGTACTGC CACGGCATT TGTATGCAGGC CT

52

(2) INFORMATION FOR SEQ ID NO: 3528:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3528:

AAAGAAAnGA TnGnnnGnnn GnAnAAAnnn nnCCATnnnn nTAAAAA

50

(2) INFORMATION FOR SEQ ID NO: 3529:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

CATTAGCCTC ATCCCCTTCG TTTAGACTCG CTATAGATGC ACTAAATGGC GATATATTTT 60

TC 62

5 (2) INFORMATION FOR SEQ ID NO: 3530:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
10 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3530:

CACTACCACA AAAATTATAG GTGTTGACCT TCAGGnGCAA GTAGTATGAT 50

(2) INFORMATION FOR SEQ ID NO: 3531:

20 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3531:

30 GAATGCAAAA TCCATTTGTA AGGAnATCGA ATGGTTTAGT AnCTCGTGCA 50

(2) INFORMATION FOR SEQ ID NO: 3532:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
35 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3532:

GGTAGAnCnC TGTTTAGTAC TAGGGGCCCC TCTCGGGTTA CCAATTCAGA 50

(2) INFORMATION FOR SEQ ID NO: 3533:

45 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3533:

55

## (2) INFORMATION FOR SEQ ID NO: 3534:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 52 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3534:

CGTCAACGAT GTAAAGTAAA GCCTTGCCA GTTTAATTGA CGAGTGGCGT AA 52

## (2) INFORMATION FOR SEQ ID NO: 3535:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3535:

TTAATCCAGA AGTACCGGTG GATTAGTTA TTGACCACTC AGTTCAAGTG GATAGCTATG 60  
 CAAATCCAGA AGCTCTTGAA CGTAATATGA AATTAGAATT TGAACGTAAC TATGAACGTT 120  
 ATCAGTTTTT AAATTGGGCA ACGAAAGCAT TTGATAATTA CAATGCAGTT CCTCCTGCAA 180  
 CTGGAATAGT TCACCAAGTT AACTTAGAAT ATTTAGCAAG TGTGTACAT GTTCGTGATG 240  
 TAGATGGTGA AAAAAGTGCA TTTCCAGATA CATTAGTTGG TACTGATTCA CATAACAACAA 300  
 TGATAAATGG TATTGGCGTA CTAGGATGGG GTGTTGGTGG TATTGAAGCT GAAGCTGGAA 360  
 TGCTTGGACA ACCTTCTTAT TTCCAATTC CAGAGGTTAT 400

## (2) INFORMATION FOR SEQ ID NO: 3536:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1118 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3536:

CGTATAGAGT GTCCTACAAC CCCAACAAGC AAGCTTGTTG GTTTGGGCTC TTCCCGTTTC 60  
 GCTCGCCGCT ACTAAGGGAA TCGAATTTTC TTTCTCTTCC TCCGGGTACT AAGATGTTTC 120  
 AGTTCTCCGG GTGTGCCTTC TGATATGCTA TGTATTCACA TATCGATAAC ATGACATAAC 180

GCATATCGTC GTTAGTAACG TCCTTCATCG GCTTCTAGTG CCAAGGCATC CACCGTGCGC 300  
 CCTTAATAAC TTAATCTATG TTTCCACCAT TTTTATAAGT CAAACGCTCA CATACGGCTT 360  
 5 CGTTTTCAAT ATTTTAAATG CTCATTTACA TAAGTAACT CTGCTTTAAA ATAATTTAAC 420  
 TCATTGTCTG CTAAACGTTT TCTTTTATAA AAAGATTAA ACGCGTTATT AATCTTGTGA 480  
 GTGTTCTTTC GAACACTAGC GATTATTTCT TATGAATTCA AGCTTATTTA AAACCTCTTTA 540  
 10 TTCACTCGGT TTTGCTTGGT AAAATCTATA TTTTACTTAC TTATCTAGTT TTCAATGTAC 600  
 AATTTCTTTT TAGTCAAGCG CTCGCATACT GCTTTATTTT CAAAAAATCA AATGCTCAAT 660  
 15 TACAAAAGTA AACTCCGCTT TAATTTTTCT TAATGCATTG TCTAACAACC GCTTTCTTTA 720  
 AAAAGAATAG ATTGTCAAGC GCTCGCATAA GCAATATCAC TTTAACCAAA AAATATTTGA 780  
 ATGTTAAATA AACATTCAA ACTGAATACA ATATGTCACG TTATTCCGCA TCTTCTGAAG 840  
 20 AAGATGTTCC GAATATATCC TTAGAAAGGA GGTGATCCAG CCGCACCTTC CGATACGGCT 900  
 ACCTTGTTAC GACTTCACCC CAATCATTTG TCCCACCTTC GACGGCTAGC TCCTAAAAGG 960  
 TTAATCCACC GGCTTCGGGT GTTACAACT CTCGTGGTGT GACGGGCGGT GTGTACAAGA 1020  
 25 CCCGGGaaCG TATTCACCGT AGCATGCTGA TCTACGaTTA CTAGCGeTCC AGCTTCATGT 1080  
 AGTCGAGTGC AGACTACCAT CCGGACTGnG GACCAACT 1118

30 (2) INFORMATION FOR SEQ ID NO: 3537:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 424 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3537:

40 GGGGATCCCC AGCCAGAAGA TTTATTCAGT GCGATGATTC GTGAAATTGA AACGCAAGAT 60  
 TTCGATATCG AACACCTGGC GACGGCAATT CGTAaGTTG AAACATCAAC ATTAGGTGAA 120  
 45 GAAAGTGAAA ATGACTTTAT CGGTCTGTTC AGCGATATGG ATTTGAGTTC AACGCGACTA 180  
 GGTAACAATG TCAAAGAACG TACTGCTTTA ATCTCTAAAG TCATGGTTAA TCTTGACGAC 240  
 TTACCATTTC TTCACAGTGA CATGGAAATT GATATGTTAG GTGATGCATA TGAATTCCTA 300  
 50 ATTGGGCGCT TTGnGCGACA CGGGTAAAAA AAGCAGGCGA GTTCTATACA CCACAACAAG 360  
 TATCTAAGAT ACTGGCGaG ATTGTCACAG ACGGTAAAGA TAAATTACGT CACGTGTATG 420  
 ACCC 424

55

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3538:

ATCTCATATG TTAAAAGGTA AACAAGGTCG TTTCCGTCAA AACTTACTTG GTAAACGTGT 60  
 TGACTATTCA GGACGTTTCA TTATTGCAGT AGGTCCAAGC TTGAAAATGT ACCAATGTGG 120  
 TTTACCAAAA GAAATGGCAC TTGAACTATT TAAACCATTG GTAATGAAAG AATTAGTTCA 180  
 ACGTGAAATT GCAACTAACA TTAAAAATGC GAAGAGTAAA ATCGAACGTA TGGATGATGA 240  
 AGTTTGGGAC GTATTGGAAG AAGTAATTAG AGAACATCCT GTATTACTTA ACCGTGCACC 300  
 AACACTTCAT AGACTTGGTA TTCAAGCATT TGAACCAACT TTAGTTGAAA GGTCGTGCGA 360  
 TTCGTCTACA TCCACTTGTA ACAACAGCTT ATAACGCTGA 400

## (2) INFORMATION FOR SEQ ID NO: 3539:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1171 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3539:

AATAAGTAAG TTATTTTGTC TGGTGACTAT AGCAAGGAGG TCACACCTGT TCCCATGCCG 60  
 AACACAGAAG TTAAGCTCCT TAGCGTCGAT GGTAGTCGAA CTTACGTTCC GCTAGAGTAG 120  
 AACGTTGCCA GGCAAATGAC AAATCGGAGA ATTAGCTCAG CTGGGAGAGC ATCTGCCTTA 180  
 CAAGCAGAGG GTCGGCGGTT CGAACCCGTC ATTCTCCACC ATTTATTCTT AGATATAGCC 240  
 GGCCTAGCTC AATTGGTAGA GCAACTGACT TGTAATCAGT AGGTTGGGGG TTCAAGTCCT 300  
 CTGGCCGGCA CCATCTTTTG AGCCATTAGC TCAGCTGGTA GAGCATCTGA CTTTAAATCA 360  
 GAGGGTCAGA GGTTCGAATC CTCTATGGCT CATTACGATT TAATTTTAT ATTTAGCAAA 420  
 ATAATGCAGA AGTAGTTCAG CGGTAGAATA CAACCTTGCC AAGGTTGGGG TCGCGGGTTC 480  
 GAATCCCGTC TTCTGCTCCA TTATTTTGCC GGGGTGGCGG AACTGGCAGA CGCACAGGAC 540  
 TTAAAATCCT GCGGTGAGAG ATCACCGTAC CGGTTGATT CCGGTCCTCG GCACCATTTT 600  
 AGCGCCCGTA GCTCAATTGG ATAGAGCGTT TGACTACGGA TCAAGAGGTT ATGGGTTCTGA 660

5 GAGCACTTGG TTTGGGACCA AGGGGTCGCA GGTTCGAATC CTGTCTTCCC GATTACTTCT 780  
 TAAATTCCAT TTTATGGGGG CTTAGCTCAG CTGGGAGAGC GCCTGCTTTG CACGCAGGAG 840  
 10 GTCAGCGGTT CGATCCCGCT AGTCTCCACC ATTTATTTTT TACACGATGA ACATTGAAAA 900  
 CTGAATGACA ATATGTCAAC GTTAATTCCA AAAAACGTAA CTATAAGTTA CAAACATTAT 960  
 TTAGTATTTA TGAGCTAATC AAACATCATA ATTTTATGAG AGAGTTTGAT CCTGGCTCAG 1020  
 15 GATGAACGCT GCGGCGGTGC CTAATACATG CAAGTCGAGC GAACGGACGA GAAGCTTGCT 1080  
 TCTCTGaTGT TAGCGGCGGA CGGGTGAGTA ACACGTGGgA TAACCTACCT ATAAGACTGG 1140  
 GaTAACTTCG GGaAACCGGA GCTAATACCG G 1171

## (2) INFORMATION FOR SEQ ID NO: 3540:

20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 601 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3540:

CTCGGCAGTG TGAAATCAAC GACTCGAAGA CACAATGTCT TCTCCCCATC ACAGCTCAGC 60  
 30 CTTAACGAGT ACCGGATTTG CCTAATACTC AGCCTTACTG CTTAGACGTG CAATCCAATC 120  
 GCACGCTTCG CCTATCCTAC TGCGTCCCCC CATCGATTAA AACGATTATA GGTGGTACAG 180  
 GAATATCAAC CTGTTATCCA TCGCCTACGC CTGTCGGCCT CAGCTTAGGA CCCGACTAAC 240  
 35 CCAGAGCGGA CGAGCCTTCC TCTGGAAACC TTAGTCAATC GGTGGACGGG ATTCTCACCC 300  
 GTCTTTCGCT ACTCACACCG GCATTCTCAC tTCTAAGCGC TCCACATGTC CTTACGATCA 360  
 TGCTTCAACG CCCTTAGAAC GCTCTCCTAC CATTGTCCAA AGGCATwCtC ACAGCTTCGG 420  
 40 TaATATGTTT AGCCCCGGTA CATTTTCGGC GCaGTGTCAC TCGACTAGTG AGCTATTACG 480  
 CACTCTTTAA ATGATGGCTG CTTCTnAGCC AACATCCTAG GTTGGTCTGG GGCACGChAC 540  
 45 ATCCTTTTCC ACTTAACATA TATTTTGGGG ACCTTGGCTG GTGGGTCTGG GGCTGhTTCC 600  
 C 601

## (2) INFORMATION FOR SEQ ID NO: 3541:

50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1311 base pairs.  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 55 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3541:

5 GCnAGGACCT TnCCAAATTT GAAATCCTTT GACCACnTTT GGGGTAGAGC CCTTTCCnC 60  
 GGGGACAAAG TGACCAGGTG GTGCATGGTT GTCGTCAGCT CGTGTCTGA GATGTTGGGT 120  
 TAAGTCCCCG CAACGAGCGC AACCTTAAG CTTAGTTGCC ATCATTAAAGT TGGGCACTCT 180  
 10 AAGTTGACTG CCGGTGACAA ACCGGAGGAA GGTGGGGATG ACGTCAAATC ATCATGCCCC 240  
 TTATGATTTG GGCTACACAC GTGCTACAAT GGACAATACA AAGGGCAGCG AAACCGTGAG 300  
 nTCAAGCAAA TCCATAAAG TTGTTCTCAG TTCGGATTGT AGTCTGCAAC TCGACTACAT 360  
 15 GAAGCTGGAA TCGCTAGTAA TCGTAGATCA GCATGCTACG GTGAATACGT TCCCGGGTCT 420  
 TGTACACACC GCCCCTCACA CCACGAGAGT TTGTAACACC CGAAGCCGGT GGAGTAACCT 480  
 TTTAGGAGCT AGCCGTCGAA GGTGGGACAA ATGATTGGGG TGAAGTCGTA ACAAGGTAGC 540  
 20 CGTATCGGAA GGTGCGGCTG GATCACCTCC TTTCTAAGGA TATATTCGGA ACATCTTCTT 600  
 CAGAAGATGC GGAATAACGT GACATATTGT ATTCAAGTTT GAATGTTTGT TCATTCAAAT 660  
 25 TAATGGGCCT ATAGCTCAGC TGGTTAGAGC GCACGCCTGA TAAGCGTGAG GTCGGTGGTT 720  
 CGAGTCCACT TAGGCCCACC ATTAATTTAA TACCTATTTG GGGGCTTAGC TCAGCTGGGA 780  
 GAGCGCCTGC TTTGCACGCA GGAGGTCAGC GGTTCGATCC CGCTAGTCTC CACCATTATT 840  
 30 TGTACATTGA AAAGTAGATA AGTAAGTAAA ATATAGATTT TACCAAGCAA AACCGAGTGA 900  
 ATAAAGAGTT TTAAATAAGC TTGAATTCAT AAGAAATAAT CGCTAGTGTT CGAAAGAACA 960  
 CTCACAAGAT TAATAACGCG TTTAAATCTT TTTATAAAAG AACGTAACTT CATGTTAACG 1020  
 35 TTTGACTTAT AAAAATGGTG GAAACATAGA TTAAGTTATT AAGGGCGCAC GGTGGATGCC 1080  
 TTGGCACTAG AAGCCGATGA AGGACGTTAC TAACGACGAT ATGCTTTGGG GAGCTGTAAG 1140  
 TAAGCTTTGA TCCAGAGATT TCCGAATGGG GAAACCCAGC ATGAGTTATG TCATGTTATC 1200  
 40 GATATGTGAA TACATAGCAT ATCAGAAGGC ACACCCGGAG AACTGAAACA TCTTAGTACC 1260  
 CGGAGGAAGA GAAAGAAAAT TCGATTCCCT TAGTAGCGGC GAGCGAAATG G 1311

## (2) INFORMATION FOR SEQ ID NO: 3542:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3542:



CGCTAGAGTA GAACGTTGCC AGGCAAATGA CAAATCGGAG AATTAGCTCA GCTGGGAGAG 120  
 CATCTGCCTT ACAAGCAGAG GGTCCGCGGT TCGAACCCGT CATTCTCCAC CATTTATTCT 180  
 5 TAGATATAGC CGGCCTAGCT CAATTGGTAG AGCAACTGAC TTGTAATCAG TAGGTTGGGG 240  
 GTTCAAGTCC TCTGGCCGGC ACCATCTTTT GAGCCATTAG CTCAGCTGGT AGAGCATCTG 300  
 ACTTTTAATC AGAGGGTCAG AGGTTGGAAT CCTCTATGGC TCATTACGAT TTAATTTTAA 360  
 10 TATTTAGCAA AATAATGCAG AAGTAGTTCA GCGGTAGAAT 400

## (2) INFORMATION FOR SEQ ID NO: 3543:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 804 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3543:

GTGAGAGTGA CGTTATGTTA TGTAATAAC AGTTAATTAT ACCGGTGGTC GGGGTGCAAC 60  
 25 CGCACTCCAC AAGTGAAGA GaTTTTGAGT CCCGCGCGTC TGCCAATTCC GCCACACCGG 120  
 CTTAATGGTA AACAAAAAC TTCCCTTTGG AAGCAATTAT GGAGCGGAAG ATAGGATTTA 180  
 CACCTATACC TCGTTCCGGG aAGGAACTGg TTcTAAAGT TGAACTACTC CCGCAAATAT 240  
 30 TAAATTATGG AGCGGAAGAT AGGATTTACA CCTATACCTC ATTCCAGGAA GGAATGTATT 300  
 CTAAGAGTTG AAATACTCCC GCATTATTAT TAAATTATGG AGCGGAAGAT AGGATTTGCA 360  
 35 CCTATACCTC GTTCCGGGAA GGAckTGTTt CTAAAGTTG AACTACTCCC GCATAAACCT 420  
 GGAGGCGGCA ACCGGATTG AACC GG TGAT AAAGGTTTTG CAGACCTCTG CCTTACCACT 480  
 TGGCTATGcG CcAATAACTG GGCTAGCTGG ATTCGAACCA ACGAGTGACG GATmAAAGTC 540  
 40 CGTTGCCTTA CCGCTTGGCT ATAGCCCATT AATAATAAGG GCGGCTGAAG GGGATCGAAC 600  
 CCTCGAATGT CGGAACCACA ATCCGATGTG TTAACCACTT cACCACAGCC GCCATGGCAG 660  
 GGGCAGTAGG AATCGAACCC ACACCAAAGT TTTGGaGACC TCTATTCTAC CGTTGAACTA 720  
 45 TGCCCCATT aAAAAATaaTA ATkGGAGGGG GGCAGATTCG AAntGCCGAA CCCGAAGGAG 780  
 CGGGATTTAC ATTCCGCCGG GTTT 804

## (2) INFORMATION FOR SEQ ID NO: 3544:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3544:

5 ATGATGTCGT TGCACAATCA ATTGATAAAT TACATTATAG CTTTAATCGT TTGAAGTATA 60  
 GTTTGAAACC AGTAGTCACA GCTGTTCAAG GTCGTGCCCT AGGCGGTGGC TGTGAGCTTG 120  
 TACTTTACTC ACCTATTGTT GTCGCTGCAA GTGAAACATA TATCGGTCTT GTTGAAGCAG 180  
 10 GTGTTGGCTT ATTACCGAGT GCGGTGGCC TTGCAGAAAT GGCTGATCGC ATATTACGCA 240  
 CATCGCATAA GTTTGATKAC AAACAAGCTT CCATGACAAA AGTACTGACG AATATCGCAT 300  
 TTGCGAAAGT CTCTACAAAT GCCTTTGAGG CACGTCGTTA TGGTTATTTA CGTGGATACA 360  
 15 GATACGATTA TTTTCAATAC AGCACAACGT GTCCGAAGTT 400

## (2) INFORMATION FOR SEQ ID NO: 3545:

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 474 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3545:

25 CCGGCATTCT CACTTCTAAG CGCTCCACAT GTCCTTACGA TCATGCTTCA ACGCCCTTAG 60  
 AACGCTCTCC TACCATTGTC CAAAGGnATC nCACAGCTTC GGTAATATGT TTAGCCCCGG 120  
 30 TACATTTTCG GCGCAGTGTC ACTCGACTAG TGAGCTATTA CGCACTCTTT AAATGATGGC 180  
 TGCTTCTAAG CCAACATCCT AGTTGTCTGG GCAACGCaCA TCCTTTTCCA CTTAACATAT 240  
 35 ATTTTGGGAC CTTAGCTGGT GGTCTGGGCT GTTTCCTTT CGAACACGGA CCTTATCACC 300  
 CATGTTCTGA CTCCCAAGTT AAATTAATTG GcATTCTGGAG TTTGTCTGAA TTCGGTAACC 360  
 CGAGAGGGGC ccCTCGTCCA AACAGTGGCT CTACCTCCAA TAATCATCAn TTGAGGCTAG 420  
 40 CCCTAAAGCT AATTCGGAGA GAACCAGTAT CTCCAGTTCG ATTGGAATTC TnCG 474

## (2) INFORMATION FOR SEQ ID NO: 3546:

## (i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3546:

GCAATTCGTA AAGTTGAAAC ATCAACATTA GGTGAAGAAA GTGAAAATGA CTTTATCGGT 120  
 CTGTTACAGG ATATGGATTT GAGTTCAACG CGACTAGGTA ACAATGTCAA AGAACGTACT 180  
 5 GCTTTAATCT CTAAAGTCAT GGTTAATCTT GACGACTTAC CATTGCTTCA CAGTGACATG 240  
 GAAATTGATA TGTTAGGTGA TGCATATGAA TTCCTAATTG GCGGCTTTGn GCGACACGGG 300  
 10 TAAAAAAGC AGGCGAGTTC TATACACCAC AACAAATATC TAAGATACTG GCGAGATTGT 360  
 CACAGACGGT AAAGATAANT ACGTCACGTG TATGACCCAA 400

## (2) INFORMATION FOR SEQ ID NO: 3547:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3547:

AACGTTTTCA CTCGCCAAG CCATTTTTCT TTGTGTTTAC TTTTATTTT GACGTTTTAG 60  
 25 ACATAAAAAA AAGAGACCTT GCGGTCTCAA TCGGCTCAT CGCATCCATT TTTGCTTG 120  
 CAACGTTCTA CTCTAGCGGA ACGTAAGTTG GCTACCATCG ACGCTAAGAA CCTTTCTTGA 180  
 30 CTTGTGACAA TCGCTTGCTT CTTTCCTCTT CTTGCGCTCT CGCTTACTCA TTTAGCTCTA 240  
 CTAAACTCGT TCGGCTCTTT TCTCGTTTCG TCAGATTCAA ACGTTTTTAC TCGCCAAGC 300  
 CATTTTTCTT TGTGTTTGCT TTTTATTTTG ACGTTTTAGA CATAAAAAA AGAGACCTTG 360  
 35 CGGTCTCAAT GCGGCTCATC GCATCCANTT TTTGCTTGGC 400

## (2) INFORMATION FOR SEQ ID NO: 3548:

40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3548:

ATGATGTCGT TGCACAATCA ATTGATAAAT TACATTATAG CTTTAATCGT TTGAAGTATA 60  
 50 GTTTGAAACC AGTAGTCACA GCTGTTCAAG GTCGTGCCTT AGGCGGTGGC TGTGAGCTTG 120  
 TACTTTACTC ACCTATTGTT GTCGCTGCAA GTGAAACATA TATCGGTCTT GTTGAAGCAG 180  
 GTGTTGGCTT ATTACCGAGT GCGGTGGCC TTGCAGAAAT GGCTGATCGC ATATTACGCA 240

55

TTGCAAAGTC TCTACAAATG CCTTTGAGGC ACGTCGTTAT GGTTATTAC GTGATACAGA 360  
TACGATTATT TTCAATACAG CACAACGTGT CCGAAGTTGG 400

(2) INFORMATION FOR SEQ ID NO: 3549:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3549:

AGGTTACTCC ACCGGCTTCG GGTGTTACAA ACTCTCGTGG TGTGACGGGC GGTGTGTACA 60  
AGACCCGGGA ACGTATTCAC CGTAGCATGC TGATCTACGA TTACTAGCGA TTCCAGCTTC 120  
ATGTAGTCGA GTTGCACT ACAATCCGAA CTGAGAACAA CTTTATGGGA TTTGCTTGAC 180  
CTCGCGGTTT CGCTGCCCTT TGTATTGTCC ATTGTAGCAC GTGTGTAGCC CAAATCATAA 240  
GGGGCATGAT GATTTGACGT CATCCCCACC TTCCTCCGGT TTGTCACCGG CAGTCAACTT 300  
AGAGTGCCCA ACTTAATGAT GGCAACTAAG CTTAAGGGTT GCGCTCGTTG CGGGACTTAA 360  
CCCAACATCT CACGACACGA GCTGACGACA ACCATGCACC 400

(2) INFORMATION FOR SEQ ID NO: 3550:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3550:

CGAACGGACG AGAAGCTTGC TTCTCTGATG TTAGCGGCGG ACGGGTGAGT AACACGTGGA 60  
TAACCTACCT ATAAGACTGG GATAACTTCG GGAAACCGGA GCTAATACCG GATAATATTT 120  
TGAACCGCAT GGTTCAAAAG TGAAGACGG TCTTGCTGTC ACTTATAGAT GGATCCGCGC 180  
TGCAATTAGCT AGTTGGTAAG GTAACGGCTT ACCAAGGCAA CGATGCATAG CCGACCTGAG 240  
AGGGTGATCG GCCCACTGG AACTGAGACA CGGTCCAGAC TCCTACGGGA GGCAGCAGTA 300  
GGGAATCTTC CGCAATGGGC GAAACCTGAC GGAGCAACGC CGCGTGAGTG ATGAAGGTCT 360  
TCGGATCGTA AAACCTGTGTT ATTAGGGAAG AACATATGTG 400

(2) INFORMATION FOR SEQ ID NO: 3551:

(A) LENGTH: 506 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3551:

10	ACAAGGTAGC CGTATCGGAA GGTGCGGCTG GATCACCTCC TTTCTAAGGA TATATTCGGA	60
	ACATCTTCTT CAGAAGATGC GGAATAACGT GACATATTGT ATTCAGTTTT GAATGTTTAT	120
	TTAACATTCA AATATTTTTT GGTAAAGTG ATATTGCTTA TGCGAGCGCT TGACAATCTA	180
15	TTCTTTTTTA AGAAAGCGGT TGTTAGACAA TGCATTAAGA AAAATTAAAG CGGAGTTTAC	240
	TTTTGTAAAT GAGCATTGGA TTTTTTGAAA ATAAAGCAGT ATGCGAGCGC TTGACTAAAA	300
	AGAAATTGTA CATTGAAAAC TAGATAAGTA AGTAAAATAT AGATTTTACC AAGCAAAACC	360
20	GAGTGAATAA AGAGTTTTAA ATAAGCTTGA ATTCATAAGA aTAATCGCTA GTGTTGAAA	420
	GAACACTCAC AAGATTAATA ACGCGTTTTAA ATCTTTTTAT AAAAGAAAC GTTTAGCAGA	480
25	CAATGAGTTA AATTATTTTA AAGCAG	506

## (2) INFORMATION FOR SEQ ID NO: 3552:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2209 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3552:

35	AAGCTGAGGC CGACAGTGGn GCGATGGATA ACAGGTTGAT ATTCCTGTAC CACCTATAAT	60
	CGTTTTAATC GATGGGGGGA CGCATAGGAT AGGCGACGTG TCGATTGGAT TGCACGTCTA	120
40	AGCAGTAAGG CTGAGTATTA GGCAAATCCG GTACTCGTTA AGGCTGAGCT GTGATGGGGA	180
	GAAGACATTG TGTCTTCgAG GTCGTTGATT TCACACTGCC GAGAAAAGCC TCTAGATAGA	240
45	AAATAGGTGC CCGTACCGCA AACCGACACA GGTAGTCAAG ATGAGAATTC TAAGGTGAGC	300
	GAGCGAACTC TCGTTAAGGA ACTCGGCAAA ATGACCCCGT AACTTCGGGA GAAGGGGTGC	360
	TCTTTAGGGT TAACGCCAG AAGAGCCGCA GTGAATAGGC CCAAGCGACT GTTTATCAAA	420
50	AACACAGGTC TCTGCTAAAC CGTAAGtGAn TGTATAGGGG CTGACGCCTG CCCGGTGCTG	480
	GAAGGTTAAG AGGAGTGGTT AGCTTCTGCG AActAcGaAT CGAAGCCCCA GTAAACGGCG	540
55	GCCGTAAC TAACGGTCCT AAGGTAGCGA AATTCCTTGT CGGGTAAGTT CCGACCCGCA	600

	GTGAAGATGC AGGTTACCCG CGACAGGACG GAAAGACCCC GTGGAGCTTT ACTGTAGCCT	720
5	GATATTGAAA TTCGGCACAG CTTGTACAGG ATAGGTAGGA GCCTTTGAAA CGTGAGCGCT	780
	AcTTaCgTGG aGGCGCTGGT GGGATACTAC CCTAGCTGTG TTGGCTTTCT AACCCGCACC	840
	ACTTATCGTG GTGGGAGACA GTGTCAGGCG GGCAGTTTGA CTGGGGCGGT CGCCTCCTAA	900
10	AAGGTAACGG AGGCGCTCAA AGGTTCCCTC AGAATGGTTG GAAATCATT C ATAGAGTGTA	960
	AAGGCATAAG GGAGCTTGAC TGCAGACCT ACAAGTCGAG CAGGGTCGAA AGACGGACTT	1020
	AGTGATCCGG TGGTTCGCA TGGAAAGGCC ATCGCTCAAC GGATAAAAGC TACCCCGGGG	1080
15	ATAACAGGCT TATCTCCCCC AAGAGTTCAC ATCGACGGGG AGGTTTGGCA CCTCGATGTC	1140
	GGCTCATCGC ATCCTGGGGC TGTAGTCGGT CCCAAGGGTT GGGCTGTTCG CCCATTAAAG	1200
	CGGTACrmGg CTGGGTTcAG AACGTCGTGA GaCAGTTcGG TCCCTATCCG TCGTGGGCGT	1260
20	AGGAAATTTG AGAGGAGCTG TCCTTAGTAC GAGAGGACCG GGATGGACAT ACCTCTGGTG	1320
	TACCAgTTGT CGTGCCAAcG cATnAGCTGG GTAGCTATGT GTGGACGGGA TAAGTGCTGA	1380
	AACaTnCTnA AGCATGAAGC CCCCTCAAG ATGAGATTT C CCAACTTCGG TTATAAGATC	1440
25	CCTCAAAGAT GATGAGGTTA ATAGGTTCGA GGTGGAAGCA TGGTGACATG TgGGAGCTGA	1500
	CGAATACTAA TCGATCGAAG ACTTAATCAA AATAAATGTT TTGCGACAAA tnCaCTTTTA	1560
30	CTTACTATCT AGTTTTGAAT GTATAAATTA CATTcATATG TCTGGTGA CT ATAGCAAGGA	1620
	GGTCACACCT GTTCCCATGC CGAACACAGA AGTTAAGCTC CTTAGCGTCG ATGGTAGTCG	1680
	AACTTACGTT CCGCTAGAGT AGAACGTTGC CAGGCAGTTT TTTAATCAAA TTTTGgTTAA	1740
35	AAAATAAAAT GGACAAGATA AAAAAAGTTA TTGACTTAAA TGTTAATAAA ATGTATAATT	1800
	AATTCTTGTC GGTAAGAAAA ATGAACATTG AAAACTGAAT GACAATATGT CAACGTTAAT	1860
	TCCAAAAAAC GTAACTATAA GTTACAAACA TTATTTAGTA TTTATGAGCT AATCAAACAT	1920
40	CATAATTTTT ATGGAGAGTT TGATCCTGGC TCAGGATGAA CGCTGGCGGC GTGCCTAATA	1980
	CATGCAAGTC GAGCGAACGG ACGAGAAGCT TGCTTCTCTG ATGTTAGCGG CGGACGGGTG	2040
	AGTAACACGT GGATAACCTA CCTATAAGAC TGGGATAACT TCGGGAAACC GGAGCTAATA	2100
45	CCGATAATA TTTTGAACCG CATGGTTCAA AAGTGAAAGA CGGTCTTGCT GTCAC TTATA	2160
	GATGGATCCg CGCTGCATTA GCTAGTTGGt AAGGtAACGG CTTTACCCA	2209

(2) INFORMATION FOR SEQ ID NO: 3553:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 518 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3553:

5 CTAGATAAGT AAGTAAAATA TAGATTTTAC CAAGCAAAAC CGAGTGAATA AAGAGTTTTA 60  
 AATAAGCTTG AATTCATAAG AAATAATCGC TAGTGTTTGA AAGAACACTC ACAAGATTAA 120  
 10 TAACGCGTTT CCTGTAGGAT GGAAACATAG ATTAAGTTAT TAAGGGCGCA CGGTGGATGC 180  
 CTTGGCACTA GAAGCCGATG AAGGACGTTA CTAACGACGA TATGCTTTGG GGAGCTGTAA 240  
 GTAAGCTTTG ATCCAGAGAT TTCCGAATGG GGAAACCCAG CATGAGTTAT GTCATGTTAT 300  
 15 CGATATGTGA ATACATAGCA TATCAGAAGG CACACCCGGA GAACTGAAAC ATCTTAGTAC 360  
 CCGGAGGAAG AGAAAGAAAA TTCGATTCCC TTAGTAGCGG CGAGCGAAAC GGAAGAGCC 420  
 CAAACCAACA AGCTTGCTTG TTGGGGTTGT AGGACTCTCT ATACGGAGTT ACaAAGGmCG 480  
 20 ACATTgGACG AaTCATCTGG gAAAGwTGaT CCAAGGAA 518

## (2) INFORMATION FOR SEQ ID NO: 3554:

## (i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 587 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3554:

AGAATGACGG GTTCGAACCG CCGACCCTCT GCTTGTAAGG CAGATGCTCT CCCAGCTGAG 60  
 CTAATTCTCC GATTTAAAC TGCCTGGCAA CGTTCTACTC TAGCGGAACG TAAGTTsGAC 120  
 35 TACCATCGAC GCTAAGGAGC TTAACCTCTG TGTTCCGGCAT GGAACAGGT GTGACCTCCT 180  
 TGCTATAGTC ACCAGACATA TGAATGTAAT TTATACATTC AAAACTAGAT AGTAAGTAAA 240  
 40 AGTGATTTTG CTTGCAAAA CATTTATTTT GATTAAGTCT TCGATCGATT AGTATTCGTC 300  
 AGCTCCACAT GTCACCATGC TTCCACCTCG AACCTATTAA CCTCATCATC TTTGAGGGAT 360  
 CTTATAACCG AAGTTGGGAA ATCTCATCTT GAGGGGGGCT TCATGCTTAG ATGCTTTCAG 420  
 45 CACTTAatCCC GTCCACACAT AGCTACCCAG CTATGCCGTT GGCACGACAA CTGGTACACC 480  
 AGAGGTATGT CCATCCCGGT CCTCTCGTAC TAAGGACAGC TCCTCTCAA TTTCTACGC 540  
 CCACGACGGa TAGGGaCCGA ACTGtCTCAC GACGTTCTGA ACCCAGA 587

## (2) INFORMATION FOR SEQ ID NO: 3555:

## (i) SEQUENCE CHARACTERISTICS:

55 (A) LENGTH: 399 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3555:

	GAATCTGAAT CGCTATCTGA ATCCGAGTCA CTGTCGGAAT CTGAGTCACT GTCGGAATCT	60
10	GAATCGCTAT CTGAATCTGA ATCGCTGTCT GAATCTGAAT CGCTGTCTGA ATCTGAGTCG	120
	CTATCTGAGT CGGAATCGCT ATCTGAGTCG GAATCACTGT CGGAATCTGA ATCGCTGTCT	180
	GAGTCGGAAT CACTGTCGGA GTCAGAATCG CTGTCTGAGT CGGAATCACT GTCGGAATCT	240
15	GAATCGCTAT CTGAATCTGA ATCGCTATCT GAATCCGAGT CACTGTCTGa GTCAGAATCG	300
	CTATCTGGAA TCTGGAGTCA CTGTCGGAAT CTGAGTCACT GGTCTGGAGT CAGAATCGCT	360
20	ATCTGGAATC CGAGTTCATG GTCTGAGTCG GGaATCGCT	399

(2) INFORMATION FOR SEQ ID NO: 3556:

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 400 base pairs
25	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3556:

	ATTCATCTTT CCAGATGATT CGTCTAATGT CGTCCTTTGT AACTCCGTAT AGAGTGTCTT	60
	ACAACCCCAA CAAGCAAGCT TGTTGGTTTG GGCTCTTCCC GTTTCGCTCG CCGCTACTAA	120
35	GGGAATCGAA TTTCTTTCT CTTCCTCCGG GTACTAAGAT GTTTCAGTTC TCCGGGTGTG	180
	CCTTCTGATA TGCTATGTAT TCACATATCG ATAACATGAC ATAACATG CTGGGTTTCC	240
40	CCATTCGGAA ATCTCTGGAT CAAAGCTTAC TTACAGCTCC CCAAAGCATA TCGTCGTTAG	300
	TAACGTCCTT CATCGGCTTC TAGTGCCAAG GCATCCACCG TGCGCCCTTA ATAACCTAAT	360
	CTATGTTTCC ATCCTACAGG AAACGCGTTA TTAATCTTGT	400

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(2) INFORMATION FOR SEQ ID NO: 3557:

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 657 base pairs
	(B) TYPE: nucleic acid
50	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3557:



5      ACAACTGGTA CACCAGAGGT ATGTCCATCC CGGTCCTCTC GTACTAAGGA CAGCTCCTCT      120  
       CAAATTTCTT ACGCCACGA CGGATAGGGA CCGAACTGTC TCACGACGTT CTGAACCCAG      180  
       CTCGCGTACC GCTTTAATGG GCGAACAGCA AnCCCTTGGG ACCGACTACA GCCCCAGGAT      240  
       GCGATGAGCc GACATCGAGG TGCCAAACCT CCCCCTCGAT GTGAACTCTT GGGGGAGATA      300  
 10      AGCCTGTTAT CCCCAGGGTA GCTTTTATCC GTTGAGCGAT GGCCCTTCCA TGCGGAACCA      360  
       CCGGATCACT AAGTCCGTCT TTCGAcCCTG CTCGACTTGT AGGTCTCGCA GTCAAGCTCC      420  
       CTTATGCCCTT TACACTCTAT GAATGATTTC CAACCATTCCT GAGGGAACcT TGAGCGCCTC      480  
 15      CGTTACCTTT TAGGAGGCGA CCGCCCCAGT CAAACTGCCc GCcTGACACT GTCTACcmCC      540  
       ACGATAAGTG GTGCGGGTTm GmAAGCCAAC ACAGCTAGGG TAGTATCCCA CCAGCGCCTn      600  
       CCCACTAATA GCGCTCACGT TTCAAAGGCT CCTACCTATC CTGTACAAGC TGTGCCG      657

(2) INFORMATION FOR SEQ ID NO: 3558:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3558:

30      GAGTCCATGG GTGAAAGAAG CATCTGCAGC AACTGTAGCA GGTATTGCTG GAACTAATAA      60  
       TGGTATTACT GTTGACAGCAG GTACTTTCAA CCCTGCTGAT ACAATTCAAG TTGTTGCAAC      120  
 35      GCAAGGACAG CGGAGAGACA GTGAGTGATG AGCAACGTAT nnTnGATTTC ACAGTTGTCTG      180  
       CACCACAACC GAACCAAGCG ACTACTAAGA TTTGGCAAAA TGGTCATATT GATATCACGC      240  
       CTAATAATCC ATCAGGACAT TTAATTAATC CAACTCAAGC AATGGATATT GCTTACACTG      300  
 40      AAAAAGTGGG TAATGGTGCA GAACATACTA AGACAATTAA TGTGTTCGT GGTCAAATA      360  
       ATCAATGGAC AATTGCGAAT AAGCCTGACT ATGTAACGTT      400

(2) INFORMATION FOR SEQ ID NO: 3559:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3559:

CGACACAAAA CAAGCCAAGC AAAACAAACG CATATAACGT AACACACAT GGAAACGGCC 120  
 AAGTATCATA TGGCGCTCGC CAACACAAAA CAAGCCAAGC AAAACAAATG CATACAACGT 180  
 5 AACACACAT GCAAACGGTC AAGTGTCTATA CGGAGCTCGC CCGACATACA AGAAGCCAAG 240  
 TAAAACAAAT GCATACAATG TAACAACACA TGCAGATGGT ACTGCGACAT ATGGGCCTAG 300  
 10 AGTAACAAAA TAAGTTTGTA ACTCTATCCA AAGACATACA GTCAATACAA AACATTACGT 360  
 ATCTTTACAA CAGTAATCAT GCATTCTATG ATGCTTCTAA 400

## (2) INFORMATION FOR SEQ ID NO: 3560:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 485 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3560:

TTTAGGTTAT ACAGCATTGC AGGCAGGATA CTTATCAATT ACTTATTTAA TCATGGTGTT 60  
 25 ATTGATGATT CGAGTTGGTG AAAAATTATT ACAAAAAATG GGTCTAAGC GACCAATGTT 120  
 ATTAGGTACA TTCATTGTGG TCATTGGTAT TGCATTATT TCATTAGTAT TCTTACCAGG 180  
 30 CATATTTTAT GTTATCAGTT GTGTCGTAGG ATATTTATGT TTCGGACTAG GCTTAGGTAT 240  
 TTATGCAACA CCTTCTACAG ATACAGCTAT TTCGAATGCA CCGTTAGATA AAGTTGGCGT 300  
 TGCTTCAGGT ATTTATAAAA TGGCTTCATC ACTTGGTGGG CGCATTCCGT GTCGCAATTA 360  
 35 GTGGTGCTGT ATATGCTGGT GCAGTTGCTG CAACGAGCAT TCCATACAGG TCGGATGATT 420  
 GCACTTTGGG TTAACGTATT GAATGGGGAA TCCATGGCCA TTTATCGCAA TTTTAATnCG 480  
 CGATT 485

## (2) INFORMATION FOR SEQ ID NO: 3561:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3561:

AAATTATGTG AAGTAAAAGG AGTACGTCCA TGCAAAATTT AGATAAGAAT TTTCGACaTT 60  
 TATCtCGTAA AGAAAAGTTA CaACAATTGG TTGATAAGCA ATGGTTATCA GAAGAACAAT 120

ATGTCATCGC GCAAGGTGCA TTACCCGTTG GATTATTACC GAATATCATT GTGGACGATA 240  
 AGGCATATGT TGTACCTATG ATGGTGAAG AGCCTTCAGT TGTGCTGCA GCTAGTTATG 300  
 5 GTGCAAAGCT AGTGAATCAG ACTGGCGGAT TTAAACGGT ATCTTCTGAA CGTATTATGA 360  
 TAGGTCAAAT CGTCTTTGAT GCGGTTGACG ATACTGAAAA ATTATCAGCA GACATTAAAG 420  
 10 CTTTAGAAAA GCAAATTCAT AAAATTGCGG ATGAGGCATA TCC 463

## (2) INFORMATION FOR SEQ ID NO: 3562:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 643 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3562:

AATTTAAACC CAATTGTCTG GCAAAACGTT TTCCTTTATA AAAAGATTTA AACGCGTTAA 60  
 TTAATCTTGG TGCGGTCTT TCGAACACTA GCGATTATTT CTTATGAATT CAAGCTTATT 120  
 25 TAAACTCTT TATTCACCTG GTTTTGCTTG GTAAATCTA TATTTTACTT ACTTATCTAG 180  
 TTTTCAATGT ACAATTTCTT TTTAGTCAAG CGCTCGCATA CTGCTTTATT TTCAAAAAAT 240  
 CAAATGCTCA TTTACAAAAG TAACTCCGC TTTAATTTTT CTTAATGCAT TGTCTAACAA 300  
 CCGCTTTCTT TAAAAAGAAT AGATTGTCAA GCGCTCGCAT AAGCAATATC ACTTTAACCA 360  
 AAAAATATTT GAATGTAAA TAAACATTCA AACTGAATA CAATATGTCA CGTTATTCCg 420  
 35 CATCTTCTGA AGAAGATGTT CCGAATATAT CCTTAGAAAAG GAGGTGATCC AGCCGCACCT 480  
 TCCGATACGG CTACCTTGCT ACGACTTCAC CCAATCATT TGTCCCACCT TCGACGGCTA 540  
 GCTCCTAAAA GGTTACTCCA CCGGCTTCGG GTGTTACAAA CTCTCGTGGT GTGACGGGCG 600  
 40 GTGTGTACAA GACCCGGGAA CGTATTCACC GTAGCATGCC TCG 643

## (2) INFORMATION FOR SEQ ID NO: 3563:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3563:

GATAAATCCA AATAGTGCAC TATAAAAAAT AATATCTACT AAAGTATCTT TATGTAATCC 60

TTCCATACCA TCGTACACTC AGTGGTCCTA AGTTAAATGC CACAGGATCT ATATAGTTAA 180  
 ATACAATACC CATTCAACCT ACTCCTCACT CTTATGACTG TTCTTGATAA TTTCTTCATT 240  
 5 TAATCTTTCA CTAAATTCTT CGGCCGTGTT AATGCCCATG ATATTTAATC GATAGTTCAT 300  
 TGCAGCGACC TCAATAATTA CCGCAACATT TCTACCAGGT CTTACAGGTA TTGGTTTTTT 360  
 10 TTAGTGGnTT TCAGTATCTA AAATACTTAG CGTCTCTTCA 400

## (2) INFORMATION FOR SEQ ID NO: 3564:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3564:

TCGTCAgCnC nTGTCGTGAG ACGTTGGGTT AAGTCCCGCA ACGAGCGCAA CCCTTAAGCT 60  
 TAGTTGCCAT CATTAAAGTTG GGCACCTCTAA GTTGACTGCC GGTGACAAAC CGGAGGAAGG 120  
 25 TGGGGATGAC GTCAAATCAT CATGCCCTT ATGATTTGGG CTACACACGT GCTACAATGG 180  
 ACAATACAAA GGGCAGCGAA ACCGCGAnGT CAAGCAAATC CCATAAAGTT GTTCTCAGTT 240  
 CGGATTGTAG TCTGCAACTC GACTACATGA AGCTGGAATC GCTAGTAATC GTAGATCAGC 300  
 30 ATGCTACGGT GAATACGTTT CCGGGTCTTG TACACACCGC CCGTCACACC ACGAGAGTTT 360  
 GTAACACCCG AAGCCGGTGG AGTAACTTTT AGGAGCTAGC 400

## (2) INFORMATION FOR SEQ ID NO: 3565:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3565:

CAAACCATTT GTAGCTATTT GTAACCTTA TATTGATATT GTTCCTGGAC ATGTTCACTT 60  
 GAGAGAGCTT GCAGATATAG CTAAAGAAGC AATTAGAGAA GCCGGTGCCA TTCCATTTGA 120  
 45 ATTCAATACA ATTGGTGTG ATGATGGAAT AGCTATGGGA CATATCGGAA TGCGATATTC 180  
 50 TCTACCATCA CGTGAAATTA TTGCAGATGC AGCTGAAACT GTAATTAAAC CTCATTGGTT 240  
 TGACGGCGTA TTTTACATTC CTAATTGTGA CAAGATTACA CCCGGTATGA TTTTAGCAGC 300

TGCACATGGA AAAGCATTAA CACTTTCATC AATGTTTGAA

400

## (2) INFORMATION FOR SEQ ID NO: 3566:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3566:

15 AAATTACGTA CATATTTAAA GCTGACGGCA CTATGACTGC AGGAACATCT GCCCCACTTT 60  
 CTGATGGTGC AGGATTTGTA GTTTTAATGT CTGGAGATAA AGTGAAAGAA CTCGGcGTGA 120  
 CACCTATTGC ACGATTCGTT GGTTTTAAGG CAGTAGGCGT TGACCCGAAA ATTATGGSTA 180  
 20 TTGGGCCTGC ATATGCGATT CCTGAAGTAT TGCTACTCAG CAATCTATCT GTTGAAGACA 240  
 TTGATTTGAT CGAATTGAAC GAAGCATTTC CTTCTCAAAC GATTGCATCT ATTAAAGAAG 300  
 TAGGTCTAGA TATATCACGT ACGAATGTGA ATGGTGGCGC TATTGCTTka GGTCATCCAT 360  
 25 TAGGTGCTAC AGGCGCaATG TTAACCGCGC GTTTACTTAA TGAAATGGGT AGACGTCCCG 420

## (2) INFORMATION FOR SEQ ID NO: 3567:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3567:

TACGGGAAGT AGCTCAGCTT GGGTAGAGCA CTTGGTTTGG GACCAAGGGG TCGCAGGTTT 60  
 40 GAATCCTGTC TTCCCGATAT ACTGTAATTA TTATGGGGGC TTAGCTCAGC TGGGAGAGCG 120  
 CCTGCTTTGC ACGCAGGAGG TCAGCGGTTT GATCCCGCTA GTCTCCACCA TATTATTTAC 180  
 45 AAATATATA AGGCGGTGTA GCTCAGCTGG CTAGAGCGTA CGGTTTATAC CCGTGAGGTC 240  
 GGGGGTTTGA TCCCTCCAC CGCCACTATT TATTAGTTGT AAAATTATAT TTAGGACCTT 300  
 TAGCTCAGTT GGTAGAGCT AACGGCTCAT AACCGTTTCG TCGCAGGTTT GAGTCCTGCA 360  
 50 GGTCCTATAT AATTTTGGAG GAATACCCAG TCCGGCTGAA 400

## (2) INFORMATION FOR SEQ ID NO: 3568:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3568:

	TTAGCCAATC CCCATTCTGG ACGTACCTCA CTCCAATCAC TCGCAAACCG CTGCGCTTCT	60
10	TCCACTGGAT GATTACACAG ACCAATCGTT GGCAGTTTGT CCAAACGTTT GCGATTCCGT	120
	GTTTCAGAAA TCATCGGCAT CGCGTCATT C AATGATTCAT ATGCATCTAA AGCAATAGAA	180
	GATAATGTGT CTGGCACATA TACCCATGCC AACGATCAG TAGACGTATG ATGTTCTGCT	240
15	ACCGCAAAAA CAGTTGTCTC TGGATATATAC ACACCTGATT GTTTTAATCC TTGTCTGACA	300
	TTTGGACGAT TACATATCAT CGCTAATAAC TTAGCATTA AAACCGCTTG ATGCGCCACC	360
20	ACAAGCCCCA CATTTCAAGT GATGGCATGG NTGTGGGTTn	400

(2) INFORMATION FOR SEQ ID NO: 3569:

	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 400 base pairs
25	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3569:

	CCCCGACCTC ACGGGTATGA ACCGTACGCT CTAGCCAGCT GAGCTACACC GCCTTATATA	60
	GTTTGTAAT AATATGGTGG AGACTAGCGG GATCGAACCG CTGACCTCCT GCGTGCAAAG	120
35	CAGGCGCTCT CCCAGCTGAG CTAAGCCCCC ATAATAATTA CAGTATATCG GGAAGACAGG	180
	ATTGGAACCT GCGACCCCTT GGTCCCAAAC CAAGTGCTCT ACCAAGCTGA GCTACTTCCC	240
	GTATAATTAA CGCGCCCGAT AGGAGTCGAA CCCATAACCT CTTGATCCGT AGTCAAACGC	300
40	TCTATCCAAT TGAGCTACGG GCGCATATGT TTTTATTGAA AATGGTGCCG AGGACCGGAA	360
	TCGAACCGGT ACGTGATCAC TCACCGCAGA TTTTAAGTCC	400

45 (2) INFORMATION FOR SEQ ID NO: 3570:

	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 542 base pairs
	(B) TYPE: nucleic acid
50	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3570:

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GTTTTATATCC GTTGAGCGAT GGCCnTCCCA TGGGGACCTA CCGGATCACT AAGTCCGTCT 120  
 TTTGACCCCT GCTTCGACTT GTAGGTCTCG CAGTCAAGCT CCCTTATGCC TTTACACTCT 180  
 5 ATGAATGATT TCCAACCATT CTGAGGGAAC CTTTGAGCGC CTCCGTTACC TTTTAGGAGG 240  
 CGACCGCCCC AGTCAAACCTG CCCGCCTGAC ACTGTCTCCC ACCACGATAA GTGGTGCGGG 300  
 10 TTAGAAAGCC AACACAGCTA GGGTAGTATC CCACCAGCGC CTCCACGTaa GyTAGCGCTC 360  
 ACGTTTCAAA GGCTCCTACC TATCCTGTAC AAGCTGTGCC GAATTTCAAT ATCAGGCTAC 420  
 AGTAAAGCTC CACGGGGTCT TTCCGTCTCG TCGCGGGTAA CCTGCATCTT CACAGGTACT 480  
 15 ATGATTTTAC CGAGTCTCTC GTTGAGACAG TGCCCAAATC GTTACGCCTT TCGTGCGGGT 540  
 CG 542

## (2) INFORMATION FOR SEQ ID NO: 3571:

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- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 619 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3571:

30 ATGCCCGACC ACATGGAGCT TCCAATCCCA TTGCTCTAAC CAATGAGCTA CTGAACCATA 60  
 aTaAAAATGT AAtGATGGCG GTCTCGACGG GAATCGAACC CGCGATCtCn GCGTGACAGG 120  
 CAGGCGTGTT AACCCCTACA CTACGAGACC TATAAAATAT TGCGGGAGGC GGATTTGAAC 180  
 35 CACCGGACTT CGGGTTATGA GCCCCGACGAG CTACCGAACT GCTCCATCCC GCGATAATAA 240  
 AAAATAATGG CGGAGGAAGA GGGATTCGAA CCCCCGCGGC CCGTTAAGGc CCTGTGCGTT 300  
 TTCAAGACCG ATCCCTTCAG CCGGACTTGG GTATTCTCTC ATTATTATAG GTAAATCGCT 360  
 40 ATTAATTATA AAATTAAATG GCGGTCTCGA CGGGAATCGA ACCCGCGATC TCCTGCGTGA 420  
 CAGGCAGGCG TGTTAACCGC TACTACTACGA GACCATTAGT AAAACGGAGG AAGAGGGATT 480  
 45 CGAACCCCGG CGAGCCGTTA AGCCCCTGTC GGTTTTCAAG ACCGATCCCT TCAGCCGGAC 540  
 TTGGGTATTCT CTCCAAAATT ATATGGACCT TGCAGGACTC GAACCTKCGA CCGAACGGTT 600  
 ATGAGCCGTT AGCTCTAAC 619

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## (2) INFORMATION FOR SEQ ID NO: 3572:

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- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3572:

5 GGTGAAGACA TCACGTATCA AGAAGCATGG GCAGATGAAG AATATCGTGA AGACTTAAAA 60  
 GCAGAATTAA TTGATCAAGC GGTACTTCA TTGAGCCACA AGATTTATTC AGTGCGATGA 120  
 TTCGTGAAAT TGAAACGCAA GATTTCGATA TAGAACATCT AGCGACGGCG ATTCGCAAAG 180  
 10 TTGAAACATC TACATTAGGT GAAGAAAGTG AAAATGACTT TATCGGGCTG TTCAGCGATA 240  
 TGGATTTGAG TTCAACGCGA CTAGGTAACA ATGTCAAAGA ACGTACTGCT TTAATCTCTA 300  
 AAGTCATGGT TAATCTTGAC GACTTACCAT TCGTTCACAG TGACATGGAA ATTGATATGT 360  
 15 TAGGTGATGC ATATGAATTC CTAATCGGGC GCTTTGCGGC 400

## (2) INFORMATION FOR SEQ ID NO: 3573:

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3573:

CAAATCGTAA CTCGCCGTT CATTCTACAA AAGGCACGCC ATCACCATT AACGGGCTCT 60  
 30 GACTACTTGT AAGCACACGG TTTCAGGTTT TATTTCACTC CCCTTCCGGG GTGCTTTTCA 120  
 CCTTTCCCTC ACGGTACTGG TTCACTATCG GTCCTAGAG AGTATTTAGC CTTAGGAGAT 180  
 GGTCCTCCCA GATTCGACG GAATTTACG TGCTCCGTCG TACTCAGGAT CCACTCAAGA 240  
 35 GAGACAACAT TTTGACTAC AGGATTATTA CCTTCTTTGA TTCATCTTTC CAGATGATTC 300  
 GTCTAATGTC GTCCTTTGTA ACTCCGTATA GAGTGTCTTA CAACCCCAAC AAGCAAGCTT 360  
 GTTGGTTTGG GGCTCTTCCC ATTCGCTCG CGGCTACTAA 400

## (2) INFORMATION FOR SEQ ID NO: 3574:

## (i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 1051 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3574:

50 TCCCTCAAAG ATGGATGAGG TTAATAGGTT CGAGGTGGAA GCATGGTGAC ATGTGGCAGC 60



TTTACTTACT ATCTAGTTTT GAATGTATAA ATTACATTCA TATGTCTGGT GACTATAGCA 180  
 AGGAGGTCAC ACCTGTTCCC ATGCCGAACA CAGAAGTTAA GCTCCTTAGC GTCGATGGTA 240  
 5' GTCGAACCTA CGTTCCGCTA GAGTAGAACG TTGCCAGGCA TAATATTAAAT CCACACTAGC 300  
 TCAGTGGTAG AGCTATCGGC TGTTAACCGA TCGGTCGTAG GTTCGAGTCC TACCTGTGGA 360  
 10' GCCATGGCTC cTtGGTCAAG CGGTAAAGAC ACCGCCCTTT CACGGCGGTA ACACGGGTTC 420  
 GAGTCCCGTA GnAGTCATTA TTTTGGAGAA TTAGCTCAGC TGGGAGAGCA TCTGCCTTAC 480  
 AAGCAGAGGG TCGGCGGTTC GAACCCGTCA TTCTCCACCA TTTTGATTAT TAAATTATAT 540  
 15' GAATAAGCTG GAGGGGTAGC GAAGTGGCTA AACGCGGCGG ACTGTAAATC CGCTcCTTCG 600  
 GGTTCGGCAG TTCGAATCTG CCCCCCTCCA CCATCTATAT ATTGGGCTAT AGCCAAGCGG 660  
 TAAGGCAACG GACTTTGACT CCGTCACTCG TTGGTTCGAA TCCAGCTAGC CCAGCCATTA 720  
 20' GAGCCATTAG CTCAGTTGGT AGAGCATCTG ACTTTTAATC AGAGGGTCAG AGGTTCGAAT 780  
 CCTCTATGGC TCACTACTTG CACTTTCCAT TTTTGGGAAG TGCTTTTTTT TAGGTTCTcC 840  
 ACCAAATGTG GTGGGtATAT AATTAAAGA ACTATTTTTA AAATACAACT TTTAGAGCTT 900  
 25' TTATTATTAG GCGGCCAGTC CATTATTGGG CTTGGTTGTC TTCTTTTTTT CTCCTTTGtA 960  
 CAAGCTGAAA ATCATCATTA TACGTGctTA AAGTGTGAAA TTTCTGTAAC CAAAAGAATH 1020  
 30' CACTTGATTA ATThnATCTA TATAATGCCT C 1051

## (2) INFORMATION FOR SEQ ID NO: 3575:

## (i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 476 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3575:

GTGGAGCGCT TAGAAGTGAG AATGCAAGTG TGAgTAGCGA AAGACGGGTG AGAATCCCCGT 60  
 45' CCACCGATTG ACTAAGGTTT CCAGAGGAAG GCTCGTCCGC TCTGGGTTAG TCGGGTCCTA 120  
 AGCTGAGGCC GACACGTATG GCGATGGATA ACAGGTTGAT ATTCTGTAC CACCTATAAT 180  
 CGTTTTAATC GATGGGGGGA CGCATAGGAT AGGCGAcGTG sCGATTGGAT TGCACGTCTA 240  
 50' AGCAGTAAGG CTGAGTATTA GGCAAATCCG GTACTCGTTA AGGCTGAGCT GTgATGGGGA 300  
 GAAGACATTG TGTCTTCGAG TCGTTgATTT CACACTGCCG AGAAAAGCCT CTAGATAGAA 360  
 AATAgTGCC CGTaCCGCAA AaCCGACACA GGTAGTCAA GATGnGAATT CTAAnGTGAA 420

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## (2) INFORMATION FOR SEQ ID NO: 3576:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3576:

TTTGTTTCCTT TTTTAATTTA TATATTTAAA ATACACATAT TCAAGAGCTC GAGATATAAG 60  
 TCAATGTACT AGGCACACAA TTTAATATTG ACAGTAATTA ACCGAACGAA AATGCGCCCC 120  
 GGGGCCCCAA CATAGAGAAT TTCGAAAAGA AATTCTACAG ACAATGCAAG TTGGCGGGGC 180  
 CCCAACATAG AAGCTGGCCA ATAGTTAGCT TTCAATAATG TGCAAGTTGG GGTAAAGGGCC 240  
 CCAACACAGA AGCTGGCCAA TAGTCAGCTT TCAATAATGT GCAAGTTGGG GTAAGGGCCC 300  
 CAACACAGAG AATTTGAAA AGAAATTCTA CAGACAATGC AAGTTGGCGG GGGCCCAACA 360  
 CAGAAGCTGG GCCAATAGTC AGCTTTTCCA ATAATGTGGC 400

## (2) INFORMATION FOR SEQ ID NO: 3577:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3577:

TGCATCTTCA CAGGTACTAT GATTTACCG AGTCTCTCGT TGAGACAGTG CCCAAATCGT 60  
 TACGCCCTTC GTGCGGGTCG GAACTTACCC GACAAGGAAT TTCGCTACCT TAGGACCGTT 120  
 ATAGTTACGG CCGCCGTTTA CTGGGGCTTC GATTCGTAGC TTCGCAGAAC TAACCACTCC 180  
 TCTTAACCTT CCAGCACCGG GCAGGCGTCA GCCCTATACA TCACCTTACG GTTTAGCAGA 240  
 GACCTGTGTT TTTGATAAAC AGTCGCTTGG GCCTATTAC TGCGGCTCTT CTGGGCGTTA 300  
 ACCCTAAAGA GCACCCCTTC TCCCGAAGTT ACGGGGTCAT TTTGCCGAGT TCCTTAACGA 360  
 GAGTTCGCTC GCTCACCTTA GAATTCTCAT CTTGACTAAC 400

## (2) INFORMATION FOR SEQ ID NO: 3578:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3578:

5 TAACTTAACA CGACTTCTTA AGTCATTTAG TTTTAATGTT TGATGTGTTT CTGCTAAACC 60  
 AATCTCCCAA GGAACACCGG CATGCTGAAT ACTCGTTTTG GGTGAAGCCC TGTACCACCA 120  
 TCGTAACCAC TGATGACAAT TTTATCTGCA AATGCTTTTG CCACCCAGCA TGCAATGGTA 180  
 10 CCAACACCTG TTTTCGAAAC TAATTTTACC GCGATATCTG CATCTTTATT CGCATTTTTC 240  
 AAATCATGTA TCAGTTGCGC TAAATCTTCT ATTGAATAAA TATCATGATG TGGCGGTGGT 300  
 GAAATCAGAC CGATACCTGG CGTTGGACCC TCTTGCTTTC GCAATCCACG GATATACCTT 360  
 15 AGTACCAGGT AATTGGACCA CCTTCACCAG GCTTTGCACC 400

(2) INFORMATION FOR SEQ ID NO: 3579:

20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3579:

AGCTACACCG CCTTATATAG TTTGTAAATA ATATGGTGGA GACTAGCGGG ATCGAACCGC 60  
 30 TGACCTCCTG CGTGCAAAGC AGGCGCTCTC CCAGCTGAGC TAAGCCCCCA TAATAATTAC 120  
 AGTATATCGG GAAGACAGGA TTCGAACCTG CGACCCCTTG GTCCCAAACC AAGTGCTCTA 180  
 CCAAGCTGAG CTACTTCCCG TATAATTAAC GCGCCCATA GGAGTCGAAC CCATAACCTC 240  
 35 TTGATCCGTA GTCAAACGCT CTATCCAATT GAGCTACGGG CGCATATGTT TTTATTGAAA 300  
 ATGGTGCCGA GGACCGGAAT CGAACCGGTA CGTGATCACT CACCGCAGGA TTTTAAGTCC 360  
 TGTGCGTCTG CCAGTTCCGC CACCCCGGCA CTATAAAAAAT 400

40 (2) INFORMATION FOR SEQ ID NO: 3580:

45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3580:

ACGTAAATAA CCATAACGAC GTGCCTCAAA GGCATTTGTA GAGACTTTCG CAAATGCGAT 60

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TATGCGATCA GCCATTTCTG CAAGGCCACC GCCACTCGGT AATAAGCCAA CACCTGCTTC 180  
 AACAAAGACCG ATATATGTTT CACTTGACGC GACAACAATA GGTGAGTAAA GTACAAGCTC 240  
 5 ACAGCCACCG CCTAAGGCAC GACCTTGAAC AGCTGTGACT ACTGGTTTCA AACTATACTT 300  
 CAAACGATTA AAGCTATAAT GTAATTTATC AATTGATTGT GCACGACATC ATCTACAAGA 360  
 10 CCGTCTTCCA TGC GCCTTTT TCCATTAAGA AAGGGTTAGC 400

## (2) INFORMATION FOR SEQ ID NO: 3581:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 15 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3581:

ATGTCATTGT TGSTACGGCT TTTCCAGAAG GATTACAAGG CAAAACATT GCACGAACGA 60  
 TTGCATTGCG TGC GGATTAT CTGACACGGT ACCGGGTCAA ACAGTGAATC GCTACTGCTC 120  
 25 ATCAGGATTA CAAACCATGC GATTGCAGCC AATCAAATTA TGGCTGGTCA AGGAGATATA 180  
 CTTGTAGCTG GTGCGTTGAA TTGATGAGTG CCGTACCAAT GGGTGGCAAC GAGCCCCACAA 240  
 30 ACAATCCAAC CTTACAATAT GATGATATAG GTGCGTCATA TCCTATGGGT TTAAC TGCTG 300  
 AAAATGTAGC ATCCCAATTT GACGTATCAC GCGAAGATCA AGATGCTTAT GCTGTCAGAA 360  
 GTCATCAACG TGCCTATGAC GCACAACGTG ATGGGTCCGG 400

35 (2) INFORMATION FOR SEQ ID NO: 3582:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 40 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3582:

AACTCGTTGC GCTCTTTTCT CGTTTCGTCA GATTCAAACG TTTTCACTTC GCCAAGCCAT 60  
 TTTTCTTTGT GTTTACTTTT TATTTTGACG TTTTAGACAT AAAAAAAGA GACCTTGCGG 120  
 50 TCTCAATGCG GTCATCGCA TCCATTTTTT GCCTGGCAAC GTTCTACTCT AGCGGAACGT 180  
 AAGTTGGCTA CCATCGACGC TAAGAACCTT TCTTGACTTG TGACAATCGC TTGCTTCTTT 240  
 CCTCTTCTTC GGCTCTCGCT TACTCATTTA GCTCTACTAA ACTCGTTGCG CTCTTTTCTC 300

55

ATTTTGACGT TTTAGACATA AAAAAAGAG ACCTTGCGGT

400

(2) INFORMATION FOR SEQ ID NO: 3583:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3583:

15	AAGCAGGCGC TCTCCAGCT GAGCTAAGCC CCCAAATAGG TATTAAATTA ATGGTGGGCC	60
	TAAGTGGACT CGAACCACCG ACCTCACGCT TATCAGGCGT GCGCTCTAAC CAGCTGAGCT	120
	ATAGGCCCAT TAATTGAAT GAACAAACAT TCAAACTGA ATACAATATG TCACGTTATT	180
20	CCGCATCTTC TGAAGAAGAT GTTCCGAATA TATCCTTAGA AAGGAGGTGA TCCAGCCGCA	240
	CCTTCCGATA CGGCTACCTT GTTACGACTT CACCCCAATC ATTTGTCCCA CCTTCGACGG	300
	CTAGCTCCTA AAAAGGTTAC TCCACCGGCT TCGGGTGTTA CAACTCTCG TGGTGTGACG	360
25	GGCGGTGTGT ACAAGACCCG GGAACGTATT TCACCGTAGC	400

(2) INFORMATION FOR SEQ ID NO: 3584:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3584:

	ACTTATTTGG CGATATTTTA AGTGATGAAG CTTCACTGAT TCCTGGTTCA CTTGGTTTAT	60
40	CACCTTCTGC TAGTTTTAGT AACGATGGTC CAAGATTGTA TGAGCCTATT CATGGATCAG	120
	CACCAGATAT TGCAGGTAAA AACGTTGCCA ATCCATTTGG AATGATTCTA TCTTTAGCGA	180
	TGTGTTTACG TGAAGCTTA AATCAACCAG ATGCTGCAGA TGAATTAGAA CAACATATTT	240
45	ATAGCATGAT TGAACATGGG CAAACGACAG CAGATTTAGG CGGCAAATTG AATACTACTG	300
	ATATTTTCGA AATTCTATCT CAAAATTGA ATCACTAAGG GGGGAGATGT AAATGGGGTC	360
50	AAACATTATT TGACAANGTG TGGGACAGAC ATGTGTTATA	400

(2) INFORMATION FOR SEQ ID NO: 3585:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3585:

ACTGATGACA ATTTTATCTG CAAATGCTTT TGCCACCCCA GATGCAATGG TACCAACACC 60  
 10 TGTTTTCGAA ACTAATTTTA CCGCGATATC TGCATCTTTA TTCGCATTTT TCAAATCATG 120  
 TATCAGTTGC GCTAAATCTT CTATTGAATA AATATCATGA TGTGGCGGTG GTGAAATCAG 180  
 ACCGATACCT GGCCTTGACC CTCTTGCTTT CGCAATCCAC GGATATACCT TAGTACCAGG 240  
 15 TAATTGACCA CCTTCACCAG GCTTTGCACC TTGCGCAACT TTAATTTGAA TTTCTTTGGG 300  
 CATGTTGTAA ATAATCACTA GTTACACCAA AACGCCCAGA AGCAACTTGT TTAATCGCAC 360  
 TTACTTTGGT GGCTTCCATC AACTTGTACT TCATAACGGT 400

20

(2) INFORMATION FOR SEQ ID NO: 3586:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 25 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3586:

TACAAGTATT ACCATTATCT CnAGAGGATT CTAGATAAGG GGCATGGATC ATTTGTCTTC 60  
 TTATGAATTT GAGCCAGATA AAGAATCTAT CTTAAGTGTA ATCTTGACCT CAATATGTTG 120  
 35 AGAGTTTGAT TTACGGAACA ATATTAGACG CAAAAGCAAG TGAGCATGCA ACACGTATGA 180  
 CTGCGATGAA AAATGCCACT GATAATGCAA CTGAACTTAT TGATGACTTA TCATTAGAAT 240  
 ATAACAGAGC GAGACAAGCA GAAATTACGC AACAAATTAC TGAAATTGTT GGTGGTTCCG 300  
 40 CAGCGCTTGA ATAATATTTA AnGGAGGAAA ATAGCATGGG AATTGGCCGT GTACTCAAGT 360  
 TATGGGTCCT GTAATTGATG TTCGATTGA ACATAACGAG 400

45

(2) INFORMATION FOR SEQ ID NO: 3587:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 50 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3587:

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AGGATTCGAA CCTGCGACCC CTTGGTCCCA AACCAAGTGC TCTACCAAGC TGAGCTACTT 120  
 CCCGTATAAT TAACGCGCCC GATAGGAGTC GAACCCATAA CCTCTTGATC CGTAGTCAAA 180  
 5 CGCTCTATCC AATTGAGCTA CGGGCGCATA TGTTTTTATT GAAAATGGTG CCGAGGACCG 240  
 GAATCGAACC GGTACGTGAT CACTCACCGC AGGATTTTAA GTCCTGTGCG TCTGCCAGTT 300  
 CCGCCACCCC GGCCTATAA AAATGGAGCA GAAGACGGGA TTCGAACCCG CGACCCCAAC 360  
 10 CTTGGCAAGG TTGTATTCTA CCGCTGAACT ACTTCTGCAT 400

(2) INFORMATION FOR SEQ ID NO: 3588:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3588:

TACTATTGAC ATGTGTGAAC CCTATGTCCG ATTATTTTCG GACCTATTTT CTAATGCAGC 60  
 25 TATTATTTTT GACAGATTCC ATATCGTTCA ACATTTAAAT AGAGAACTTA ATAAGTATCG 120  
 TGTACAAGTT ATGAATGAAT ACCGTAATAA AAAAGGACCT GATTATACAA TTTTAAAGAA 180  
 TAACTGGAAA GTCCTATTGA TGGATACTAG TAAAACCATA TTTAGTAAAT ACAGATGGAA 240  
 30 TAAATCTTTT AAGGGCTTAT AAACGCTCAT CTGACATTGT AGAATTCATG CTTTCAAAG 300  
 ACGATATACT ACGACACTCC TACGAACTTG TCCAGGGATT ACGAAAAGAC CTAAGGGTAT 360  
 35 GTAATTGGGC CTAAATTAT TAATCGTTTA AATTCCGTTA 400

(2) INFORMATION FOR SEQ ID NO: 3589:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3589:

AGAGCGAACG GACGAGAAGC TTGCTTCTCT GATGTTAGCn GCGGACGGGT GAGTAACACG 60  
 TGGATAACCT ACCTATAAGA CTGGGATAAC TTCGGGAAAC CGGAGCTAAT ACCGGATAAT 120  
 50 ATTTTGAACC GCATGGTTCA AAAGTGAAAG ACGGTCTTGC TGTCATTAT AGATGGATCC 180  
 GCGCTGCATT AGCTAGTTGG TAAGGTAACG GCTTACCAAG GCAACGATGC ATAGCCGACC 240

AGTAGGGAAT CTTCCGCAAT GGGCGAAAGC TGACGGAGCA ACGnCGCGTG AGTGATGAAG 360  
 GTCTTCGGAT CGTAAAACTC TGTATTAGG GAAGAACATA 400

(2) INFORMATION FOR SEQ ID NO: 3590:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3590:

GTTAgGAGAG CGTTCTAAGG GCGTTGAAGC ATGATCGTAA GGACATGTGG AGCGCTTAGA 60  
 AGTGAGAATG CCGGTGTGAG TAGCGAAAGA CCGGTGAGAA TCCctCCACC GATTGACTAA 120  
 GGTtTCCAGA GGAAGGCTCG TCCGCTCTGG GTTAGTCGGG TCCTAAGCTG AGGCCGACag 180  
 gTAaGGCGAT GGATAACAGG TTGATATTCC TGTACCACCT ATAATCGTTT TaATCGATGG 240  
 GGGGACGCAT AGGATAGGCG AAcGTGcGAT TGGATTGCAC GTCTAAGCAG TAAGGCTGAG 300  
 TATTAGGCAA ATCCGGTACT CGTTaAGGCT GAGCTGTGAT GGGGAGAAGA CATTGwGTCT 360  
 TCGAGTCGTT GATTTCACAC TGCCGAGAAA AgCCTCTAGA TAGAAAATAG GTGCCCCGTAC 420  
 CGCAAACCGA CACAGGTAAT CCAAGATGAG AATTCTAAGG TGAGCGAGCG AACTCTCGTT 480  
 AAGGAACTCG GCAAAATGAC CCCGTAAct 509

(2) INFORMATION FOR SEQ ID NO: 3591:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3591:

ATTTCTTATG AATTCAAGCT TATTTAAAC TCTTTATTCA CTCGGTTTTG CTTGGTAAAA 60  
 TCTATATTTT ACTTACTTAT CTAGTTTTCA ATGTACAAAT AATGGTGGAG ACTAGCGGGA 120  
 TCGAACCGCT GACCTCCTGC GTGCAAAGCA GCGCTCTCC CAGCTGAGCT AAGCCCCCAA 180  
 ATAGGTATTA AATTAAATGGT GGGCCTAAGT GGA CTGGAAC CACCGACCTC ACGCTTATCA 240  
 GCGTGCGCT CTAACCAGCT GAGCTATAGG CCCATTAATT TGAATGAACA AACATTCAAA 300  
 ACTGAATACA ATATGTCACG TTATTCGCA TCTTCTGAAG AAGATGTTCC GAATATATCC 360



## (2) INFORMATION FOR SEQ ID NO: 3592:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 440 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3592:

TGGGnAACGC AACATCCTTT TCCAACTTAA CATATATTTT GGGACCTTAg CTGGTGGTCT 60  
 GGGCTGTTTC CCTTTCGAAC ACGGACCTTA TCACCCATGT TCTGACTCCC aAGTTAAATT 120  
 AATTGGCATT CGGAGTTTGT CTGAATTCGG TAACCCGAGA GGGGCCCTC GTCCAAACAG 180  
 TGCTCTACCT CCAATAATCA TCACTTGAGG CTAGCCCTAA AGCTATTTTCG GAGAGAACCA 240  
 GCTATCTCCA GGTTCGATTG GAATTTCTCC GCTACCCTCA GTTCATCCGC TCACTTTTCA 300  
 ACGTAAGTCG GTTCGGTCct CCATTCAGTG TTACCTGAAC TTCAACCTGa CCAAGGGTAG 360  
 ATCACCTGGT TTCcGsGTsT ACGACCAAAT AsTAAACGCC CTATTCAGAC TCGCTTTTCGC 420  
 TAnGGCTCCA CATTACTGGn 440

## (2) INFORMATION FOR SEQ ID NO: 3593:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3593:

TAAACGAACC AATTTTATTT GGTGCACCAC TAGTATTGAA TCCTGTGTTT TTTATTCCAT 60  
 TTGTATTAGC ACCAATTGTT AACGTATGGA TTTTCAAAC TTTTCGTTGAA GTGTTAGGAA 120  
 TGAATAGTTT TAGTGTGAAT TTACCTTGGA CAACACCAGG TCCATTGGGC ATTATCATGG 180  
 GTACAGGTTT TGGTTTATGG TCATTCGTAC TAGCTATTAC TTTGATTGTT GTAGATATTA 240  
 TTATnTACTA CCCATTCCCTA AAAGTTTATG ATAGTGAAAT TCTTGATGAA GAAGAAGGAC 300  
 GTAAAGAAAG TAATTCAGAT TTAAAGAAA AAGTTCAGC AAACCTTTGA TACGAAAAAA 360  
 GCTGATTCAA TTTTAGCGGC AAGTGGTGTA TCAGACGATG 400

## (2) INFORMATION FOR SEQ ID NO: 3594:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 409 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3594:

	AAGGGAATCG AATTTTCTTT CTCTTCCTCC GGGTACTAAG ATGTTTTCAGT TCTCCGGGTG	60
10	TGCCTTCTGa TATGCTATGT ATTCACATAT CGATAACATG ACATAACTCA TGCTGGGTTT	120
	CCCCATTTCGG AAATCTCTGG ATCAAAGCTT aCTaCAGCTC CCCAAAGCAT ATCGTCGTTA	180
	GTAACGTCCT TCATCGGCTT CTAGTGCCAA GGCATCCACC GTGCGCCCTT AATAACTTAA	240
15	TCTATGTTTC CACCATTTTT ATAAGTCAAA CGCTCACATA CGGCTTCGTT TTCATTATTT	300
	TAAATGCTCA TTTACATAAG TAAACTCTGC TTTAAATAA TTAACTCAT TGTCTGCTAA	360
	ACGTTTTCTT TTATAAAAAG ATTTAAAcGC GTTAaTAATC CTCTCGCTC	409

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(2) INFORMATION FOR SEQ ID NO: 3595:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3595:

	AATATAAGCC CTGGATCATA CATGACCTGT ATTTGGGCAA TCCCTTCTGC TACATCTTCT	60
	GCCCACTCAT TCAATATTTG TTTTGCAATA TCATCACCTT CTTAGCTGC TTCAAACAAT	120
35	ACTGGCACAT GTGTGCTTCT CGTAAATCCT CCGGCAATCA TGCGCTTTTT CAATGCACTC	180
	GTTGCAGCAC GTTGCTCAAA CGTTGTATTT TCAGTTGGAC GATACAATAA ATACCCAAC	240
	TCATTGCTT TATGAAGCTC ACCATTATCA ATATGACCTT GGATTATTCT TGTACGCACC	300
40	CCCAATGGCC TGGTACCAAG CGTCCATACA AAAGATCCGT TCTGGCTTGG ATATTGGATG	360
	GTAATTTCCA ATTCGGCCTA GTTAATGGCA GCGGTTTTAA	400

(2) INFORMATION FOR SEQ ID NO: 3596:

45

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 596 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3596:

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CTGCCGAACC CGAAGAGCGG ATTTACAGTC CGCCGCGTTT AGCCACTTCG CTACCCCTCCA 120  
 GCTTATTCAT ATAATTTAAT AATCAAAATG GTGGAGAATG ACGGGTTCGA CCGCCGACCC 180  
 5 TCTGCTTGTA AGGCAGATGC TCTCCCAGCT GaGCTAATTC TCCAAAATAA TGA CTCTAC 240  
 GGGACTCGAA CCCGTGTTAC CGCCGTGAAA GGGCGtGTCT TAACCGCTTG ACCAAGGAGC 300  
 CATGGCTCCA CaGGTAGGAC TCGAACCTAC GACCGATCGG TTAACAGCCG ATAGCTCTAC 360  
 10 CACTGAGCTA CTGTGGaTTA ATATTATGCC TGGcAACGTT CTACTCTAGC GGAACGTAAG 420  
 TTCGACTACC ATCGACGCTA AGGAGCTTAA CTTCTGTGTT CGGCATGGGA ACAGGTGTGA 480  
 CCTCCTTGCT ATAGTCACCA GACATATGAA TGTAATTTAT ACATTCAAAA CTAGATAGTA 540  
 15 AGTAAAAGTG ATTTTGCTTC GCAAAACATT TATTTTGATT AAGTCTTCGA TCGATT 596

(2) INFORMATION FOR SEQ ID NO: 3597:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3597:

TCATCTTGAG GGGGGCTTCA TGCTTAGATG CTTTCAGCAC TTATCCCGTC CACACATAGC 60  
 30 TACCCAGCTA TGCCGTTGGC ACGACAATG GTACACCAGA GGTATGTCCA TCCCGGTCCT 120  
 CTCGTACTAA GGACAGCTCC TCTCAAATTT CCTACGCCCA CGACGGATAG GGACCGAACT 180  
 GTCTCAGGAC GTTCTGAACC CAGCTCGCGT ACCGCTTTAA TGGGCGAACA GCCCAACCCT 240  
 35 TGGGACCGAC TACAGCCCCA GGATGCGATG AGCCGACATC GAGGTGCCAA ACCTCCCCGT 300  
 CGATGTGAAC TCTTGGGGGA GATAAGCCTG TTATCCCCGG GGTAGCTTTT ATCCGTTGAG 360  
 40 CGATGGCCCT TCCATGCGGA ACCACCGGAT CAATAAAGTC 400

(2) INFORMATION FOR SEQ ID NO: 3598:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 397 base pairs  
 45 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3598:

AACCAACGGC AGCAACTACA TGACCTAATT CTTGTGCTGA CTCTACATTT AGTAGCTCTA 60

CACTTCAATT GTACCAATCA ATCGTTGACG ATCTTGATCG TAACGCCATG TAGCAATACC 180  
 ACGATACTGT CCGTCACGAC TCGCGTATGC ATGCGCACTT GCTTCTGCAC CACGCGTATC 240  
 5. ATTTCTCTGTT GCTAAAACAA CAGCATGTAT GCCATTCATA ACACCTTTAT TATGTGTTGC 300  
 TGCACGATGA ATATCTACTT GGGCCAATAC AGAAGCACGT TCCATCGTTT GcaACCTCTT 360  
 CTCCAGTTCT CTCGCCCCCTT GGCTAAATCT TTAACAT 397

## (2) INFORMATION FOR SEQ ID NO: 3599:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3599:

AACCCTTGGG ACCGACTACA GCCCCAGGAT GCGATGAGCC GACATCGAGG TGCCAAACCT 60  
 CCCCCTCGAT GTGAACTCTT GGGGGAGATA AGCCTGTTAT CCCCAGGGTA GCTTTTATCC 120  
 25. GTTGAGCGAT GGCCCTTCCA TCGGAACCA CCGGATCACT AAGTCCGTCT TTCGACCCTG 180  
 CTCGACTTGT AGGTCTCGCA GTCAAGCTCC CTTATGCCTT TACTCTAT GAATGATTTT 240  
 CAACCATTCT GAGGGAACCT TTGAGCGCCT CCGTTACCTT TTAGGAGGCG ACCGCCCCAG 300  
 30. TCAAAGTGCC CGCCTGACAC TGTCTCCAC CACGATAAGT GTGCGGGTTA GAAAGCCAAC 360  
 ACAGCTAGGG TAGTATCCCA CCAGCGCCTC CAACGTAAGC 400

## (2) INFORMATION FOR SEQ ID NO: 3600:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3600:

ATCTGAATCT GAGTCGTTGT CTGAGTCCGA ATCGCTATCT GAATCTGAGT CGCTATCTGA 60  
 GTCTGAGTCG CTATCTGAAT CTGAGTCGCT GTCTGAATCT GAATCACTGT CTGAGTCTGA 120  
 50. GTCGCTGTCT GAGTCTGAAT CGCTGTCAGA ATCTGAGTCG CTATCTGAGT CTGAATCTGA 180  
 ATCACTGTCT GAGTCCGAAT CGCTATCTGA ATCTGAATCG CTATCTGAGT CTGAGTCGCT 240  
 ATCCGAATCT GAGTCGCTAT CTGAGTCTGA GTCGCTATCC GAGTCTGAAT CGCTGTCTGA 300

GGTCTGGAAT CTGAnTCGCT AACTGAAATC TGAGTCGCTA

400

## (2) INFORMATION FOR SEQ ID NO: 3601:

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## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3601:

15 ATTTAATACC TATTTGGGGG CTTAGCTCAG CTGGGAGAGC GCCTGCTTTG CACGCAGGAG 60  
 GTCAGCGGTT CGATCCCGCT AGTCTCCACC ATTATTTGTA CATTGAAAAC TAGATAAGTA 120  
 AGTAAAATAT AGATTTTACC AAGCAAAACC GAGTGAATAA AGAGTTTTAA ATAAGCTTGA 180  
 20 ATTCATAAGA AATAATCGCT AGTGTTGCGAA AGAACATCCA CAAGATTAAT AACGCGTTTA 240  
 AATCTTTTTA TAAAAGAACG TAACTTCATG TTAACGTTTG ACTTATAAAA ATGGTGGAAG 300  
 CATAGGTAA GTTATTAAGG GCGCACGGTG GGATGCCTTG GCACTAGAAG CCGATGAAGG 360  
 25 GncGTTACTA ACGACGATAT GCTTTGGGGA GCTGTAAGTA 400

## (2) INFORMATION FOR SEQ ID NO: 3602:

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## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3602:

GCTGTCTGAG TCGGAATCAC TGTnGGAGTC AGAATCGCTG TCTGAGTCGG AATCACTGTC 60  
 40 GGAATCTGAA TCGCTATCTG AATCTGAATC GCTATCTGAA TCCGAGTCAC TGTCTGAGTC 120  
 AGAATCGnTA TCTGAATCTG AGTCACTGTC GGAATCTGAG TCACTGTCTG AGTCAGAATC 180  
 GCTATCTGAA TCCGAGTCAT TGTCTGAGTC GGAATCGCTC GCTGAGTCGG AATCGCTTGC 240  
 45 TGAATCTGAA TCACTCGCTG AGTCTGAATC ACTTGCTGAA TCTGAATCAC TCGCTGAATC 300  
 TGAACCACTA TCTGATGTAG GAATCACTAC CCGAATCTGA AnCGCTATCT GAATAAGAAT 360  
 50 CGCTGCCAGA TCTGAACCTG GGGTCAGAAT CTGAAT 396

## (2) INFORMATION FOR SEQ ID NO: 3603:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 529 base pairs

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(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3603:

	TTTCTTATCT GTAATTTTAT CGTAAGATTT TTTCGCAATG AGATTGGAT CGTnTTTGTC	60
10	CACTACAATA TCTAATAGTT TTAATTTAAG TCCAGCATTG AAAAAAGTG CTGCCAGTTG	120
	AGCGCCCATG GTGCCTGCGC CAAGAACGGT TACTTTATTA ATTGTCATAG TGATTCCTCC	180
	AATTTAGTTG AGGATAAGAT AACCATTAAAG ATAATTGGAA TAACGTTGCT ATTTTATAAA	240
15	ATTAATTAAG TATCTTTGAC AGTCATCTTA GCCTCTTATT TAAGGaAAAA GCTTTATGCT	300
	TAAAATAAGT CTTTTTTAGT GAAATTAATG CATCTCATAT AATTATTTGC TATTTATACG	360
	AAAGCmGaAT CTCCAGTcAa AGCGCGTCCA ATTACTAAGG CATTAAATTC ATGTGTACCT	420
20	TCGTACGTGT AAATCGCTTC TGCATCAGAG AAGAAACGTG CAATATCATA ATCGTCAGCT	480
	AGTATGCCAT TACCACCTGT AATACCGCGG CCCATAGCTA CTnTCTCAC	529

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(2) INFORMATION FOR SEQ ID NO: 3604:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 399 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3604:

35	CACAAGATAA GCATTGTAGA TGTGGATGCT TTAAGTGGG AAGCGATTGG TCGTCCTAAA	60
	ACAGGTACAT ATGCGCTATC TGACCTAGTC GGTTTAGATA TTGCAGTGTC TGTAATTAAA	120
	GGCATGCAAC AAGTACCTGA AGAAACACCT TATTTTCATG ATGTCAAAT TGTAATACG	180
40	TTGTTTGACA ATGGCGCACT CGGACGTAAA ACGAAACAAG GATTTTACAA AAAGGATAAA	240
	GAAACTAAAG CTCGACTTGT TTACGATGTT GAAAAACAAG ATTATGTACC TGTATCGCAA	300
45	CCACAATTAC CAATTTTAAA TGAATTTAAT AAAGACTTAG TGCaTAACCT TGATACCATA	360
	TTCCAATGCG CAAGACGAGC GGGGACTATT TTTATGGGG	399

(2) INFORMATION FOR SEQ ID NO: 3605:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3605:

5 ATCACTTGAG GCTAGCCCTA AAGCTATTTT GGAGAGAACC AGCTATCTCC AGGTTCGATT 60  
 GGAATTTCTC CGCTACCCTC AGTTCATCCG CTCACCTTTT AACGTAATCG GTTCGGTCCT 120  
 CCATTCAGTG TTACCTGAAC TTCAACCTGA CCAAGGGTAG ATCACCTGGT TTCGGGTCTA 180  
 10 CGACCAAATA CTAACGCCCC TATTCAGACT CGCTTTCGCT ACGGCTCCAC ATTTACTGCT 240  
 TAACCTTGCA TCAAATCGTA ACTCGCCGGT TCATTCTACA AAAGGCACGC CATCACCCAT 300  
 TAACGGGCTC TGGACTACTT GTAAGCACAC GGTTCAGGT TCTATTTTAC TCCCCTTCCG 360  
 15 GGGTGGCTTT TCACCTTTCC CTCACGGTAA TGGGTTCACT 400

## (2) INFORMATION FOR SEQ ID NO: 3606:

## (i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3606:

AAATCCTGCG GTGAGTGATC ACTAACCCGG TTCGATTCCG GTCCTCGGCA CCATTTTCAA 60  
 TAAAAACATA TGCGCCCGTA GCTCAATTGG ATAGAGCGTT TGA CTACGGA TCAAGAGGTT 120  
 30 ATGGGTTCGA CTCCTATCGG GCGCGTTAAT TATACGGGAA GTAGCTCAGC TTGGTAGAGC 180  
 ACTTGGTTTG GGACCAAGGG GTCGCAGGTT CGAATCCTGT CTTCCCGATA TACTGTAATT 240  
 ATTATGGGGG CTTAGCTCAG CTGGGGAGAG CGCCTGCTTT GCACGCAGGA GGTCAGCGGT 300  
 35 TCGATCCCGC TAGTCTCCAC CATATTATTT ACAA ACTATA TAAGGCGGTG TAGCTCAGCT 360  
 GGCTAGAGCG TACGGTTCAT ACCCGTGAGG TCGGGGGTTC 400

## (2) INFORMATION FOR SEQ ID NO: 3607:

## (i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3607:

50 GGGTGTGCTT CTGATATGCT ATGTATTCAC ATATCGATAA CATGACATAA CTCATGCTGG 60  
 GTTTCCTTTC CGGAAATCTC TGGATCAAAG CTTACTTACA GCTCCCCAAA GCATATCGTC 120

TTAATCTATG TTTCCACCAT TTTTATAAGT CAAACGTTAA CATGAAGTTA CGTTCTTTTA 240  
TAAAAAGATT TAAACGCGTT ATTAATCTTG TGAGTGTCTT TTCGAACACT AGCGATTATT 300  
5 TCTTATGAAT TCAAGCTTAT TTAAACTCT TTATTCACCTC GGTTTGTGCTT GGTAAAATCT 360  
ATATTTTACT TACTTATCTA GTTnCAATG TACAAATAAT 400

## (2) INFORMATION FOR SEQ ID NO: 3608:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3608:

20 TAGTTTTCAA TGTACAAATA ATGGTGGAGA CTAGCGGGAT CGAACCGCTG ACCTCCTGCG 60  
TGCAAAAGAGC CGCTCTCCCA GCTGAGCTAA GCCCCCAAAT AGGTATTAAA TTAATGGTGG 120  
GCCTAAGTGG ACTCGAACCA CCGACCTCAC GCTTATCAGG CGTGCCTCTT AACCAGCTGA 180  
25 GCTATAGGCC CATTAAATTG AATGAACAAA CATTCAAAAC TGAATACAAT ATGTCACGTT 240  
ATTCCGCATC TTCTGAAGAA GATGTTCCGA ATATATCCTT AGAAAGGAGG TGATCCAGCC 300  
GCACCTTCCG ATACGGCTAC CTTGTTACGA CTTACCCCCA ATCATTGTGC CCACCTTCGA 360  
30 CGGCTAGCTC CTAAAAGGTT ACTCCACCGG CTTGGGGTGT 400

## (2) INFORMATION FOR SEQ ID NO: 3609:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
35 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3609:

AGGGCACTCT TACTGGGCGT GTTAAATTAC TAAnTTCAAT CAGCAGAAGA ACTAGGACAT 60  
45 GGCGCTTTTA AAATTATTGA AACACATGCA TTAAGAGATG TACAAGCAGT ATTGGGTTTT 120  
CATAATGACC CATCGCGTTC GGTAGGTACA TTTGCAATCA AAACAGGGGC AATTACATCA 180  
GCAGTAGATC GTTTTGAGTT TCATATTAAA GGCGTGGGTG GTCATGCTGC AAACCAGAAC 240  
50 AATGCAACGA TCCAGTTATT GTGTGGCGC AATTGATTAA TAGTATTCAA TCCATAGTTA 300  
GTAGAAATCT ATCTGCGTTT GATGAAGCGG TAGTAACAAT TGGACAAATA TCATGTGGTA 360



## (2) INFORMATION FOR SEQ ID NO: 3610:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3610:

```

AGGGAATCGA ATTTTCTTTC TCTTCCTCCG GGTACTAAGA TGTTTCAGTT CTCCGGGTGT      60
GCCTTCTGAT ATGCTATGTA TTCACATATC GATAACATGA CATAACTCAT GCTGGGTTTC      120
CCCATTCGGA AATCTCTGGA TCAAAGCTTA CTTACAGCTC CCCAAAGCAT ATCGTCGTTA      180
GTAACGTCCT TCATCGGCTT CTAGTGCCAA GGCATCCACC GTGCGCCCTT AATAACTTAA      240
TCTATGTTTC CACCATTTTT ATAAGTCAAA CGCTCACATA CGGCTTCGTT TTCATTATTT      300
TAAATGCTCA TTTACATAAG TAAACTCTGC TTTAAATGA ATTTAACTCA TTGTCTGCTA      360
AACGTTTTGC TTTTATAAAA AGATTTAAAC GCGTTGATTT      400

```

## (2) INFORMATION FOR SEQ ID NO: 3611:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3611:

```

GAGCTAGGCC GGCAATATGT AAGAATAAAT GGTGGAGAAT GACGGGTTTC AACCGCCGAC      60
CCTCTGCTTG TAAGGCAGAT GCTCTCCAG CTGAGCTAAT TCTCCGATT AAAACTGCCT      120
GGCAACGTTT TACTCTAGCG GAATAAGTT GNACTACCAT CGACGCTAAG GAGCTTAACT      180
TCTGTGTTTC GCATGGGAAC AGGTGTGACC TCCTTGCTAT AGTCACCAGA CATATGAATG      240
TAATTTATAC ATTCAAACT AGATAGTAAG TAAAAGTGAT TTTGCTTCGC AAAACATTTA      300
TTTTGATTAA GTCTTCGATC GATTAGTATT CGTCAGCTCC ACATGTCACC ATGCTTCCAC      360
CTCGAACCTA TTAACCTCAT CATCTTTGAG GGATCTTAAT      400

```

## (2) INFORMATION FOR SEQ ID NO: 3612:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3612:

5 ACCCAGCTCG CGTACCGCTT TAATGGGCGA ACAGCAATCC CTTGGGACCG ACTACAGCCC 60  
 CAGGATGCGA TGAGCCGACA TCGAGGTGCC AAACCTCCCC GTCGATGTGA ACTCTTGGGG 120  
 GAGATAAGCC TGTATATCCCC GGGGTAGCTT TTATCCGTTG AGCGATGGCC CTTCCATGCG 180  
 10 GAACCACCGG ATCACTAAGT CCGTCTTTTCG ACCCTGCTCG ACTTGTAGGT CTCGCAGTCA 240  
 AGCTCCCTTA TGCCTTTACA CTCTATGAAT GATTTCCAAC CATTCTGAGG GAACCTTTGA 300  
 15 GNGCCTCCGT TACCTTTTATG GAGGCGACCG CCCCAGTCAA ACTGCCCCGCC TGACACTGTC 360  
 TCCCACCACG ATAAGTGTnG GGGGGTTAGA AAGCCAACAC 400

## (2) INFORMATION FOR SEQ ID NO: 3613:

20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 487 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3613:

ACTTACAGCT CCCCAAAGCA TATCGTCGTT AGTAACGTCC TTCATCGGCT TCTAGTGCaA 60  
 30 GGCATCCACC GTGCGCCCTT AATAACTTAA TCTATGTTTC CACCATTTTT ATAAGTCAAA 120  
 CGCTCACATA CGGCTTCGTT TTCATTATTT TAAATGCTCA TTTACATAAG TAAACTCTGC 180  
 TTTAAAATAA TTAACTCAT TGTCTGCTAA ACGTTTTCTT TTATAAAAAG ATTTAAACGC 240  
 35 GTTATTAATC TTGTGAGTGT TCTTTCGAAC ACTAGCGATT ATTTCTTATG AATTCAAGCT 300  
 TATTTAAAAC TCTTTATTCA CTCGGTTTTG CTTGGTAAAA TCTATATTTT ACTTACTTAT 360  
 CTAGTTTTCA ATGTACAAAT AATGGTGGGC CTAAGTGGAC TCGAACCACC GACCTCACGC 420  
 40 TTATCAGGCG TCGCTCTAA CCAGCTGAGC TATAGGCCCA TTTTTTTGaa TGTTAAATAA 480  
 ACATTCA 487

## (2) INFORMATION FOR SEQ ID NO: 3614:

45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 50 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

ACCGTACGCT CTAGCCAGCT GAGCTACACC GCCTTATATA GTTTGTAAAT AATATGGTGG 60  
 AGACTAGCGG GATCGAACCG CTGACCTCCT GCGTGCAAAG CAGGCGCTCT CCCAGCTGAG 120  
 5 CTAAGCCCCC ATAATAATTA CAGTATATCG GGAAGACAGG ATTCGAACCT GCGACCCCTT 180  
 GGTCCCAAAC CAAGTGnTCT ACCAAGCTGA GCTACTTCCC GTATAATTAA CGCGCCCGAT 240  
 AGGAGTCGAA CCCATAACCT CTTGATCCGT AGTCAAACGC TCTATnCAAT TGAGCTACGG 300  
 10 GCGCATATGT TTTTATTGAA AATGGTGCCG AGGACCGGAA TCGAACCGGT ACGGTGATCA 360  
 CTCACCGCAG ATTTTAAGTC CTGTGCGTCT GcnAGTTCCG 400

(2) INFORMATION FOR SEQ ID NO: 3615:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3615:

TCGGCTCTCG CTTACTCATT TAGCTCTACT AAACCTCGTTG CGCTCTTTTC TCGTTTCGTC 60  
 AGATTCAAAC GTTTTCACTT CGCCAAGCCA TTTTCTTTG TGTTTACTTT TTATTTTGAC 120  
 30 GTTTTAGACA TAAAAAAGA GACCTCACGG TCTCAACTTG CCTGGCAACG TTCTACTCTA 180  
 GCGGAACGTA AGTTGGCTAC CATCGTCGCT AAAGACCTTT CTTGACTTGT GACAATCGCT 240  
 TGCTTCTTTC CTCTCCTTCG GCTCTCGCTT ACTCATTTAG CTCTACTAAA CTCGTTGCGC 300  
 35 TCTTTTCTCG TTTCTGCAGA TTCAAACGTT TTCACTTCGC CAAGCCATTT TTCTTTGTGT 360  
 TTACTTTTTTA TTTTGACGTT TAGGCATAAA AAAAAGAGAC 400

(2) INFORMATION FOR SEQ ID NO: 3616:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3616:

TrGTGTCTTT CGAACACTAG CGATTATTTT TTATGAATTC AAGCTTATTT AAAACTCTTT 60  
 ATTCACTCGG TTTTGCTTGG KAAAATCTAT ATTTTACTTA CTTATCTAGT TTTCAATGTA 120  
 55 CAATTTCTTT TTAGTCAAGC GCTCGCATAA GCAATATCAC TTTAACCAAA AAATATTTGA 180

AAGATGTTCC GAATATATCC TTAGAAAGGA GGNATCCAG CCGCACCTTC CGATACGGCT 300  
 ACCTTGTTAC GACTTCACCC CAATCATTG TCCCACCTTC GACGGCTAGC TCCTAAAAGG 360  
 5 TTACTCCACC GGCTTCGGGT GTTACAAACT CTCGTnGGTG TGACGGGCGG TGTGTACAAG 420

## (2) INFORMATION FOR SEQ ID NO: 3617:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3617:

CACTAGCGAT TATTTCTTAT GAATTCAAGC TTATTTAAAA CTCTTTATTC ACTCGGTTTT 60  
 20 GCTTGGTAAA ATCTATATTT TACTTACTTA TCTAGTTTTC AATGTACAAT TTCTTTTATG 120  
 TCAAGCGCTC GCATAAGCAA TATCACTTTA ACCAAAAAAT ATTTGAATGT TAAATAAACA 180  
 25 TTCAAAACTG AATACAATAT GTCACATTAT TCCGCATCTT CTGAAGAAGA TGTTCGGAAT 240  
 ATATCCTTAG AAAGGAGGTG ATCCAGCCGC ACCTTCGGAT ACGGCTACCT TGTACGACT 300  
 TCAnCCCAAT CATTTGTCCC ACCTTCGACG GCTAGCTCCT AAAAGGTTAC TCCACCGGCT 360  
 30 TCGGGTGTTA CAACTCTCG TGGTGTGACG GCGGGTGTGT 400

## (2) INFORMATION FOR SEQ ID NO: 3618:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3618:

GATATACGCT ATGGCTGGAG CAGTGTGGCC AAATGGCGGA AGACAAACGT TTAATGCGAT 60  
 45 AACTTTAGCG CAAAATATTG GTGTGGCTGT CGGTGCTGCA ATGGGCGGCT TTGTGCGAGA 120  
 ATTTAGCTTT AACTATATCT TTTTAGCCAA TCTTATTATG TATGTTGTGT TTGCGCTTGT 180  
 CCGGTTAACn AATTTAATAT TGAAATTAAT GCGAAAGTTA AATATCCAAC TCATTTAGAT 240  
 50 ATTACTGGTA AAAAGAATAA AGCAAGATTT ATTTCAATAG TACTAATTTG TGCAATGTTT 300  
 GCAATTTGTT GGGTTGCATA TATTCAATGG GGAGTCTACA ATCGCTTCAT TTTACACAAT 360  
 55 CTATTAATAT TTCAATGGGC ACAATATAGT GTTTTATGGG 400

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3619:

TCGCACGCCT TCGCCTATCC TACTGCGTCC CCCCATCGAT TAAAACGATT ATAGGTGGTA 60  
 CAGGnAATAT CAACCTGTTA TCCATCGCCT ACGCCTGTCT GCCTCAGCTT AGGACCCGAC 120  
 TAACCCAGAG CGGACGAGCC TTCCTCTGGA AACCTTAGTC AATCGGTGGA CGGGATTCTC 180  
 ACCCGTCTTT CGCTACTCAC ACCGGCATTC TCACTTCTAA GCGCTCCACA TGTCTTACG 240  
 ATCATGCTTC AACGCCCTTA GAACGCTCTC CTACCATTGT CCAAAGGAAA TCCACAGCTT 300  
 CGGTAATATG TTTAGCCCCG GTACATTTTC GGCGCAGTGT CACTCGACTA GTGAGCTATT 360  
 ACGCACTCTT TAAATGATGG CTGCTTCTAA GCCAACATCC 400

## (2) INFORMATION FOR SEQ ID NO: 3620:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3620:

TTAAGTCTTC GATCGATTAG TATTCGTCAG CTCCACATGT CACCATGCTT CCACCTCGAA 60  
 CCTATTAACC TCATCATCTT TGAGGGATCT TATAACCGAA GTTGGGAAAT CTCATCTTGA 120  
 GGGGGGCTTC ATGCTTAGAT GCTTTTCAGCA CTTATCCCGT CCACACATAG CTACCCAGCT 180  
 ATGCCGTTGG CACGACAACT GGTACACCAG AGGTATGTCC ATCCCGGTCC TCTCGTACTA 240  
 AGGACAGCTC CTCTCAAATT TCCTACGCCC ACGACGGATA GGGACCGAAC TGTCTCACGA 300  
 CGTTCTGAAC CCAGCTCGCG TACCGCTTTA ATGGGCGAAC AGCCCAACCC TTGGGACCGA 360  
 CTACAGnCCC AAGGATGCGA TGAGCCGACA TCGAGGTGCC 400

## (2) INFORMATION FOR SEQ ID NO: 3621:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 475 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3621:

5 CCACACCCGc AAATGGTGag CCATAGcAGG ATTCGgaACC TCTGcACCCT CTGATTAAAA 60  
 GTCAGcATGC TCTACCAACT GaGCTAATGG CTCTTCCATG GTGCCGGCCA GAGGACTTGA 120  
 ACCCCCAACC TACTGATTAC AAGTCAGTTG CTCTACCAAT TGAGCTAGGC CGGCAATATG 180  
 10 TAAGAATAAA TGGTGGAGAA TGACGGGTTT GAACCGCCGA CCCTCTGCTT GTAAGGCAGA 240  
 TGCTCTCCCA GCTGAGCTAA TTCTCCGATT TAAACTGCC TGGCAACGTT CTA CTCTAGC 300  
 GGAACGTAAG TTCGACTACC ATCGACGCTA AGGAGCTTAA CTTCTGTGTT CGGCATGGGA 360  
 15 ACAGGTGTGA CCTCCTTGCT ATAGTCACCA GACATATGGA ATGTAATTTA TACATTCAAA 420  
 ACTAGATAGT AAGTAAAAGT GATTTTGCTT CGCAAAACAT TTATTTTGAT TAAGT 475

## (2) INFORMATION FOR SEQ ID NO: 3622:

20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 25 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3622:

30 TGGACGAAAC TTTATATCGA TCAATTTCTA TCGAGTTGGA CAATGCCGAA GCGTGACAAA 60  
 AGTTTTTACC ATGCATGGTT GCATTTAGCG CAACATGACC ATAGTTTTAC TAAAGCACAG 120  
 CGCnCAAGTG ATTAAAGGCT TACCCAATGA TCCTGAAATG ACGATAGAGT CAGTATTAAC 180  
 35 TCATTTTTCA ATAGATCAGG AAGACTACCA AGCTTATGTT GAAGGACATC TTTTGCGGTT 240  
 ACCGGGTTGG GCAGGTATGT TGTATTACCG TTCACAACAG CATCACTTTG AACAACTTT 300  
 40 GTTAACGGAT TATTTGGCAA TTCGGTTAGT TGTCGAACAA TTGCTAGTTG GTGGATGAGT 360  
 TTTAAGTCAG TCGCTAAAGA TTGTGGAAAG TAAGATCCGG 400

## (2) INFORMATION FOR SEQ ID NO: 3623:

45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 50 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3623:

55 TAGATGCTTT CASACTTATC CCGTCCACAC ATAGCTACCC AGCTATGCCG TTGGACGACA 60

ATTCCTACG CCCACGACGG ATAGGGACCG AACTGTCTCA CGACGTTCTG AACCCAGCTC 180  
 GCGTACCGCT TTAATGGGCG AACAGCCAAC CCTTGGGACC GACTACAGCC CCAGGATGCG 240  
 5 ATGACCGACA TCGAGGTGCC AAACCTCCCC GTCGATGTGA ACTCTTGGGG GAGATAAGCC 300  
 TGTATCCCC GGGGTAGCTT TTATCCGTTG AGCGATGGCC TTCCATGCGG GAACACCGGA 360  
 TCACTAAGTC CGTCTTTCGA CCCTGCTCGA CTTTGTAGGn 400

(2) INFORMATION FOR SEQ ID NO: 3624:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3624:

GAGCTAGGCC GGCAATATGT AAGAATAAAT GGTGGAGAAT GACGGGTTCTG AACCGCCGAC 60  
 CCTCTGCTTG TAAGGCAGAT GCTCTCCCAG CTGAGCTAAT TCTCCGATTT AAAACTGCCT 120  
 25 GGCAACGTTT TACTCTAGCG GAANTAAAGTn GnACTACCAT CGACGCTAAG GAGCTTAACT 180  
 TCTGTGTTCTG GCATGGGAAC AGGTGTGACC TCCTTGCTAT AGTCACCAGA CATATGAATG 240  
 30 TAATTTATAC ATTCAAACCT AGATAGTAAG TAAAAGTGAT TTTGCTTCGC AAACATTTAT 300  
 TTTGATTAAG TCTTCGATCG ATTAGTATTC GTCAGCTCCA CATGTCACCA TGCTTCCACC 360  
 TCGAACCTAT TAACCTCATC ATCTTTGAGG GGATCTTATA 400

(2) INFORMATION FOR SEQ ID NO: 3625:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3625:

TTAAGAACG CTAATAACTG ATCGTAACCA CTATATATAT TGTTGTGACC TCTAACAGCA 60  
 TAATGTCTAA ATGTTTGTGG GATATATTGA AGCAATCCTT TTGCTGGATT GCCCTGTAAA 120  
 50 ACGTTGATGT CTCTAAGCGA ACTAGATTGA GTTATACCTG CATTTCTCTC TGATTCGTGT 180  
 TGAATCAAGC TAATGATATT TCCTACGTCA GCCGAAGTAA CATTAAACACC CATTCGTTTT 240  
 55 GCTGCACGAC GTATATCGCC TGCCCAAGCA GATGCAGCCT TATTAAACACC TGAACCACTT 300

CCTGGATGCG ACCCTTGCAT CAnTTGGGAA ATGTAnGTGT

400

## (2) INFORMATION FOR SEQ ID NO: 3626:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 461 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3626:

GATTGTGGTT CCGACATTCG AGGGTTCGAT CCCCTTCAGC CGCCCTTATT ATTAATGGGC 60  
 TATAGCCAAG CGGTAAGGCA ACGGACTTTG ACTCCGTCAC TCGTTGGTTC GAATCCAGCT 120  
 AGCCCAGTTA TTGGCGGCAT AGCAAGTGGT AAGGCAGAGG TCTGCAAAAC CTTTATCACC 180  
 GGTTCAAATC CGGTTGCCGC CTCCAGGTTT ATGCGGGAGT AGTTCAACTT TTAGAACACG 240  
 TTCCTTCCCG GAAGAGGTAT AGGTGCAAAT CCTATCTTCC GCTCCATAAT TTAATAATAA 300  
 TGCGGGAGTA TTTCAACTCT TAGAATACAT TCCTTCCTGG AATgAGGTAT AGGTGTAAAT 360  
 CCTATCTTCC GCTCCATAAT TTAATATTTG cGGGAGTAGT TCAACTTTTA GAAACAGCTC 420  
 CTTCCCGGAA CCGAGGTATA GGTGTAAATC CTATCTTCCG C 461

## (2) INFORMATION FOR SEQ ID NO: 3627:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3627:

TGCGGTCTCA ATGCGGCTCA TCGCATCCAT TTTTGCCTG GCAACGTTCT ACTCTAGCGG 60  
 AACGTAAGTT GGCTnAnATC GACGCTAAGA ACCTTTCTTG ACTTGTGACA ATCGCTTGCT 120  
 TCTTTCCTCT TCTTCGGCTC TCGTTACTC ATTTAGCTCT ACTAAACTCG TTGCGCTCTT 180  
 TTCTCGTTTC GTCAGATTCA AACGTTTCA CTTCGCCAAG CCATTTTTCT TTGTGTTTGC 240  
 TTTTtATTTT GACGTTTTAG ACATAAAAAA AAGAGACCTT GCGGTCTCAA TGCGGCTCAT 300  
 CGCATCCATT TTTTGCCTGG CAACGTTCTA CTCTAGCGGA ACGTAAGTTC GACTACCATC 360  
 GACGCTAAGG GAGCTTAACT TCTGTGTnCG GGCATGGGGG 400

## (2) INFORMATION FOR SEQ ID NO: 3628:



- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3628:

10 ATGCTTTTCAG CACTTATCCC GTCCACACAT AGCTACCCAC CTATGCCGTT GGCACGACAA 60  
 CTGGGTACAC CAGAGGTATG TCCATCCCGG TCCTCTCGTA CTAAGGACAG CTCCTCTCAA 120  
 ATTTCTTACG ACCCAGCAGG GATAGGGACC GAACTGTCTC ACGACGTTCT GAACCCAGCT 180  
 15 CGCGTACCGC TTTAATGGGC GAACAGCCCA ACCCTTGGGA CCGACTACAG CCCCAGGATG 240  
 CGATGAGCCG ACATCGAGGT GCCAAACCTC CCCGTCGATG TGAACCTCTG GGGGAGATAA 300  
 GCCTGTTATC CCCGGGGTAG CTTTATCCG nTGAGCGATG GGCCTTCCAT GCGGnACCAC 360  
 20 CGGnTTACTA AGTCCGTCTT TCGAnCCTGC TCGACTTGTA 400

## (2) INFORMATION FOR SEQ ID NO: 3629:

- 25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3629:

35 TTTATAAATA TCCAGTCTG AACGCGATTG CCATAACGGA TCAATGGCAG GATTGAAAGG 60  
 ATGTACATAT GGATGCATAT CCGTTGATGA TAAATCATGT TTTTCATACC AAGTCGCTGC 120  
 CGGCAAAACA ATGTCAGAAT ATAACGGTGT TGCCGTCATT CTGAAGTCTA AAGAGACCAC 180  
 40 TAAATCTAAC TTACCTGTTG TTTCTTCACG CCACGTAATT TCTTCTGGCT TTTCATCTTC 240  
 ATTTGGTGTA GCTAATAACC CTGATTTTGT GCCAAGTAAA TGCTTCATAA AGTATTCTTG 300  
 ACCTTTTGCA GAACTTGAAA TTAAGTTTGA ACGCCATATA AATAATGATT TTGGATGATT 360  
 45 CTnTTTCAAA TCAGGATCTT CTATTGCAAA TGGGGTTTGT 400

## (2) INFORMATION FOR SEQ ID NO: 3630:

- 50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 589 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

55

TTTAAGTTGT ngATTtAAAA TATTaATAAA GTGTAAATTT GACTATTGAn ATTCKrACaA 60  
 ATACATATTA AAATAATATT TGTTGAATTA ATTGAGTTAG GAAATTTATT TTTTAGAAAT 120  
 5 AAAATAATTA AAAATAATTC TTGACTTACA AAAACTTACG AGTTATAATT AAATCTTGTA 180  
 AGTGACAAAC GAACATTGAA AACTGAATGA CAATATGTCA ACGTTAATTC CAAAAACGTA 240  
 ACTATAAGTT ACAAACATTA TTTAGTATTT ATGAGCTAAT CAAACATCAT AATTTTTATG 300  
 10 GAGAGTTTGA TCCTGGCTCA GGATGAACGC TGGCGGCGTG CCTAATACAT GCAAGTCGAG 360  
 CGAACGGACG AGAAGCTTGC TTCTCTGATG TTAGCGGCGG ACGGGTGAGT AACACGTGGA 420  
 15 TAACCTACCT ATAAGACTGG GATAACTTCG GGAAACCGGA GCTAATACCG GATTATATTT 480  
 TGAACCGCAT GGTTCAAAAG TGAAAGACGG TCTTGCTGTC ACTTATAGAT GGATCCGCGC 540  
 TGCATTAGCT AGTTGGTAAG GTAACGGCTT ACCAAGGCAA CGATGCATA 589

20 (2) INFORMATION FOR SEQ ID NO: 3631:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 25 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3631:

CCAACTGAGC TAATGGCTCT TCCATGGTGC CGGCCAGAGG ACTTGAACCC CCAACCTACT 60  
 GATTACAAGT CAGTTGCTCT ACCAATTGAG CTAGGCCGCGC AATATGTAAG AATAAATGGT 120  
 35 GGAGAATGAC GGGTTGGAAC CGCCGACCCT CTGCTTGTA A GGCAGATGCT CTCCCAGCTG 180  
 AGCTAATTCT CCGATTtAAA ACTGCCTGGC AACGTTCTAC TCTAGCGGAA CGTAAGTTTCG 240  
 ACTACCATCG ACGCTAAGGA GCTTAACTTC TGTGTTTCGGC ATGGGAACAG GTGTGACCTC 300  
 40 CTTGCTATAG TCACCAGACA TATGAATGTA ATTTATACAT TCAAAACTAG ATAGTAAGTA 360  
 AAAGTGATTT GCTTCGCAAA ACATTTATTT TGATTAAGTC 400

45 (2) INFORMATION FOR SEQ ID NO: 3632:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 50 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3632:

TTCCACCATT TTTATAAGTC AAACGTTAAC ATGAAGTTAC GTTCTTTTAT AAAAAGATTT 120  
 AAACGCGTTA TTAATCTTGT GAGTGTTCCTT TCGAACACTA GCGATTATTT CTTATGAATT 180  
 5 CAAGCTTATT TAAAACTCTT TATTCACCTCG GTTTTGCTTG GTAAAATCTA TATnTTACTT 240  
 ACTTATCTAG TTTTCAATGT ACAAATAATG GTGGAGACTA GCGGGATCGA ACCGCTGACC 300  
 10 TCCTGGCGTG CAAAGCAGGC GCTCTCCCAG CTGAGCTAAn GCCCCCAnAT AGGTATTAAA 360  
 TTAATGGGGG GGCCTAAGTG GACTCGAACC ACCGACCTCA 400

## (2) INFORMATION FOR SEQ ID NO: 3633:

- 15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 20 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3633:

25 ATATGTCAAC GTTAATTCCA AAAAACGTAA CTATAAGTTA CAAACATTAT TTAGTATTTA 60  
 TGAGCTAATC AAACATCATA ATTTTTATGG AGAGTTTGAT CCTGGCTCAG GATGAACGCT 120  
 GCGGGCGTGC CTAATACATG CAAGTCGAGC GAACGGACGA GAAGCTTGCT TCTCTGATGT 180  
 30 TAGCGGCGGA CGGGTGAGTA ACACGTGGAT AACCTACCTA TAAGACTGGG ATAACTTCGG 240  
 GAAACCGGAG CTAATACCGG ATAATATTTT GAACCGCATG GTTCAAAAGT GAAAGACGGT 300  
 CTTGCTGTCA CTTATAGATG GATCCGCGCT GCATTAGCTA GTTGGTAAGG TAACGGCTTA 360  
 35 CCAAGGChAC GATGCATAGC CGACCTGAGA nGGTGATCGG 400

## (2) INFORMATION FOR SEQ ID NO: 3634:

- 40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 45 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3634:

50 TGAGCTAGGC CGGCAATATG TAAGAATAAA TGGTGGAGAA TGACGGGTTG GAACCGCCGA 60  
 CCCTCTGCTT GTAAGGCAGA TGCTCTCCCA GCTGAGCTAA TTCTCCGATT TAAAACTGCC 120  
 TGGCAACGTT CTA CTCTAGC GGAACGTAAG TTCGACTACC ATCGACGCTA AGGAGCTTAA 180  
 55 CTTCTGTGTT CGGCATGGGA ACAGGTGTGA CCTCCTTGCT ATAGTCACCA GACATATGAA 240

TATTTTGATT AAGTCTTCGA TCGATTAGTA TTGTCAGCT CCACATGTCA CCATGCTTCC 360  
 ACCTCGAACC TATTAACCTC ATCATCTTTG AGGGATCTTA 400

(2) INFORMATION FOR SEQ ID NO: 3635:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3635:

TTGTGACAAT CGCTTGCTTC TTTCCTCTCC TTCGGCTCTC GCTTACTCAT TTAGCTCTAC 60  
 TAAACTCGTT GCGCTCTTTT CTCGTTTCGT CAGATTCAAA CGTTTTCACT TCGCCAAGCC 120  
 ATTTTCTTT GTGTTTACTT TTTATTTTGA CGTTTGTAGAC ATAAAAAAAA GAGACCTTGC 180  
 GGTCTCAAAT GCGGCTCATC GCATCCATTT TTTGCCTGGC AACGTTCTAC TCTAGCGGAA 240  
 CGTAAGTTGG GCTACCATCG ACGTAAGAA CCTTTCTTGA CTTGTGACAA TCGCTTGCTT 300  
 CTTTCTCTT CTTCGGCTCT CGCTTACTCA TTTAGCTCTA CTAACTCGT TCGCTCTTT 360  
 TCTCGTTTCG TCAGATTCAA ACGTTTTCAC TTCGCCAAGC 400

(2) INFORMATION FOR SEQ ID NO: 3636:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3636:

TACTTATCTA GTTTTCAATG TACAATTTCT TTTAGTCAA GCGCTCGCAT ACTGATTTTC 60  
 AAAAAATCAA ATGCTCATTT ACAAAGTAA ACTCCGCTTT ATTTTCTTA ATGCATTGTC 120  
 TAACAACCGC TTTCTTTAAA AAGAATAGAT TGTCAAGCGC TCGCATAAGC AATATCACTT 180  
 TAACCAAAAA ATATTTGAAT GTTAAATAAA CATTCAAAAC TGAATACAAT ATGTCACGTT 240  
 ATTCCGCATC TTCTGAAGAA GATGTTCCGA ATATATCCTT AGAAAGGAGG TGATCCAGCC 300  
 GCACCTTnCG ATACGGCTAC CTTGTTACGA CTTACCCCA nTCATTTGTh CCACCTTCGA 360  
 CGGCTAGCTC CTAAAAGGTT ACTCCACCGG CTTCCGGGTGT 400

(2) INFORMATION FOR SEQ ID NO: 3637:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3637:

10 AGCGCTCGCA TAAGCAATAT CACTTTAACC AAAAAATATT TGAATGTTA AATAACATT 60  
 CAAAACTGnA ATACAATATG TCACATTATT CCGCATCTTC TGAAGAAGAT GTTCCGAATA 120  
 TATCCTTAGA AAGGAGGTGA TCCAGCCGCA CCTTCCGATA CGGCTACCTT GTTACGACTT 180  
 15 CACCCCAATC ATTTGTCCCA CCTTCGACGG CTAGCTCCTA AAAGGTTACT CCACCGGCTT 240  
 CGGGTGTTAC AAACTCTCGT GGTGTGACGG GCGGTGTGTA CAAGACCCGG GAACGTATTC 300  
 ACCGTAGCAT GCTGATCTAC GATTACTAGC GATTCCAGCT TCATGTAGTC GAGTTGCAGA 360  
 20 CTACAATCCG AACTGAGAAC CACTTATGGG ATTGCCTnAC 400

## (2) INFORMATION FOR SEQ ID NO: 3638:

- 25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3638:

35 TTCTCCGATT TAAAACTGCC TGGCAACGTT CTA CTCTAGC GGAAGTAAGT CGAnCTACCA 60  
 TCGACGCTAA GGAGCTTAAC TTCTGTGTTT GGCATGGGAA CAGGTGTGAC CTCCTTGCTA 120  
 TAGTCACCAG ACATATGAAT GTAATTTATA CATTCAAAC TAGATAGTAA GTAAAAGTGA 180  
 40 TTTTGCTTCG CAAAACATTT ATTTTGATTA AGTCTTCGAT CGATTAGTAT TCGTCAGCTC 240  
 CACATGTCAC CATGCTTCCA CCTCGAACCT ATTAACCTCA TCATCTTTGA GGGATCTTAT 300  
 AACCGAAGTT GGGGAAATCT CATCTTGAGG GGGGCTTCAT GCTTAGATGC TTTCAGCACT 360  
 45 TATCCCGTCC ACACATAGCT ACCCAGCTAT GCCGTTGGCA 400

## (2) INFORMATION FOR SEQ ID NO: 3639:

- 50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 551 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

55

ATGTCTCTAA CGCCTTTAAT AGTATTGAAC ACAATTGGGA AAAAAGCAGC GATAAAAATA 60  
 ATCGCAATCG CTGGCAAACT ACCAATACCA AACCATAGAA CAACAAATGG TGCCCATGCT 120  
 5 ATCGGAGATA TCGGCCTAAT CAATTGAAAT AGCGGTTCTGA TAGCGTTGTA TAGCCAACGA 180  
 TTCCTTCCAA GCAAGAAGCC CAATGGAATA GCAACCAACA ATGCGACAAC AAAGCCCGCT 240  
 ACAAATCTCC ATAAACTAAT TGCTAAATGT TGGAAAATTT CTCCAGTAAC AATGAAAGAC 300  
 10 CATATACTTT TTCCTACAAG AGCAGGACCC GGTAACAATA CAGGTTGGTA ATGCCCAATA 360  
 ATAaTGACCA TTTCCCAAaT GCCTAAGAAA aTAATAAATG TGATAATAGG TAATATAAAT 420  
 15 TTGTTATTTG TGGGACGTGT CATGAACGCG ATGCCTCCTT ATACAATGAC GGTTCACAA 480  
 AGTCATCCAT ATGCAGGTGG ATTAAACAAA TGATGTTGTT TTACCAngTC GTAATTTCTT 540  
 GATAGCCGGA T 551

20 (2) INFORMATION FOR SEQ ID NO: 3640:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 25 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3640:

CACTAAACTA AATTAATGAA GTGCCTTATG TATAAAAATT ATAAC TTGAT CCAACTTACA 60  
 CTACCAATAG AAAC TTCTGT TAGAATTCCT CAAATTGATA TTTCGCGATA TGTTAATGAA 120  
 35 ATTGTTGAAA CGATACCTGA TAGCGAATTC GATAAATTCA GACATCATCG TGGCGCAACA 180  
 TCCTATCATC CAAAATGAT GTTAAAAATC ACCTTATATG CATATACTCA ATCTGTATTT 240  
 TCTGGTCGTA GAATAGAGAA ATTACTTCAT GACAGTATTC GAATGATGTG GTTAGCTCAA 300  
 40 AATCAAACAC CTTCTTATAA AACTATTAAT CGTATTAGAG TGAATCCTAA TACTGATGCG 360  
 TTAATTGAAT CTTTATTTAT CCAGTTTCAT AGTCAATGTT 400

45 (2) INFORMATION FOR SEQ ID NO: 3641:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 398 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 50 (D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3641:

GATTGTCCTT TGGCAATGGT AGGAGAGCGT TCTAAGGGCG TTGAAGCATG ATCGTAAGGA 120  
 CATGTGGAGC GCTTAGAAGT GAGAATGCCG GTGTGAGTAG CGAAAGACGG GTGAGAATCC 180  
 5 CGTCCACCGA TTGACTAAGG TTTCCAGAGG AAGGCTCGTC CGCTCTGGGT TAGTCGGGTC 240  
 CTAAGCTGAG GCCGACAGnG TAGGCGATGG ATAACAGGTT GATATTCCTG TACCACCTAT 300  
 AATCGTTTTA ATCGATGGGG GGrCGCATAG GATAGCGGAA CGTTGCGATT GGATTGCACG 360  
 10 TCTAAGCAGT AAGGCTGGAG TATTAGGCAA ATCCGGTA 398

## (2) INFORMATION FOR SEQ ID NO: 3642:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 439 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3642:

TAATGTCTAC ACTTTGCTTG CGATCATTCA TTTTAAAGCC AGACTTTTTA TAATCTTGTA 60  
 25 CAAATGCTTG CGCTACATCC TTGTGTTGAT CAAGCAATTC CCCTCTCAGT ACTAGCACAC 120  
 AGCAATACGC ATCAGGtATA ACGTCATCAC CATGTTTCAA AGTCTTACCT TTGCCTAACT 180  
 TTTCACCCAG TGCACCGAAT GGTTCGGCTA CAGAATACCC TGTaATTCTG TGTTCACTCA 240  
 30 ATGCGGCTGG CATTTCTGCT GGCACATTT CATGATAGCT AAAATGCCCC GGTTTAATCT 300  
 TTAATTGTTT ACGTAATTCC TCAAGTAAAA GATAATGTGt TGAATAACgA TGTGGtATAC 360  
 CAAATGGka ATCATCGCCA TTAAtATTAA ATTCaTTTAA GTGCATACCT TTTTGTCCCA 420  
 35 TAATGACATT GCCTTCATG 439

## (2) INFORMATION FOR SEQ ID NO: 3643:

40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3643:

ATTTCTTATG AATTCAAGCT TATTTAAAC TCTTTATTCA CTCGGTTTGT CTTGGTAAAA 60  
 50 TCTATATTTT ACTTACTTAT CTAGTTTTCa ATGTACAAAT AATGGTGGAG ACTAGCGGGA 120  
 TCGAACCGTG ACCTCCTGCG TGCAAAGCAG GCGCTCTCCC AGCTGAGCTA AGCCCCCAA 180

55

GGTGCCTC TAACCAGCTG AGCTATAGGC CCATTAATTT GAATGAACAA ACATTCAAAA 300  
 CTGAATACAA TATGTCACGT TATTCCGCAT CTTCTGAAGA AGATGTTCCG AATATATCCT 360  
 5 TAGAAAGGAG GTGATCCAGC CGCACCTTnC GATACGGTTA 400

## (2) INFORMATION FOR SEQ ID NO: 3644:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3644:

GCGAACTGT ACGGAGCAAC GCCGCGTGAG TGATGAAGGT CTTGGGATCG TAAAACTCTG 60  
 20 TTATTAGGGA AGAACATATG TGTAAGTAAC TGTGCACATC TTGACGGTAC CTAATCAGAA 120  
 AGCCACGGCT AACaCGTGCC AGCAGCCGCG GTAATACGTA GGTGGCAAGC GTTATCCGGA 180  
 ATTATTGGGC GTAAAGCGCG CGTAGGnGTT TTTTAAGTCT GATGTGAAAG CCCACGGnTC 240  
 25 AACCGTGGAG GGTCAATTGGA AACTGGAAAA CTTGAGTGCA GAAGAGGAAA GTGGAATTCC 300  
 ATGTGTAGCG GTGAAATGCG CAGAGATATG GAGGAACACC AGTGGCGAAG GCGACTTTCT 360  
 GGTCTGTAAC TGACGCTGAT GTGCGAAACG TGGGGATCA 399

## (2) INFORMATION FOR SEQ ID NO: 3645:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3645:

TATTATACTT TACATTTCTC GTTTCGTCAG ATTCAAACGT TTTCACCTCG CCAAGCCATC 60  
 TTTCTTTGTG TTTGCTTTTA TTTTGACGTT TTAGACATAA AAAAAGAGAC CTTGCGGTCT 120  
 45 CAATGCGGCT CATCGCATCC ACTTTTTTGCC TGGCAACGTT CTACTCTAGC GGAACGTAAG 180  
 TnCGACTACC ATCGACGCTA AGGAGCTTAA CTTCTGTGTT CGGCATGGGA ACAGGTGTGA 240  
 CCTCCTTGCT ATAGTCACCA GACATATGAA TGTAAATnAT ACATTCAAAA CTAGATAGTA 300  
 50 AGTAAAAGTG GATTTTGCTT CGCAAACAT TTATTTTGGG TTAAGTCTTC GATCGGATTA 360  
 GTATTCGTCA GCTCCACATG TCACCATGGC TTCCACCTCG 400



## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 758 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3646:

AGATAAGTAA GTAAATATA GATTTTACCA AGCAAACCG AGTGAATAAA GAGTTTAAAA 60  
 TAAGCTTGAA TTCATAAATA ATCGCTAGTG TTCGAAAGAC ACGAnCAAGA TTAATAACGC 120  
 GTTTAAATCT TTTTATAAAA GAACGTAAC TCATGTTAAC GTTTGACTTA TAAAAATGGT 180  
 GGAAACATAG ATTAAGTTAT TAAGGGCGCA CGGTGGATGC CTTGGCACTA GAAGCCrATG 240  
 AAGGACGTTA CTAACGACGA TATGCTTTGG GGAGCTGTAA GTAAGCTTTG ATCCAGAGAT 300  
 TTCCGAATGG GGAAACCCAG CATGAGTTAT GTCATGTTAT CGATATGTGA ATACATAGCA 360  
 TATCAGAAGG CACACCCGGA GAACTGAAAC ATCTTAGTAC CCGGAGAAGA GAAAGAAAAT 420  
 TCGATTCCCT TAGTAGCGGC GAGCAnAACG GGAAGAGCCC AAACCAACAA GCTTGCTtGg 480  
 GGGTnTGTA GACACTCTAT ACGGATTACA AAGGACGACA TTAGACGAAT CATCTGGaAA 540  
 GATGAATCAA AGAAGGTAAT AATCCTGTAG TCGAAAATGT TGTCTCTCTT GAGTGGATCC 600  
 TGaGTACGAC GGAGCACGTG AAATTCCGTC GGAATCTGGG GAGGaCCATC TCCTAAGGCT 660  
 AAATACTCTC TAGTGACCGA TAGTGGAACC aGTaCCGTGA GGGAAAGGTg AAAAGCACCC 720  
 gGAAGnAGT TGAAATaGAA ctGGAAACCG TGTGCTTA 758

## (2) INFORMATION FOR SEQ ID NO: 3647:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3647:

ACAAACTCCG AATGCCAATT AATTTAACTT GGGAGTCAGA ACATGGGTGA TAAGGTCCGT 60  
 GTTCGAAAGG GAAACAGCCC AGACCACCAG CTAAGGTCCC AAAATATATG TTAAGTGGAA 120  
 AAGGATGTGG CGTTGCCCAG ACAACTAGGA TGTTGGCTTA GAAGCAGCCA TCATTTAAAG 180  
 AGTGCGTAAT AGCTCACTAG TCGAGTGACA CTGCGCCGAA AATGTACCGG GGCTAAACAT 240  
 ATTACCGAAG CTGTGGATTG TCCTTTGGnA TGGGTAAGGA GAGCGTTCTA AGGGCGTTGA 300

AAGACGGGTG AGAATCCCGT CCACCGATTG ACTAAAGGTT

400

## (2) INFORMATION FOR SEQ ID NO: 3648:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 521 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3648:

GTCATTGGAA ACTGGAAAAC TTGAGTGCAG AAGAGGAAAG TGAATTCCA TGTGTAGCGG 60  
 TGAAATGCCG AGAGATATGG AGGAACACCA GTGGnCGAAG GCGACTTTCT GGTCTGTAAC 120  
 TGACGCTGAT GTGCGAAACG TGGGGATCAA ACAGGATTAG ATACCCTGGT AGTCCACGCC 180  
 GTAAACGATG AGTGCTAAGT GTTAGGGGGT TTCCGCCCTT TAGTGCTGCA GCTAACGCAT 240  
 TAAGCACTCC GCCTGGGGGAG TACGACCGCA AnGTTGAAAC TCAAAGGAAT TGACGGGGGAC 300  
 CCGCACAAAGC GgTGGaGcAT GTGGTTTAAT TCGAAGCAAC GCGAAGAACC TTACCAAATC 360  
 TTGACATCCT TTGACAACTC TAGAGATAGA GCcTTCCCCT TCGGGGGACA AAGTGACAAG 420  
 TGGTGCATGG TGTCGTCAAC TCCTGTCTGT GAGATGTTGG GGTAAnTCCC CGCAAnGAGC 480  
 GCACCCTTAA GCCTTAGTTT nCATCATTAA GTTGGGCACT C 521

## (2) INFORMATION FOR SEQ ID NO: 3649:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3649:

CCAAAGTTCA TCTTTTACGA ATGAGAAATA GGTGTTGCAT ATTCAATGGT CTCATCTTGT 60  
 TTATAAAAGC CACCATCTAA ATCACTAATC CATTGTGGTA AGTCTCCAAG TTCGTCTTCC 120  
 ATACGTGTTT TAACACGTTT GTATCCCATT GCATCCCATA ATTGGAATGG ACCAAGTTTC 180  
 CAGTTGAACC CCCAGACAAG CGCACGGTCT ATGTCTCGGA AATCATCGGT AGCTTTAGGT 240  
 ACATTGATAG CAGAGTAATA GAAATTATTA CGTAATGTCT CCCATAAAAA TAGTCCCGCT 300  
 TCGTCTTGcG CATTGAATAT GGTATCAaG TTATGCACTA aGTCTTTATT AAATTCATTT 360  
 AAAATTGGTA ATTGTGGTTG CGATACAGGT ACATAATCTT 400

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3650:

GCATAATAA AAAATAATGG CGGAGGAAGA GGGATTGAA CCCCCGCGGn CCGTTAAGGC 60  
 CCTGTCGGTT TTCAAGACCG ATCCCTTCAG CCGGACTTGG GTATTCCTCC ATTATTATAG 120  
 GTAAATCGCT ATTAATTATA AAATTAAATG GCGGTCTCGA CGGGAATCGA ACCCGCGATC 180  
 TCCTGCGTGA CAGGCAGGCG TGTTAACCGC TACTACTACGA GACCATTAGT AAAACGGAGG 240  
 AAGAGGGATT CGAACCCCCG CGAGCCGTTA AGCCCCGTGC GGTTTTCAAG ACCGATCCCT 300  
 TCAGCCGGAC TTGGGTATTC CTCCAAAT ATATGGACCT TGCAGGACTC GAACCTGCGA 360  
 CCGAACGGTT ATGGAGCCGT TAGCTCTAAn CAACTTGAGC 400

(2) INFORMATION FOR SEQ ID NO: 3651:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3651:

TGGCGCTGTG CTTTAGTAAA ACTATGGTCA TGTTGCGCTA AATGCAACCA TGCATGGTAA 60  
 AAACTTTGCT CACGCTTCGG CATTGTCCAA CTCGATAGAA ATTGATCGAT ATAAAGTTTC 120  
 GTCCATTTAA TCATTTGACG ATTCACTTGT TCGCTAAGTG GCTCACCTTG TTCATCTATT 180  
 ATTGCATCAC TCATCGGACG TACATCATAG TGATGATATG ATTCAGCCAT ATCACGTTTT 240  
 GATTTTTCTA ATAGTAGATC AGCAACAACA TCAACATTG AATGATTCAT ATATGATGGC 300  
 AGGTACGTCT TTTAATGTTT TAATGTTATC AATATAAAGA TGATGTAGTG TTGCGGGATA 360  
 TGTAGTGAnG TTCAAGTAAC ATATCAGTAA CAAGTTGATT 400

(2) INFORMATION FOR SEQ ID NO: 3652:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3652:

CATTGTCCAA AGGACAATCC ACAGCTTCGG TAATATGTTT AGCCCCGGTA CATTTTCGGC 60  
 5 GCAGTGTAC TCGACTAGTG AGCTATTACG CACTCTTTAA ATGATGGCTG CTTCTAAGCC 120  
 AACATCCTAG TTGTCTGGGC AACGCCACAT CCTTTTCCAC TTAACATATA TTTTGGGACC 180  
 TTAGCTGGTG GTCTGGGCTG TTTCCCTTTC GAACACGGAC CTTATCACCC ATGTTCTGAC 240  
 10 TCCCAAGTTA AATTAATTGG CATTTCGGAGT TTGTCTGAAT TCGGTAACCC GAGAGGGGCC 300  
 CCTCGTCCAA ACAGTGCTCT ACCTCCAATA ATCATCACTT GAGGGCTAGC CCTAAAGCTA 360  
 ATTTTCGGAGA GAACCAGCTA TCTCCAGGTT CGATGGAATT 400

## (2) INFORMATION FOR SEQ ID NO: 3653:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3653:

GGTTCGGTCC TCCATTCAGT GTTACCTGAA CTTCAACCTG ACCAAGGGTA GATCACCTGG 60  
 TTTCGGGTCT ACGACCAAAT ACTAAACGCC CTATTCAGAC TCGCTTTCGC TACGGCTCCA 120  
 30 CATTTACTGC TTAACCTTGC ATCAAATCGT AACTCGnCGG TTCATTCTAC AAAAGGCACG 180  
 CCATCACCCA TTAACGGGCT CTGACTACTT GTAAGCACAC GGTTCAGGT TCTATTTTAC 240  
 TCCCCTTCCG GGGTGCTTTT CACCTTTCCC TCACGGTACT GGTTCACTAT CGGTCACTAG 300  
 35 AGAGTATTTA GCCTTAGGAG ATGGTCCTCC CAGATTCCGA CGGAATTTCA CGTGCTCCGT 360  
 CGTACTCAAG NATCCACTCA AGAGAGACAA CATTTTCGAC 400

## (2) INFORMATION FOR SEQ ID NO: 3654:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3654:

AAAGGTCCTA AATATAATTT TACAACTAAT AAATAGTGGC GGTGGAGGGG ATCGAACCCC 60  
 CGACCTCAGG GGTATGAACC GTACGCTCTA GCCAGCTGAG CTACACCGCC TTATATAGTT 120

GCGCTCTCCC AGCTGAGCTA AGCCCCCATA ATAATTACAG TATATCGGGA AGACAGGATT 240  
 CGAACCTGCG ACCCCTTGGT CCCAAACCAA GTGCTCTACC AAGCTGAGCT ACTTCCCCTA 300  
 5 TAATTAACGC GCCCGATAGG AGTCGAACCC ATAACCTCTT GATCCGTAGT CAAACGnTCT 360  
 ATCCAATTGA GCTACGGGCG CATATGTTTT TATTGAAAAT 400

(2) INFORMATION FOR SEQ ID NO: 3655:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3655:

20 TATTGAAGCC TGAGTCAACA CGTACGCAAA TCGATCAAAT CATCGATGAA GCGAAACATA 60  
 CAATTTTAAA TCTGTATGTG TGAATCCAAC ACATGTTAAA TATGCAGCAG AGCnnCTAGC 120  
 TGATTCAGAG GTGCTCGTTT GTACGGTAAT AGGATTCCCA TTAGGTGCGT CGACAACTGC 180  
 25 AACGAAAGCA TTTGAAACAG AAGATGCAAT TCAAAATGGT GCAGATGAAA TTGACATGGT 240  
 CATCAACATC GGCGCATTAA AAGATGGACG TTTTGATGAT GTACAACAAG ACATTGAAGC 300  
 AGTGGTTAAA GCTGCGAAAG GTCACACAGT AAAAGTGGAT TATTGAGACG GTATTGTTGG 360  
 30 GACCATGACG AAATTGTAAG AGCGAGTGGG ATTAACCAAA 400

(2) INFORMATION FOR SEQ ID NO: 3656:

- (i) SEQUENCE CHARACTERISTICS:  
 35 (A) LENGTH: 530 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3656:

GATGAGTCGC TGnCTGATCT GAACGCTGTC TGAGnCCGAA CGCTACTGAA CTGAGTCGCT 60  
 45 GTCTGAGTCT GAATCGCTAT CTGAATCTGA GTCGCTATCT GAGTCTGAGT CGCTGTCTGA 120  
 GTCTGAGTCG CTGTCTGAGT CTGAATCGCT ATCTGAATCT GAGTCGCTGT CTGAGTCTGA 180  
 GTCGCTATCT GAGTCTGAGT CGCTGTCTGA ATCTGAGTCG CTGTCTGAAT CTGAATCGCT 240  
 50 GTCTGAGTCT GAATCGCTAT CTGAGTCTGA ATCGCTATCT GAGTCTGAAT CACTGTCTGA 300  
 GTCCGAGTCA CTGTCTGAAT CTGACTCACT ATCTGATTCT GAGTCGCTAT CTGATTCTGA 360

ATCTGAACCT GAGTCGCTGT CTGAGCCTGA AGTCACTGGT CTGAATCCGA ATCCGGATCC 480  
GGGTCTGGGG CTTGGGTTCC GGTTCCTGGGT CTGGGACTTG GGTTCCTGGGA 530

(2) INFORMATION FOR SEQ ID NO: 3657:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3657:

GTTTTAACTA CGCAAGACAT CGAAGAAGCT GACGGTGTCA TAATTGCAGC TGATAAACAA 60  
GTTGATCTGT CCCGATTTGT TGGTAAACGG TTGATTAATG AAAATGTTTCG CGAAGGGATT 120  
CATAATCCGA GAGGTCTAAT TCAACGTATC ATTAATCAAG ATGCGCCTAT TTATCAATCT 180  
GAAACAAATT ATCATTGCGAA AGATCGCGGT AAGTCTAAAA ATGGTATTCA AATGGTGTAT 240  
CAACATTTAA TGAACGGTGT ATCGTTTATG GTTCCTTTTA TCGTAGTTGG TGGACTCCTT 300  
ATCGCCATCG CGCTGGACTC TAGGCGGTGA ACGACATCAA AAGGATTAGT CATCCCAGAT 360  
GGATTCATTT TGGGAAATCC ATTGGAAAAC ATTGGGTAGT 400

(2) INFORMATION FOR SEQ ID NO: 3658:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 668 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3658:

GAAGAAGTTT ATGAAACGGT TATGAATAAG CCATACACTA GATATCCAGT GTACGAGGGA 60  
GATATTGATA ACATTATTGG GGTGTTTCAT TCTAAATATC TGTGGGCTTG GAGTAATAAA 120  
AAAGAAAATC AAATTACAAA CTATTCAGCT AAGCCATTAT TTGTGAATGA ACACAATAAA 180  
GCTGAATGGG TATTACGTAA GATGACTATT TCTAGAAAAC ATTTAGCAAT TGTGTTGGAC 240  
GAATTTGGTG GTACTGAAGC GATAGTGTCA CATGAAGACT TAATTGAAGA ATTATTAGGT 300  
ATGGaAATTG AAGATGAGAT GGaTAAAAAG GAAAAGAAA AACTTTCTCA ACAGCAAATT 360  
CmATTTCAAC AACGGAAAAA TCGCmACGTA TCTATATAAG GnGCGAACAG CTATGTGCTA 420  
ATAAGAATCG ACTTACTCAA ATGTTAAGTA TTGAATATCC AATTATACAA GCAGGTATGG 480

TAGGCGCGGT TACTTTAATA CGCAGCAATT GGAAGATGAA ATAGATTATG GTACGCCAAT 600  
 TAACGTCAAA TTCTTTTGGC GTAAATGTCT TTGGTACCAA GTCAACAATC ATATACCAGT 660  
 5 AGTCAAAT 668

(2) INFORMATION FOR SEQ ID NO: 3659:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3659:

AAAAGAATGG TAAGTTGAAT AAAGTATTGA AATCAATTGC CAATATCTTT ATACCGTTGA 60  
 20 TTCCTGnATT TATTGGAGCT GGATTAATTG GTGGTATTGC AGCAGTACTG AGTAACTTAA 120  
 TGGTGGCAGG CTATATTTCa GGTGCTTGGa TTACGCCAACT TATAACAGTA TTTAATGTCA 180  
 TTAAAGACGG TATGTTAGCA TACTTAGCTA TTTTCACTGG TATTAATGCG GCTAAAGAAT 240  
 25 TTGGTGCGAC ACCAGGACTT GGTGGCGTGA TTGGTGGTAC AACGTTATTA ACGGGTATTG 300  
 CTGGTAAAAA TATTTTAATG AATGTCTTCA CTGGAGAACC ATTGCAACCT GGACAaNGTG 360  
 GGATTATTGG CGTTATTTTG CCGTTTGGAA TTTAAGTAAT 400

(2) INFORMATION FOR SEQ ID NO: 3660:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3660:

CTGAGCTAAT GGCTCTTCCA TGGTGCCGGC CAGAGGACTT GAACCCCAAA CCTACTGATT 60  
 ACAAGTCAGT TGCTCTACCA ATTGAGCTAG GCCGGCAATA TGTAAGAATA AATGGTGGAG 120  
 45 AATGACGGGT TCGAACCGCC GACCCTCTGC TTGTAAGGCA GATGCTCTCC CAGCTGAGCT 180  
 AATTCTCCGA TTTAAACTG CCTGGCAACG TTCTACTCTA GCGGAACGTA AGTTCGGACT 240  
 ACCATCGACG CTAAGGAGCT TAACTTCTGT GTTCGGCATG GGAACAGGTG TGACCTCCTT 300  
 50 GCTATAGTCA CCAGACATAT GAATGTAATT TATACATTCA AACTAGATA GTAAGTAAAA 360  
 GTGATTTTgT TTTGCAAAA CATTATTTT GGATTAAGTC 400

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3661:

10 TGATGTTTGA TTAGCTCATA AATACTAAAT AATGTTTGTA ACTTATAGTT ACGTTTTTTG 60  
 GAATTAACGT TGACATATTG TCATTCAGTT TTCAATGTTT ATTTTTCTTA CCGACAAGAA 120  
 TTAATTATAC ATTTTATTAA CATTTAAGTC AATAACTTTT TTTATCTTGT CCATTTTATT 180  
 15 TTTTAACCAA AATTTGATTA AAAAAGTGGC TGGCAACGTT CTACTCTAGC GGAACGTAAG 240  
 TTCGACTACC ATCGACGCTA AGGAGCTTAA CTTCTGTGTT CGGCATGGGA ACAGGTGTGA 300  
 CCTCCTTGCT ATAGTCACCA GACATATGAA TGTAATTTAT ACATTCAAAA CTAGATAGTA 360  
 20 AGTAAAAGTG ATTTTGCTTC GCAAACATTT ATTTTGATTA 400

## (2) INFORMATION FOR SEQ ID NO: 3662:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 742 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3662:

CGCTCAACGT CTGCCTTCGT AATGGCTTTT GTAGAAATTC TAACTAAATA ATTTGGAATG 60  
 35 CTATCATTGA TTGTTTCAAC AGCTTGATGC TTTTGTTCAA GCTTTTTGAT CAATTTTTTA 120  
 TCGTCTTTTG TAATTTTCGG AATGTCTTCA AACATTGATA AGACAATCTG ACCCACATTT 180  
 TGTAATTCTT TTTGAGTTTC TTGTAATGCA ACACCAGGTG CGTGATAAAC AAGATCTTTG 240  
 40 TTTAAGTGCT GAGGTTTATA GTCATCAGCA ATATCTTTAC CTGGGACAAG CTTTGTAACA 300  
 ATCCATGCTA AACCTGCTAC AAATGGTAAT TGAATCAAAG TATTTGTTAT GTTGAAGATA 360  
 CCATGTGATA CTGCAATCGT CATCGCTGGT TTTAAGTGCC ATAAATCTTG TAACAAACTA 420  
 ATCAAATGAA TCACAACTGG CAAGAAAATT GTGAAGATAA TTACCCCGAT TAAGTTAAAG 480  
 ATGACGTGTA CAAGCGCCGC ACGTTTTGCA GCGATTGAGC CGGCTAAACT AGCTAAGATA 540  
 50 GCTGTAATCG TGGTACCAAT GTTATCGCCT AGTAACACAG GGATKGTGC GTTTAAGCTA 600  
 ATTAAATCTT GTTGATAAAA TTCTTGTAAG ATACCAATCG TCGCACTTGA ACTTTGAACT 660



AGCATTAAAT TGGCTTnAAA TC

742

## (2) INFORMATION FOR SEQ ID NO: 3663:

- 5 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear
- 10

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3663:

15 ATGAATTCAA GCTTATTTAA AACTCTTTAT TCACTCGGTT TTGCTTGGTA AAATCTATAT 60  
 TTTACTTACT TATCTAGTTT TCAATGTACA ATTTCTTTTT AGTCAAGCGC TCGCATACTG 120  
 CTTTATTTTC AAAAAATCAA ATGCTCATT TACAAAAGTAA ACTCCGCTTT AATTTTTCTT 180  
 20 AATGCATTGT CTAACAACCG CTTTCTTTAA AAAGAATAGA TTGTCAAGCG CTCGCATAAG 240  
 CAATATCACT TTAACCAAAA AATATTTGAA TGTTAAATAA ACATTCaAA CTGAATACAA 300  
 TATGTCACGT nATTCCGCAT CTTCTGAAGA AGATGTTCCG AATATATCCT TAGAAAGGAG 360  
 25 GTGATCCAGC CGCACCTTCC GATACGGGCT ACCTnGTnAC 400

## (2) INFORMATION FOR SEQ ID NO: 3664:

- 30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 636 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear
- 35

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3664:

AACTAATAGT TCACTTTTAC TTTTCTTTT TTCAATTATTA TCCATTATTT TTTCACCGCC 60  
 40 AAAACGAATT TCATGATGTT AATTAAATG TTCTATGACA AAATTAAGCA ACGATGTTtT 120  
 ATATTTATTT CCAACTATGT CTAGATTAAA TTTCTAAAAA TAKACATCAT TTAAAAGGAG 180  
 CTTGGGACAT AAATCAATGT CCTAGGGTCT ATAATATTAT AktGCTAGTA GTTGACTGAA 240  
 45 TGAAATGCG CTTGCAACAA GCTTTTTTCA ACTCTAGTCA GGGGCCCAAA CACAGAGAAT 300  
 TTCGAAAAGA AATTCTACAG GCAATGCGAG TTGGGGTGTG GGCCCAACA CAGAGAATTT 360  
 CGAAAAGAAA TTCTACAGGC AATGCGAGTT GGGGTGTGGG CCCCAACACA GAGAATTTCTG 420  
 50 AAAAGAAATt CTACAGGCAA TGCGAGTTGG GGTGTGGGCC CCAACATAGA GAAATGGaTT 480  
 CCCaattTCT ACAGACAATG CAAGTTGGCG GGGCCCCAAC ACAGAAGCTG ACGAAAAGTC 540

55

TACAATAATG nGCAAGTTGG CGGGGnCCCC AACACA

636

(2) INFORMATION FOR SEQ ID NO: 3665:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 404 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3665:

TATCATTTCC	TGTTGCTAAA	ACAACAGCAT	GTATGCCATT	CATAACACCT	TTATTATGTG	60
TTGCTGCACG	ATGAATATCT	ACTTGGGCCA	ATACAGAAGC	ACGTTCCATT	CGTTTGGCAA	120
CCTCTTCTCC	AGTTCTCTCG	CCCCTTGCTA	AATCTTTAAC	ATCAATTTCTG	CCTTGAACCT	180
TAACAACGGA	CGCTGTTGCA	TGATTGGATA	AAATACTCAT	TAAAATGTCG	CTTTGGGAAA	240
CTCATTTTTT	AAAAATGCAG	TTATGGCCTC	TAAAATCGTA	TTAAGCATAT	TAGCGCCCAT	300
AGCATCTTTC	GTATCAACAA	ATACTTTTAA	AGATAGTAAC	TGtTGctCAG	GrAATGTaKc	360
matCGCTATA	CGtTGGTAAC	CACCACCACG	CGCTTTAATA	GGAA		404

(2) INFORMATION FOR SEQ ID NO: 3666:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3666:

GTGGTTCCAG	TAGCAATTAT	TGAACGATAT	TAGGCTATCT	AGTCGGCATA	TTTGTA AAAAC	60
AAGATCCAAT	TAAATATCAA	CAGGAATAAC	GAATAATATA	AAAGAGGTTG	GGACATAAAT	120
CCCTAAAAAA	ACAGCAGTAA	GATAATTTTC	AATTAGAAAA	TATCTTACTG	CTGTTCTCTA	180
TTTATACAAT	ACTTCGTATT	GAATGGCTTC	GCTTTCCTAG	GGTGCCGTCT	CAGCCTCGGT	240
CTTCGACTGG	CACTGCTCCC	TCAGGAGTCT	CGCCATTAAT	ACTACGTATT	AACGTGTAAT	300
TTTACTTTGA	AATACTTTAA	AAAAATAAGA	CACTTTGCCC	AACCTGCACA	TAAATGTAAA	360
ATTCAATAAA	ATAAATTTCT	GTGTTGGATC	CCTnCGTATA			400

(2) INFORMATION FOR SEQ ID NO: 3667:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3667:

	CCAACAAATC TGTCTGTGCG ATCGCCTTTG TCGTTCCAAA TAAATATGTA CAAACGAATC	60
10	CACCAGCATA CGCnCCAAGT AATCCTGCAA TATAACCTAA ATACATATTA TCTGAGATTA	120
	ATGGTAATAG TGACACACCA CTTGGGCCTA TTGCTTTGGC ACCAATATGT CCAATTCCAC	180
	CTATTACAGC GCCACCAATA CCACCACCAA TACAAGCAGT TAAGAAAGGT CGACCTAATG	240
15	GCAAAGTCAC ACCATAGATT AATGGTTCTC CGATACCTAG GGAAACCAAC TGGCAATGCA	300
	CCTTTTAAAG TATTACGTAA TGTGTGTTG CGGTTTACAT CTTACCCAAA GTGCTAATGC	360
20	GGGCACCTAC TTGGTCCCAG CACCAGCCAT CGCTGCAATT	400

(2) INFORMATION FOR SEQ ID NO: 3668:

(i) SEQUENCE CHARACTERISTICS:

25

(A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3668:

	ACTAAGATGT TTCAGTTCTC CGGGTGTGCC TTCTGATATG CTATGTATTC ACATATCGAT	60
	AACATGACAT AACTCATGAC TGGGTTTCCC CATTGCGAAA TCTCTGGATC AAAGCTTACT	120
35	TACAGCTCCC CAAAGCATAT CGTCGTTAGT AACGTCCTTC ATCGGCTTCT AGTGCCAAGG	180
	CATCCACCGT GCGCCCTTAA TAACTTAATC TATGTTTCCA TCCTACAGGA AACGCGTTAT	240
40	TAATCTTGTG AGTGTTCTTT CGAACACTAG CGATTATTTT TTATGAATTC AAGCTTATTT	300
	AAAACCTCTT ATTCACTCGG TTTTGCTTGG TAAAATCTAT ATTTTACTTA CTTATCTAGT	360
	TTTCAATGTA CAATTTCTTT TTAGTCAAGC GCTCGCATAA	400

45

(2) INFORMATION FOR SEQ ID NO: 3669:

(i) SEQUENCE CHARACTERISTICS:

50

(A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3669:

5 GAGCGCTACT TACTGGnAGG CGCTGGTGGG ATACTACCCT AGCTGTGTTG GCTTTCTAAC 120  
 CCGCACCCT TATCGTGGTG GGAGACAGTG TCAGGCGGGC AGTTTGACTG GGGCGGTGCG 180  
 CTCCTAAAAG GTAACGGAGG CGCTCAAAGG TTCCCTCAGA ATGGTTGGAA ATCATTCTATA 240  
 GAGTGTAAG GCATAAGGGA GCTTGACTGC GAGACCTACA AGTCGAGCAN GGTGAAAGA 300  
 10 CGGACTTAGT GATCCGGTGG TTCCGCATGG AAGGGCCATC GCTCAACGGA TAAAAGCTAC 360  
 CCCGGGGGAT AACAGGCTTA TCTCCCCCAA GAGTTCACAT 400

## (2) INFORMATION FOR SEQ ID NO: 3670:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3670:

25 ATACTTTACA TTTCTCGTTT CGTCAGATTC AAACGTTTTT ACTTCGCCAA GCCATCTTTC 60  
 TTTGTGTTTG CTTTTATTTT GACGTTTTAG ACATAAAAAA AGAGACCTTG CGGTCTCAAT 120  
 GCGGCTCATC GCATCCACTT TTTGCCTGGC AACGTTCTAC TCTAGCGGAA CGTAAGTTTG 180  
 30 ACTACCATCG ACGCTAAGGA GCTTAACTTC TGTGTTCCGC ATGGGAACAG GTGTGACCTC 240  
 CTTGCTATAG TCACCAGACA TATGAATGTA AATTATACAT TCAAACTAG ATAGTAAGTA 300  
 AAAGTGATTT TGCTTCGCAA AACATTTATT TTGATTAGT CTTCCGATCG ATTAGTATTC 360  
 35 CGTCAGTCC ACATGTCACC ATGCTTCCAC CTCGAACTT 400

## (2) INFORMATION FOR SEQ ID NO: 3671:

40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3671:

50 CACCCGAAGA TATTGCTCAG ACAAAGTCAT CATATACAGG AAAGTATTTA AAAGAAGTAC 60  
 TTGAACGAGA TAAACAAAAT ACTGAAGATA AATAAGATTA AAAGAAGTGA AGGATGTTAT 120  
 AAATTTATCC TTCGCTTCTT TTTATTAATT TAGTAATGAA TAGTAGAAAG AAAAGATGCG 180  
 TAAAAAGAAT TATGTTAAGA TAGGGTCAAT CTAGAGTAGT TAAACATAAA TCGAACTGGG 240

55

TTAGCCACAG CTATTGTGTA CTTAAAAATA GGAATGCATG AGTGCACCA nAGGnAGAAT 360  
 ACTAATTTCC AAAGAAAAAG TATTCCTTAT GTTGGGGCCC 400

(2) INFORMATION FOR SEQ ID NO: 3672:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 461 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3672:

TGGACCTGTA AAAGGAGACT CGATTGTAGA AAAAGAAGAG ATTCCATTCT AGAAAGAACG 60  
 TAAATTTAAT cCTGATTAG CmCCaGGGAC aGAAAAAGTA mCmAGaGAAG GACaAAAAGG 120  
 TGAGAAGACA ATaACGACAC CAACACTAAA AAATCCATTA ACTGGAGTAA TTATTAGTAA 180  
 AGGTGAACCA AAAGAAGAAA TCACAAAAGA TCCGATTAAT GAATTAACAG AATACGGACC 240  
 AGAAACGATA ACACCAGGTC ATCGAGACGA ATTTGATCCG AAGTTACCAA CAGGAGAGAA 300  
 AGAAGAAGTT CCAGGTAAAC CAGGAATTAA GAATCCAGAA ACAGGAGACG TaGTTAGACC 360  
 ACCGGTCGAT AGCGTAACAA AATATGGACC TGTAAGGA GACTCGATTG TAGAAAAAGA 420  
 AGAGATTCCA TTCAAAACGT AAATTTAATC CGGATTTAGC A 461

(2) INFORMATION FOR SEQ ID NO: 3673:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3673:

CTTATGAATT CAAGCTTATT TAAAACTCTT TATTCACCTG GTTTTGCTTG GTAAAAATCTA 60  
 TATTTTACTT ACTTATCTAG TTTTCAATGT ACAAATAATG GTGGAGACTA GCGGGATCGA 120  
 ACCGCTGACC TCCTGCGTGC AAAGCAGGCG CTCTCCAGC TGAGCTAAGC CCCCAnAG 180  
 GTATTAAATT AATGGGGGGC CTAAGTGGAC TCGAACCACC GACCTCACGC TTATCAGGCG 240  
 TGCCTCTAA CCAGCTGAGC TATAGGCCCA TTAATTTGAA TGAACAAACA TTCAAACTG 300  
 AATACAATAT GTCACGTTAT TCCGCATCTT CnGAAGAAGA TGTTCCGAAT ATATCCTTAG 360  
 AAAGGAGGTG ATCCAGCCGC ACCTTCCGAn ACGGCTACCT 400

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3674:

ACATGAAGAC TTAATTGAAG AATTATTAGG TATGGAAATT GAAGATGAGA TGGATAAAAA 60  
 GGAAAAAGAA AAACCTTCTC AACAGCAAAT TCAATTTCAA CAACGGAAAA ATCGCAACGT 120  
 ATCTATATAA GGAGCGAACA GCTATGTGGG AATAAGAATC GACTTACTCA AATGTTAAGT 180  
 ATTGAATATC CAATTATACA AGCAGGTATG GCAGGAAGTA CGACACCGAA ATTAGTTGCA 240  
 TCAGTAAGTA AACAGTGGTG GGTAGGCAC AATAGGCGCG GTTACTTTAA TACGCGCCAA 300  
 TTGGANGATG GANATnGATT ATGTACGCCA TTAACGTCAA ATTCTTTTGG CGTAAATGTC 360  
 TTTGTACCAA GTCAACAATC ATATACCACT AGTCCAAATT 400

## (2) INFORMATION FOR SEQ ID NO: 3675:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3675:

AGCTAGGCCG GCAATATGTA AGAATAAATG GTGGAGAATG ACGGGTTCGA ACCGCCGACC 60  
 CTCTGCTTGT AAGGCAGATG CTCTCCCAGC TGAGCTAATT CTCCGATTTA AAACCTGCCTG 120  
 GCAACGTTCT ACTCTAGCGG AACGTAAGTT CGACTACCAT CGACGCTAAG GAGCTTAACT 180  
 TCTGTGTTTC GCATGGGAAC AGGTGTGACC TCCTTGCTAT AGTCACCAGA CATATGAATG 240  
 TAATTTATAC ATTCAAACT AGATAGTAAG TAAAAGTGAT TTTGCTTCGC AAAACATTTA 300  
 TTTTGATTAA GTCCTCGTCG TTAGTATTCG TCAGCTCCAC ATGTCACCAT GCTTCCACCT 360  
 CGGACCTATT AACCTCATCA ACCTTGAGGG nTCTTATAAA 400

## (2) INFORMATION FOR SEQ ID NO: 3676:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3676:

5 TGGACAATGG TAGGAGAGCG TTCTAAGGGC GTTGAAGCAT GATCGTAAGG ACATGTGGAG 60  
 CGCTTAGAAG TGAGAATGCC GGTGTGAGTA GCGAAAGACG GGTGAGAATC CCGTCCACCG 120  
 ATTGACTAAG TTTCCAGAGG AAGGCTCGTC CGCTCTGGGT TAGTCGGGTC CTAAGCTGAG 180  
 10 GCGACAGCG TAGGCGATGG ATAACAGTTG ATATTCCTGT ACCACCTATA ATCGTTTTAA 240  
 TCGATGGGGG GACGCATAGG ATAnGCGAAn GTGCGATTGG ATTGCACGTC TAAGCAGTAA 300  
 GGCTGAGTAT TAGGCAAATC CGGTACTCGT TAAGGCTGAG CTGTGATnGG GAGAAGACAT 360  
 15 TGAGTCTTCG AGTCGTTGAT TTCACACTGC CGAGAAAAGC 400

## (2) INFORMATION FOR SEQ ID NO: 3677:

## (i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3677:

25 AAAGCGCCAC ATGGTGCCAA GTCTGGAGTT AATCCAGCAA TTGCTTGTTT TAAGCTATTA 60  
 TATTTTTCTT CTACTTTTGT TTTTCTGCG GCAATTTGTT GGTCAGTCGC ATCACCATTG 120  
 30 TTAATAACAT TTTGTGCATT TGTTGATTCT GTTTGACCCG CACGTTTAGC ATTTTCATAT 180  
 GCTTGGATTG ATGATTGTGT CATACCATCA GTAGTTACTG ATTTATTGAT TTCTTCATCA 240  
 35 AGTTTCGTCT TAGCAGTTTT TAAAGCACTA TTATCAGCTA AAGGTACTAA TTGGATTAAT 300  
 TGCTTGCATT AATCGCTCAT TGACACGATT TACATTTGTT AACGCAGATT GCACTTCTTG 360  
 TACTGTTCTT AATGGGCTTT TGAATAATA GCATTAGCGC 400

## (2) INFORMATION FOR SEQ ID NO: 3678:

## (i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 648 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3678:

50 ACAGTCAATT GnTCTACCAA TTGAGCTAGG CCGGTTAAGA AATGGTTCCA GGACAGAGTC 60  
 GAATGCCGAC ACATGGAGCT TCAATCCATT GCTCTAACCA ACTGAGCTAC TGAACCATAA 120

AGGCGTGTTA ACCGCTACAC TACGAGACCT ATAAATATT GCGGGAGGCG GATTTGAACC 240  
 ACCGTA CTTC GGGTTATGAG CCCGACGAGC TACCGAACTG CTCCATCCCG CGATAATAAA 300  
 5 AAATAATGGC GGAGGAAGAG GGATTCTGAAC CCCC CGGCC CGTTAAGGCC tGTCGGTTTT 360  
 CAAGACCGAT CCCTTCAGCC GGACTTGGGT ATTCTCCAT TATTATAGGT AAATCGCTAT 420  
 10 TAATTATAAA ATTAAATGGC GGTCTCGACG GGAATCGAAC CCGCGATCTC tGCGTGACAG 480  
 GCAGGCGTGT TAAyCGCTAC ACTACGAGAC CATTAGTAAA ACGGAGGAAG AGGGATTCTGA 540  
 ACCCCCGCGA GCGGTTAAGC CCCTGTGGT TTTCAAGACC GATCCCTTCA GCCGGGACTT 600  
 15 GGGGTATTCC TCCAAAATTA TATGGGACCT TGCAGGACTC GAACCTGC 648

## (2) INFORMATION FOR SEQ ID NO: 3679:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 20 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3679:

CTGATCCCGT TGTGCTTCAC ACCCGATAGA TAGGGATTTA CAGATAAATT CAGGTCTCTT 60  
 30 CCACGTCATA TTTGGACCCA TCGAAAATTC GGGTTCTCAA ATCATCGAAC ATAACAAAAG 120  
 AAGCTAAGCA ACATGTAGGC CGTTGTCACT TAACTTCTTG TTTTCCGAT GACAGCTTCT 180  
 ATTTAGAGAA TGTCATGATT ATTTTATATT CACTTCAATG TTATCAATAT TAGTGCCATC 240  
 35 TATGACATCT GCCATGCGAT TTTCTTGTA TTTTTGTGC AATTCAAACG TGTACTTTCC 300  
 ACCGTTTTTC ATTTTAATAA CAATTTTACC TGAACCAACG TTACCGTACA GATTATTTTT 360  
 TTCAATAAGT TGTTTTCTCA ATTTAAATC AAGTTCTTTC 400

40 (2) INFORMATION FOR SEQ ID NO: 3680:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 45 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3680:

TCAATGCGGC TCATCGCATT CATTTCTTGT CTAGCAACGT TCTACTCTAG CGGAAnTAAG 60  
 TTAGCTACCA TCCTCGCTAA GAACCTTTCT TGA CTGTGA CAATCGCTTG CTTCTTTCCT 120

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TCGTCAGATT CAAACGTTTT CACTTCGCCA AGCCATTTTT CTTTGTGTTT ACTTTTTATT 240  
 TTGACGTTTT AGACATAAAA AAAGAGACCT CACGGTCTCA ACTTGCCTGG CAACGTTCTA 300  
 5 CTCTAGCGGA AGTAAGTTGG CTACCATCGT CGCTAAAGAC CTTTCTTGAC TTGTGACAAT 360  
 CGTTTGGCTT CTnTCCTCTC CTTCCGnTCT CGGCTTACTC 400

(2) INFORMATION FOR SEQ ID NO: 3681:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3681:

20 TCTTTCCTCT CCTTCGGCTC TCGCTTACTC ATTTAGCTCT ACTAAACTCG TTGCGCTCTT 60  
 TTCTCGTTTC GTCAGATTCA AACGTTTTCA CTTGCCCAAG CCATTTTTCT TTGTGTTTAC 120  
 TTTTATTTTT GACGTTTTAG ACATAAAAAA AGAGACCTCA CGGTCTCAAC TTGCCTGGCA 180  
 25 ACGTTCTACT CTAGCGGAAC GTAAGTTGGC TACCATCGTC GCTAAAGACC TTTCTTGACT 240  
 TGTGACAATC GCTTGCTTCT TTCCTCTCCT TCGGCTCTCG CTTACTCATT TAGCTCTACT 300  
 30 AAACTCGTTG CGCTCTTTTC TCGTTTCGTC AGATTCAAAC GTTTTCACTT CGCCAAGCCA 360  
 TTTTCTTTG TGGTTTACTT TTTATTTTGA CGGTTTAGGC 400

(2) INFORMATION FOR SEQ ID NO: 3682:

- 35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 414 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3682:

45 TTGAACATGT TGAATCTAAT GAAATTCTTG TTCGTCGTCT AGTTGAAGAG AACGGCGTTG 60  
 AGCATGAAGG TGAATTAGAT CGCTATCCAT TAGCTAAATT TAAACGTTCA AACTCAGGTA 120  
 CATGTTACAA CCAACGTCCA ATCGTTGCAG TTGGAGATGT TGTGAGTAT AACGAGATTT 180  
 50 TAGCAGATGG ACCATCTATG GAATTAGGAG AAATGGCATT AGGTAGAAAC GTATAGTTGG 240  
 TTTCATGACT TGGGACGGTT ACAACTATGA GGATGCCGTT ATCATGAGTG AAAGACTTGT 300  
 GAAAGATGAC GTGTATACTT CTATTCATAT TGAAGAGTAT GAATCAGAAG CACGTGATAC 360

## (2) INFORMATION FOR SEQ ID NO: 3683:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3683:

TTGGAATTC TCGCTACCC TCAGTTCATC CGCTCACTTT TCAACGTAAG TCGGTTCGGT 60  
 CCTCCATTCA GTGTTACCTG AACTTCAACC TGACCAAGGG TAGATCACCT GGTTCGGGT 120  
 CTACGACCAA ATACTAAACG CCCTATTGAG ACTCGCTTTC GCTACGGCTC CACATTTACT 180  
 GCTTAACCTT GCATCAAATC GTAACGCGC GGTTCATTCT ACAAAGGCA CGCCATCACC 240  
 CATTACGGG CTCTGACTAC TTGTAAGCAC ACGGTTTCAG GTTCTATTTT ACTCCCCTTC 300  
 CGGGGTGCTT TTCACCTTTC CCTCAGGTA CTGGGTTTAC TATCGGTCAC TANGAGAGTA 360  
 TTTAAGCCTT ANGAGATGGT CCTCCAGAT TCCCAGCGG 400

## (2) INFORMATION FOR SEQ ID NO: 3684:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 528 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3684:

GATnTATGAT GAAAACTAT CTGACTGCTG TTTCACTTTT TATAAGACTT CTGAATGTCT 60  
 TCACTTATAC TTCTAGTCAC AGATTnAAAT AATCAAAAGT GCACATTATT AAAATATCAA 120  
 TTTCACACTC AATGCGGCTC ATCGCATTCA TTTCTTGTCT AGCAACGTTT TACTCTAGCG 180  
 GAACGTAAGT TAGCTACCAT CCTCGCTAAG AACCTTTcTT GACTTgTGAC AATCGCTTGC 240  
 TTCTTTCTCT TCCTTCGGCT CTCGCTTACT CATTAGCTC TACTAAACTC GTTGCCTCT 300  
 TTTCTCGTTT CGTCAGATTG AAACGTTTTT ACTTCGCCAA GCCATTTTTT TTTGTGTTTA 360  
 CTTTTTATTT TGACGTTTTA GACATAAAAA AAGAGACCTC ACGGTCTCAA CTTGCCTGGG 420  
 CAACGTTCTA CTCTAGCGGA ACGTAAGTTG GCTACCATCG TCGCTAAAGA CCTTTCTTGA 480  
 CTTGTGACAA TCGCTTGCTT CTnTCCTCTC CTTGGGCTCT CGGTTACT 528

## (2) INFORMATION FOR SEQ ID NO: 3685:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3685:

10 AAATTATGGT CGATTGCGAA TGATTTAAGA GGGAnCATGG ATGCGAGTGA ATTCCGTAAT 60  
 TACATTTTAG GCTTGATTTT CTATCGCTTC TTATCTGAAA AAGCCGAACA AGAATATGCA 120  
 GATGCCTTGT CAGGTGAAGA CATCACGTAT CAAGAAGCAT GGGCAGATGA AGAATATCGT 180  
 15 GAAGACTTAA AAGCAGAATT AATTGATCAA GTCGGTTACT TCATTGAGCC ACAAGATTTA 240  
 TTCAGTGC GA TGATTCGTGA AATTGAAACG CAAGATTTCTG ATATAGAGCA TCTAGCGACG 300  
 GCGATTGCGA AAGTTGAAAC ATCTACATTA GGTGAnGAAA GTGAAAATGn CTTTATCGGG 360  
 20 CTGTTCA GCG ATATGGATTT GAGTTCAACG CGGCTAGGTA 400

## (2) INFORMATION FOR SEQ ID NO: 3686:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 403 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3686:

TTAAATTATT GGTCTATCGG TTCTTGGGGT GGCCATGGTA TCTGTTCCTT CTTCGGTGGT 60  
 35 GCAGTTGCGA CAACTATGGG TTGGAGATGG ATTTTCATCT TCTCAATTAT CGTTGCCGTA 120  
 CTTTCAATGT TACTCATCAA AGGGACGCCT GAAACGAAAT CAGAAATTAC CAATACACAT 180  
 AAATTTGACG TTGCAGGGCT AATTGTTCTA GTAGTTATGT TGCTAAGTTT AAACGTTGTC 240  
 40 ATTACTAAAG GTGCAGCACT TGGTTACACA TCATTATGGT TCTTTGGTTT GATTGCAATC 300  
 GTAATTGTAG CATTCTTTAT TTTCTTAAAT GTTGAGAAAA AAGTAGATAA TCCACTTATT 360  
 45 GATTTTAAAT TATTgAAAAAT AAACCATATA CAGGTGCAAC GGT 403

## (2) INFORMATION FOR SEQ ID NO: 3687:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 449 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

TATGAGCCCG ACGAGCTACC GAACTGCTCC ATCCGCGGAT AATAAAAAAT AATGGCGGAG 60  
 GAAGAGGGGAT TCGAACCCCC GCGGCCCCGT AAGGnCCTGT CGGTTTTCAA GACCGATCCC 120  
 5 TTCAGCCGGA CTGGGTATT CCTCCATTAT TATAGGTAAA TCGCTATTAA TTATAAAATT 180  
 AAATGGCGGT CTCGACGGGA ATCGAACCCG CGATCTCCTG CGTGACAGGC AGGCGTGTTA 240  
 ACCGCTACAC TACGAGACCA TTAGTAAAAC GGAGGAAGAG GGATTGGAAC CCCCAGGAGC 300  
 10 CGTTAAGCCC CTGTCGGTTT TCAAGACCGA TCCCTTCAGC CGGACTTGGG TATTCCTCCA 360  
 AAATTATATG GACCTTGACG GACTCGAACC TCGACCGAA CGGTATGAGC CGTAGCnCTA 420  
 ACCACTGGGC TAAAGTCCTA ATATAATTT 449

(2) INFORMATION FOR SEQ ID NO: 3688:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 20 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3688:

AAAACGTCGT AATATGCAAA TTGAAGGTGC CAAGGTTGTT ATTCAAGGTT TCnATAATGC 60  
 CGGAAGTTTC TTAGCTAAAT TCTTATATGA TTTAGGTGCA AAAATTGTAG GTATCTCTGA 120  
 30 TGCTTACGGT GCATTACACG ATCCAAATGG CTTAGATATA GATTATTTAT TAGACCGTCG 180  
 AGATAGTTTT GGTACGGTAA CAAATTTATT TGAAGAAACA ATCTCAAATA AAGAATTGTT 240  
 TGAATTAGAT TGTGACATTT TAGTACCAGC GGCTATTTCA AACCAAATTA CAGAAGACAA 300  
 35 TGCACATGAT ATTAAAGCTA GTATCGTTGT TGAAGCTGCT AATGGACCTA CAACACCAGA 360  
 AGCAACACGT ATTTTAACTG AACGTGGTAT ATTATTAGTT 400

40 (2) INFORMATION FOR SEQ ID NO: 3689:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3689:

50 CACGCTTATC AGGCGTGCGC TCTAACCAGC TGAGCTATAG GCCCATTAAT TTGAATGAAC 60  
 AAACATTCAA AACTGAATAC AATATGTCAC GTTATCCGC ATCTTCTGAA GAAGATGTTC 120

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CGACTTCACC CCAATCATT GTCCACCTT CGACGGCTAG CTCCTAAAAG GTTACTCCAC 240  
 CGGCTTCGGG TGTTACAAAC TCTCGTGGTG TGACGGGCGG TGTGTACAAG ACCCGGGAAC 300  
 5 GTATTCACCG TAGCATGCTG ATCTACGATT ACTAGCGATT CCAGCTTCAT GTAGTCGAGT 360  
 TGCAGACTAC AATCCGAAC GAGAACTT TATGGGGAA 400

## (2) INFORMATION FOR SEQ ID NO: 3690:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 553 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3690:

GCnGCGTTTT AGGCCCATTC GGTTACCCCC nTTCCATAAA TGGTGCCCGG CCAGAGGACT 60  
 TGAACCCCC AACTTACTGA TTACAAGTCA GTTGCTCTAC CAATTGAGCT AGGCCGGCTA 120  
 AGAAATGGTT CAGGACAGAG TCGAACTGCC GACACATGGA GCTTCAATCC ATTGCTCTAC 180  
 25 CAACTGAGCT ACTGAACCAT AATAAAAATG TAATGATGGC GGTCTCGACG GGAATCGAAC 240  
 CCGCGATCTC tGCGTGACAG GCAGGCGTGT TAACCGCTAC ACTACGAGAC CTATAAAATA 300  
 TTGCGGGAGG CGGATTTGAA CCACCGaCT CGGGTTATGA GCCCGACGAG CTACCGAACT 360  
 30 GCTCCATCCC GCGATAATAA AAAATAATGG CGGAGGAAGA GGGATTGAA CCCCCGCGGC 420  
 CCGTTAAGGC CCTGTGCGTT TTCAAGACCG ATCCCTTCAG CCGGACTTGG GTATTCCTCC 480  
 ATTATTATAG GTAnATCGCT ATTAAATTATA AnATTAAAT GGCGGTCTCG ACGGGAATCG 540  
 35 AACCCGCGGA TCT 553

## (2) INFORMATION FOR SEQ ID NO: 3691:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3691:

TCAATGCGGC TCATCGCATC CATTTTTTTGC CTGGCAACGT TCTACTCTAG CGGAACGTAA 60  
 50 GTTGGCTACC ATCGACGCTA AGAACCTTTC TTGACTGTG ACAATCGCTT GCTTCTTTCC 120  
 TCTTCTTCGG CTCTCGCTTA CTCATTAGC TCTACTAAAC TCGTTGCGCT CTTTCTCGT 180

TTTGACGTTT TAGACATAAA AAAAAGAGAC CTTGCGGTCT CAATGCGGCT CATCGCATCC 300  
 ATTTTTTGCC TGGCAACGTT CTA CTCTAGC GGAACGTAAG TTCGGACTAC CATCGACGCT 360  
 5 AAGGGAGCTT AACTTTCTGT GTTCGGGCAT GGGGAACAGG 400

(2) INFORMATION FOR SEQ ID NO: 3692:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 410 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3692:

TCGAATACTG TCATGAAGTA ATTTCTCTAT TCTACGACCA GAAATACAG ATTGAGTATA 60  
 20 TGCATATAAG ATGTTTTTAA CATCATTTTT GGATGATAGG ATGTTGCACC ACGATGATGT 120  
 CTGAATTCAT CGAATTCCTA TCAGGTATCG TTTCAACAAT TTCATTAACA TATCGCGAAA 180  
 TATCATTTTG AGAATCTAA CGAATTCCT ATTGGTAGTG TAAGTTGGGG TCATGTTATA 240  
 25 ATTTTATAC ATAAGGCACC TCTTTAATTT AGTTTAGTAG TATTTATTAA ATTATACGAG 300  
 GGACCCAACA CAGAAAATTC ATTTTATTGa ATTTTACATT TATGTGmCAA GTTGGGaAAA 360  
 ATGTCTTATT TTTTCAAAGT ATTTAAAAGT AAAATTACAT GTTAATACGT 410

(2) INFORMATION FOR SEQ ID NO: 3693:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3693:

ACTTCATATA ATTTATGAAA TAAACCTGTC AATTTTGGAT TGATTATGCT TTGTGATTCT 60  
 TTTTATTCT GCGTAATAAC GCTAAACCTA AAATGCTAAA TAATCCGCCG AACACATGC 120  
 45 CGTTGTTTGT TGATTCTTCT CCACCTGTTT CAGTAGTTCA GATTCTTAG ATTGTGCTTT 180  
 TTTAGTTGGT ACCACTGcTT TAACCTTTTC ATTGATTTCATA AACAGGTG TTACTACTTT 240  
 ACCTTGTTCC ACTGGTTTAG AAGGTTTTTT AGGTTCTTCT TTAGCAGGTG GTaTTGGTTT 300  
 50 ACCAGTTCA GTTGGTACCT CTGGCGTTGG CGGTGTTGGT GTTCCGGCT CGCTTGGTAC 360  
 TTCTGGTGTC GGTGGTGTG GGTGTTnCC GGCTTCGCTT GGTACTTCTG GGTGTTCCGT 420

## (2) INFORMATION FOR SEQ ID NO: 3694:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3694:

GCATCGTTGC CTTGGTAAGC CGTTACCTTA CCAACTAGCT AATGCAGCGG GAGTCCATCT 60  
 ATAAGTGACA GCAAGACCGT CTTTCACTTT TGAACCATGC GGTTCAAATn ATTATCCGGT 120  
 ATTAGCTACG GTTTCCTCGAA GTTATCCCAG TCTTATAGGT AGGTTATCCA CGTGTTACTC 180  
 ACCCGTCCGC CGCTAACATC AGAGAAGCAA GCTTCTCGTC CCGTTCGCTC GACTTGCAATG 240  
 TATTAGGCAC GCCGCCAGGT TCCATCCTGA GCCAGGATCA AACTCTCCAT AAAAATTATG 300  
 ATGTTTGATT AGCTCATAAA TACTAAATAA TGTTTGTAAC TTATAGTTAC GTTTTTTGGG 360  
 AATTAACGTT GGACATATTG TCATTCCAGT TTTCAATGTT 400

## (2) INFORMATION FOR SEQ ID NO: 3695:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3695:

ACCTAATATA TAGACAGGTT CATCACTTAA TGACTTTGCA AGTTCGGCAA TGTCTGTGTC 60  
 GTCGCGTTTG ACACGATAAT CACTGTCAGG GTTTGAAGCG GAATCAGGGA GTGGTTCAGT 120  
 TAACTCGCTT TCTCCATAAT CACGACGATC AACGGCTACA ACAGTAAAT GGTCTTTTAA 180  
 CTGTTCTGCA AGAGGCAGAA AAATGTCTCC GGTACCGTTT GCACCAGGAA TAAAGATGAG 240  
 CACGGGTCCT TGTCCGACTT GGTGGTATCG TAATTAGCG CCTTGTAATT CTAAAGTTTC 300  
 CATATTCAAT GACCTCCATT TGTTAATTGT TAGGTGATAA ACCTAATAAT TTAGCACCAT 360  
 TTGGTATAAC TTAATTTcnc CTTTTCTTC ATCnGGTTAA 400

## (2) INFORMATION FOR SEQ ID NO: 3696:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3696:

5 TTCTTTCTCT TCCTCCGGGT ACTAAGATGT TTCAGTTCTC CGGGTGTGCC TTCTGATATG 60  
 CTATGTATTC ACATATCGAT AACATGACAT AACTCATGCT GGGTTTCCCC ATTCCGAAAT 120  
 CTCTGGATCA AAGCTTACTT ACAGCTCCCC AAAGCATATC GTCGTTAGTA ACGTCCTTCA 180  
 10 TCGGCTTCTA GTGCCAAGGC ATCCACCGTG CGCCCTTAAT AACTTAATCT ATGTTTCCAC 240  
 CATTITTATA AGTCAAACGC TCACATACGG CTTCGTTTTC ATTATTTTAA ATGCTCATTT 300  
 ACATAAGTAA ACTCTGCTTT AAAATAATTT AACTCATTGT CTGCTAAACG TTTTCTTTTA 360  
 15 TAAAAAGATT TAAACGCGTT GATTAACTG TGAGTGTCT 400

## (2) INFORMATION FOR SEQ ID NO: 3697:

## (i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3697:

CACTTTAACC AAAAAATATT TGAATGTAA ATAAACATTC AAAACTGAAT ACAATATGTC 60  
 30 ACGTTATTCC GCATCTTCTG AAGAAGATGT TCCGAATATA TCCTTAGAAA GGAGGTGATC 120  
 CAGCCGCACC TTCCGATACG GCTACCTTGT TACGACTTCA CCCCAATCAT TTGTCCCACC 180  
 TTCGACGGCT AGCTCCTAAA AGGTACTCC ACCGGCTTCG GGTGTTACAA ACTCTCGTGG 240  
 35 TGTGACGGGC GGTGTGTACA AGACCCGGGA ACGTATTCAC CGTAGCATGC TGATCTACGA 300  
 TTACTAnCGA TTCCAnCTTC ATGTAGTCGA GTTGCACT ACAATCCGAA CTGAGAACAA 360  
 CTTTATGGGA TTGCTTGAC CTCGCGGTTT CGTnCCCTT 400

## (2) INFORMATION FOR SEQ ID NO: 3698:

## (i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3698:

50 AAGGGAATCG AATTTTCTTT CTCTCCTCC GGGTACTAAG ATGTTTCAGT TCTCCGGGTG 60



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CCCCATTTCGG AAATCTCTGG ATCAAAGCTT ACTTACAGCT CCCCAGCA TATCGTCGTT 180  
 AGTAACGTCC TTCATCGGCT TCTAGTGCCA AGGCATCCAC CGTGCGCCCT TAATAACTTA 240  
 ATCTATGTTT CCATCCTACA GGAAACGCGT TATTAATCTT GTGAGTGTTT TTTGGAACAC 300  
 TAGCGATTAT TTCTTATGAA TTCAAGCTTA TTTAAACTC TTTATTCACT CGGTTGTGCT 360  
 TGGTAAATC TATATTTTAC TTACTTATCT AGGTTTCAAT 400

## (2) INFORMATION FOR SEQ ID NO: 3699:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3699:

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TTTATGGCAT ACACGCATCA TAATACAGCC CAACACCACT AATGGTGCGT TTGCAAATCC 60  
 AAATTCTTCC GCTCCAAGCG CACATGCGTA CGCTACATCT TTACCAGTTA ATAACCTTACC 120  
 GTCTGTTTCT AACTTAACAC GACTTCTTAA GTCATTTAGT TTTAATGTTT GATGTGTTTC 180  
 TGCTAAACCA ATCTCCCAAG GAACACCGGC ATGCTGAATA CTCGTTTTGG GTGAAGCCCC 240  
 TGTATCACCA TCGTAACCAC TGATGACAAT TTTATCTGCA AATGCTTTTG CCACCCAGCA 300  
 TGCAATGGTA CCAACACCTG TTTTCGAAAC TAATTTTACC GCGATATCTG CATCTTTATT 360  
 CGCATTTTTC AAATCATGTA TCAGTTGCGC TAAATCTTCT 400

## (2) INFORMATION FOR SEQ ID NO: 3700:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3700:

45  
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CGACGTACCA TCGACGCTAA GGAGCTTAAC TTTCTGTGT TCGGCATGGG AACAGGTGTG 60  
 ACCTCCTTTG CTATAGTCAC CAGACATATG AATGTAATTT ATACATTCAA AACTAGATAG 120  
 TAAGTAAAG TnATTTTGCT TCGCAAAACA TTTATTTTGA TTAAGTCTTC GATCGATTAG 180  
 TATTCGTCAG CTCCACATGT CACCATGCTT CCACCTCGAA CCTATTAACC TCATCATCTT 240  
 TGAGGGATCT TATAACCGAA GTTGGGAAAT CTCATCTCnG GGGGGGCTTC ATGCTTAGAT 300

GGTACACCAG AGGTATGTCC ATCCCGGTCC TCTCGTACTA

400

## (2) INFORMATION FOR SEQ ID NO: 3701:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3701:

AACCAAGCCC AATAATGGAC TGGCCGCTA ATAATAAAG CTCTAAAAGT TGTATTTTAA	60
AAATAGTTCT TTAAATTATA TACCCACCAC ATTTGGTGGA GAACCTAAAA AAAAGCACTT	120
CCCAAAAATG GAAAGTGCAA GTAGTGAGCC ATAGAGGATT CGAACCTCTG ACCCTCTGAT	180
TAAAAGTCAG ATGCTCTACC AACTGAGCTA ATGGCTCTAA TGGCTGGGCT AGCTGGATTC	240
GAACCAACGA GTGACGGAGT CAAAGTCCGT TGCCTTACCG CTTGGCTATA GCCCAATATA	300
TAGATGGTGG AGGGGGGCGAG ATTCGAAGT CCGAACCCGA AGAGCGGnTT TACAGTCCGC	360
CGCGTTTAGC CAnTTCGnTA CCCCTCCAGn TTATTCATAT	400

## (2) INFORMATION FOR SEQ ID NO: 3702:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3702:

TTTAAGTCCT GTGCGTCTGC CAGTTCGCCC ACCCCGGCAC TATAAAAATG GAGCAGAAGA	60
CGGGATTCTGA ACCCGCGACC CCAACCTTGG CAAGGTTGTT ATTCTACCGC TGAACACTT	120
CTGCATATGC GGGTGAAGGG AGTCGAACCC CCACGCCGTA AGgTTAGaTC CTAAGTCTAG	180
TGCGTCTGCC AATTCCGCCA CACCCGCAAA TGGTGAGCCA TAGAGGATTC GAACCTCTGG	240
ACCCTCTGGA TTAAAAGTCA GATGCTCTAC CAACTGAGCT AATGGGCTCT TCCATGGTGC	300
CGGCCAGAGG ACTTGGAACC CCAACCTAC TGGATTACAA GTCAGTTGGC TCTACCAATT	360
GAnGCTAAGG CCGGCAATAT GTTAAGnATn AATGGTGGAG	400

## (2) INFORMATION FOR SEQ ID NO: 3703:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3703:

	CAACTAATAA ATAGTGGCGG TGGAGGGGAT CGAACCCCCG ACCTCACGGG TATGAACCGT	60
10	ACGCTCTAGC CAGCTGAGCT ACACCGCCTT ATATAGTTTG TAAATAATAT GGTGGAACT	120
	AGCGGGATCG AACCGCTGAC CTCCTGCGTG CAAAGCAGgC GCTCTCCAG CTGAGCTAAG	180
	CCCCATAAT AATTACAGTA TATCGGGAAG ACAGGATTG AACCTGCGAC CCCTTGGTCC	240
15	CAAACCAAGT GCTCTACCAA GCTGAGCTAC TTCCCGTATA ATTAACGCGC CCGATAGGAG	300
	TCGAACCCAT AAACCTCTTG ATCCGTAGTC AAACGCTCTA TCCAATTGAG CTAACGGGCG	360
	CATATGTTTT TAATTGAAAT GGTGCCCGAG GACCGGAATG	400

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(2) INFORMATION FOR SEQ ID NO: 3704:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3704:

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	CTAACGCCTA CGCGTTACAT GAAAAACGGA GAACAAGCAG AACAATTATT ACGTCAGCTT	60
	ATAGAAAAAG ATGAAGCACT AGCTAAGTAT GTCATGGTTT GTGATGAAAC AGCTTGGTGG	120
35	TCATATATGG GTCAAGATAA TGATATTTTC AAAGATCAAT TAGGTCATCT AACTGTTTCT	180
	CTAAGAAAGT ATCCCGAAGT GCTAGCCAAA AATGATACGC AACAGCTAGT GTCAATGGCA	240
	GCACTGCGCG CAAATGATCG CACTTTATAT CAAATGATTT GTGGAAAAGA TAATATTTCT	300
40	AAAAATGATG TCATGACGTT ATTTGAAGAT ATCGCGCAAG TCTTTTAAA GGTAACACTA	360
	TCATTTATGC AATACGGCGC ATTACCCAGA GTTGTCATGGT	400

(2) INFORMATION FOR SEQ ID NO: 3705:

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(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 478 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3705:

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5 TGACGGGGAC CCGCACAAGC GGTGGAGCAT GTGGTTTAAT TCGAAGCAAC GCGAaGaACC 120  
 TTACCAAATC TTGaCATCCT TTGaCAACTC TAGaGATAGA GCTTTCCCCT TCGGGGGTAC 180  
 AAAGTGACAG GTGGTGCATG GTTGTCGTCA GCTCGTGTCTG TGAGATGTTG GGTAAAGTCC 240  
 CGCAACGAGC GCAACCCTTA AGCTTAGTTG CCATCATTAA GTTGGGCACT CTAAGTTGAC 300  
 10 TGCCGGTGAC AAACCGGAGG AAGGTGGGGA TGACGTCAAA TCATCATGCC CCTTATGATT 360  
 TGGGgCTACA CACGTGCTAC AATGGACAAT ACAAAGGGCA GCGAAACCGT GAGTCAAGCA 420  
 AATCCCATAA AGTTGTTCTC AGTTCGGATT GTAGTCTGCA ACTCGACTAC ATGAAGCT 478

15 (2) INFORMATION FOR SEQ ID NO: 3706:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 20 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3706:

25 ATCTTAAGTC TTTGGTGAAC CGTTTTGTAG AATTAAATAA TATTACAGAG CCGCTAGCAG 60  
 TAACGATCCA AACGAATTTA CCACCATCAC GTGGATTAGG ATCGAGTGCA GCTGTCGCGA 120  
 30 TTGCTTTTGT TCGTGCAAGT TATGATTTTT TAGGGAAATC ATTAACGAAA GAAGAACTCA 180  
 TTGAAAAGGC TAATTGGGCA GAGCAAATTG CACATGGTAA ACCAAGTGGT ATTGATACGC 240  
 AAACGATTGT ATCAGGCAAA CCAGTTTGGT TCAAAAAGG TCATGCTGAA ACGTTGAAAn 300  
 35 CTCAAAGTTT AGACGGCTAT ATGGTTGTTA TAGAnACTGG TGTGAAAGGT TCACCAAGAC 360  
 AAGCAGTAGA AGATGTTCCA TAAACTTTGG TGAGGACCCT 400

40 (2) INFORMATION FOR SEQ ID NO: 3707:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 45 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3707:

50 GTCGAACTGC CGACACATGG AGCTTCAATC CATTGCTCTA CCAACTGAGC TACTGAACCA 60  
 TAATAAAAAT GTAATnnTGG CGGTCTCGAC GGGAAATCGAA CCCGCGATCT CCTGCGTGAC 120  
 AGGCAGGCGT GTTAACCGCT AACTACGAG ACCTATAAAA TATTGCGGGA GCGGATTG 180

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TAAAAAATAA TGGCGGAGGA AGAGGGATTC GAACCCCCGC GGCCCGTTAA GGCCCTGTCG 300  
 GTTTTCAAGA CCGATCCCTT CAGCCGGACT TGGGTATTCC TCCATTATTA TAGGTAAATC 360  
 5 GCTATTAATT ATAAATTAA ATGGCGGTCT CGACGGGAAT 400

## (2) INFORMATION FOR SEQ ID NO: 3708:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3708:

GTTCGCCCCAT TAAAGCGGTA CCAnGCTGGG TTCAGAACGT CGTGAGCAnG TTCGGTCCCT 60  
 20 ATChGGGGTG GGCCTAGGAA ATTTGAGAGG AGCTGTCCTT AGTACGAGAG GACCGGGATG 120  
 GACATACCTC TGGTGTACCA GTTGTCTGTC CAACGCATA GCTGGGTAGC TATGTGTGGA 180  
 CGGGATAAGT GCTGAAACAT CTAAGCATGA AGCCCCCTC AAGATGAGAT TTCCCAACTT 240  
 25 CGGTTATAAG ATCCCTCAAA GATGATGAGG TTAATAGGTT CGAGGTGGAA GCATGGTGAC 300  
 ATGTGGAGCT GACGAATACT AATCGATCGA AGACTTAATC AAAATAAATG TTTTGCGAAC 360  
 30 AAAATCCACT TTTACTTACT ATCTAGTTTT GAATGTATAA 400

## (2) INFORMATION FOR SEQ ID NO: 3709:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 424 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3709:

AATTTTATGG GCCCTTTATG GACTTTATAT TmCCTAAAT ACTATTAAGA AGTCCTGAAA 60  
 AATTCACATT AGCAGTTGGA TTGTTCAACT TTATTAATGA TAAGTATGCA AATAATTTCA 120  
 45 CAGTGTGTTGC AGCAGGGGCA ATTATGATTG CAGTACCTAT AGCAATCGTA TTCTGTGTTCT 180  
 TGCAACGCTA TTAGTATCA GGTTTAACAA CAGGTGCGAC AAAAGGTTAG TTTGAAATTr 240  
 50 GGAGTGGGGC AGAATTGATA AAGAACCACT AATGACGATA AAGATTAAAA GGAGGACGTT 300  
 ATGATGACGA TTAAAGTTGG AATCATTGGG TGTGGTGGTA TTGCGAATGG CAAGCACATG 360  
 CCAAGTTTAC AAAAAGTTGA AATGTTGAA ATGATCGCAT TTGTGACGTG GACTTTTCGAA 420

## (2) INFORMATION FOR SEQ ID NO: 3710:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 559 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3710:

```

AGTGCTCTAC CAAGCTGAGC TACTTCCCGT ATAATTAACG CGCCCGATAG GAGTCGAACC      60
CATAACCTCT TGATCCGTAG TCAAACGCTC TATCCAATTG AGCTACGGGC GCATATGTTT      120
TTATTGAAAA TGGTGCCGAG GACCGGAATC GAACCGGTAC GTGATCACTC ACCGCAGgAT      180
TTTAAGTCCT GTGCGTCTGC CAGTTCGGCC ACCCCGGCAC TATAAAAATG GAGCAGAAGA      240
CGGGATTGCA ACCCGCGACC CCAACCTTGG CAAGGTTGTa TTCTACCGCT GAACTACTTC      300
TGCATATGCG GGTGAAGGGA GTCGAACCCC CACGCCGTAA GcTkAGaTCC TgAAGTCTAG      360
TGCGTCTGCC AATTCCGCCA CACCCGCAA TGGTGAGCCA TAGAGGATTC GAACCTCTGG      420
ACCTCTGGA TTGAAAAGTh CAGATGCTCT GACCAACTGG AGCTAATGGC TCTTCCCATG      480
GTGGCCGGCC AGAAGGACTT GGAACCCCCA ACCTGATGGA TTTACAATTC AGTTGGCTCT      540
AACCAATTTG AGCTAAGGC                                     559
  
```

## (2) INFORMATION FOR SEQ ID NO: 3711:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3711:

```

AACCTTTTAG GAGCTAGCCG TCGAAGGTGG GACAAATGAT TGGGGTGAAG TCGTAACAAG      60
GTAGCCGTAT CGGAAGGTGC GGCTGGATCA CCTCCTTTCT AAGGATATAT TCGGAACATC      120
TTCTTCAGAA GATGCGGAAT AACGTGACAT ATTGTATTCA GTTTTGAATG TTTGTTTCATT      180
CAAATTAATG GGCCTATAGC TCAGCTGGTT AGAGCGCACG CCGATAAGC GTGAGGTCGG      240
TGGTTCGAGT CCACTTAGGC CCACCATTAA TTTAATACCT ATTTGGGGGC TTAGCTCAGC      300
TGGGAGAGCG CCTGCTTTGC ACGCAGGAGG TCAGCGGTTG GATCCCGCTA GTCTCCACCA      360
TTATTTGTAC ATTTGAAAAC TAGATAAGTA AGTAAAATAT                                     400
  
```

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3712:

TAGAATGAAC CGGCGAGTTA CGATTTGATG CAAGGTTAAG CAGTAAATGT GGAGCCGTAG 60  
 CGAnnTCATG TCTGAATAGG GCGTTTAGTA TTTGGTCGTA GCCTGAAACC nnGTGATCTA 120  
 CCCTTGGTCA GGTGAAGTT CAGGTAACAC TGAATGGAGG ACCGAACCGA CTTACGTTGA 180  
 AAAGTGAGCG GATGAACTGA GGGTAGCGGA GAAATCCAA TCGAACCTGG AAATAGCTGG 240  
 TTCTCTCCGA AATAGCTTTA GGGCTAGCCT CAAGTGATGG ATTATTGGAG GTAGAGCACT 300  
 GTTTGGACGA GGGGCCCCCTC TCGGGTTACC GAATTCAGAC AACTCCGAA TGCCAATTTA 360  
 ATTTAACTTG GGGAGTCAGA ACATTGGGTG ATAAGGTCCG 400

(2) INFORMATION FOR SEQ ID NO: 3713:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3713:

TTTTTAAGTC TGATGTGAAA GCCACGGCT CAACCGTGAA GGGTCATTGG AAAGTGGAAA 60  
 ACTTGAGTGC AGAAGAGGAA AGTGGAATTC CATGTGTAGC GGTGAAATGC GCAGAGATAT 120  
 GGAGGAACAC CAGTGCGGAA GCGCACTTTC TGGTCTGTAA CTGACGCTGA TGTGCGAAAC 180  
 GTGGGGATCA nACAGGATTA GATACCCGGT AGTCCACGCC GTAAACGATG AGTGCTAAAG 240  
 TGTTAGGGGG TTTCCGCCCC TTAGTGCTGC AGTAAACGCA TTnAAGCACT CCGnCTGGGG 300  
 AGTACGnCCG CAAGTTGGAA ACTTCAAAGG AATTGACGGG GGACCCGCAC AAGCGTTGGG 360  
 AGCATGTGGT TTAATTTCCA AGCAACGGAG AGGAACCTGA 400

(2) INFORMATION FOR SEQ ID NO: 3714:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 425 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3714:

5 AGGTAGGACT CGAACCTACG ACCGATCGGT TAACAGCCGA TAGCTCTACC ACTGAGCTAC 60  
 TGTGGATTAA TATTATGCCT GGCAACGTTT TACTCTAGCG GAACGTAANT CGACTACCAT 120  
 CGACGCTAAG GAGCTTAACT TCTGTGTTCT GCATGGGAAC AGGTGTGACC TCCTTGCTAT 180  
 10 AGTCACCAGA CATATGAATG TAATTATATAC ATTCAAACCT AGATAGTAAG TAAAAGTGAT 240  
 TTTGCTTCGC AAAACATTTA TTTTGATTAA GTCTTCGATC GATTAGTATT CGTCAGCTCC 300  
 CATGTCACCA TGCTTCACC TCGAACCTAT TAACCTCATC ATCTTTGAGG GATCTTATAA 360  
 15 CCGAAGTTGG GAAATCTCAT CTTGAGGGGG GCTTCATGTC TTAGCATTTC AGTCACTTAT 420  
 GCCCC 425

## (2) INFORMATION FOR SEQ ID NO: 3715:

20

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3715:

30 GTCCCTGCTG TTCCTATCAT ATAAATGATA GATTCAAATA GATTGTAGG TTTGTCATGC 60  
 CCAGTTACAA GTTGCCTTAT CGTAGACACT AACATTAATA TGA CTGGTAA TGTGCTGTT 120  
 AATAAACTCA TACCAAATCC TGGCATCTCT TGATCCGTAA ATTCTTTTGG TGCACCTAAC 180  
 35 GCTGAAATAT CGCCTTCTCG TGTATACGCA GACGGAATCA TTTTGTGTC ACTTTGTAA 240  
 ATATAGGCCC TGCAATGAGT GACTGGAAT GGCAATAATC ATACCATACA GTAATACATC 300  
 TCCAACATTT GCCTTTAATT CTTTTCGAG ACTACCGGTC CTGGGATGTG GTGGTAAAAA 360  
 40 GCCATGTGTC ACTGATAAAG CTGTTACCAT AAGTAGTCCT 400

## (2) INFORMATION FOR SEQ ID NO: 3716:

45

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3716:

55 TTATGAATTC AAGCTTATTT AAAACTCTTT ATTCACCTCGG TTTTGCTTGG TAAAATCTAT 60



5 GCAATATCAC TTTAACCAAA AAATATTTGA ATGTTAAATA AACATTCAAA ACTGAATACA 180  
 ATATGTCACA TTATTCCGCA TCTTCTGAAG AAGATGTTCC GAATATATCC TTAGAAAGGA 240  
 GGTGATCCAG CCGCACCTTC CGATACGGCT ACCTTGTTAC GACTTCACCC CAATCATTTG 300  
 TCCCACCTTC GACGGCTAGC TCCTAAAAGG TTA CTCCACC GGnTTCGGGT GTTACAAACT 360  
 10 GTTCGTGGTG TGACGGGGCG GTGTGTTACA AGACCCGGGA 400

(2) INFORMATION FOR SEQ ID NO: 3717:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3717:

AAAGGACGAC ATTAGACGAA TCATCTGGAA AGATAATTCA AAGAAGGTAA TAATCCTGTA 60  
 25 GTCGAAAATG TTGTCTCTCT TGAGTGGATC CTGGTACGAC GGAGCACGTG AAATTCCGTC 120  
 GGAATCTGGG AGGACCATCT CCTAAGGCTA AATACTCTCT AGTGACCGAT AGTGAACCAG 180  
 TACCGTGAGG AAAGGTGAAA AGCACCCCGG AAGAGTTGA AATAGAACCT GAAACCGTGT 240  
 30 GCTTACAAGT AGTCAGAGCC CGTTAATGGG TGATGGCGTG CCTTTTGTAG AATGAACCGG 300  
 CGAGTTACGA TTTGATGCAA GGTTAAGCAG TAAATGTGGA GCCGTAGCAn AAnnTGTTC 360  
 GAATAGGGCG TTTAGTATTT TGGTCGTAGC CCGAGAACCA 400

35 (2) INFORMATION FOR SEQ ID NO: 3718:

40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3718:

TAATTCATCT GCAGCATCTG GTTGATTAA GCTTTCACGT AAACACATCG CTAAAGATAG 60  
 AATCATCCA AATGGATTGG CAACGTTTTT ACCTGCAATA TCTGGTGCTG ATCCATGAAT 120  
 50 AGGCTCATAC AATCTTGGAC CATCGTTACT AAAACTAGCA GAAGGTGATA AACCAAGTGA 180  
 ACCAGGAATC ACTGAAGCTT CATCACTTAA AATATCGCCA AATAAGTTTT CACATACGAT 240  
 GACGTCAAAT TGTTTTGGnA TTTGTGATTA AATGCATACT ACAAGCATCA ACAATAAGT 300

55

TTTACTAGAA GCTAATACAT TTCCTTATCA ACGGATGTnA

400

## (2) INFORMATION FOR SEQ ID NO: 3719:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3719:

ATTTAAAACT GCCTGGCAAC GTTCTACTCT AGCGGAATA AGTnGAGCTA CCATCGACGC 60  
 TAAGGAGCTT AACTTCTGTG TTCGGCATGG GAACAGGTGT GACCTCCTTG CTATAGTCAC 120  
 CAGACATATG AATGTAATTT ATACATTCAA AACTAGATAG TAAGTAAAAG TGATTTTGCT 180  
 TCGCAAAACA TTTATTTTGA TTAAGTCTTC GATCGATTAG TATTCGTCAG CTCCACATGT 240  
 CACCATGCTT CCACCTCGAA CCTATTAACC TCATCATCTT TGAGGGATCT TATAACCGAA 300  
 GTTGGGAAAT CTCATCTTGA GGGGGGCTTC ATGCTTAGAT GCTTTCAGCA CTTATCCCGT 360  
 CCACACATAG CTACCCAGCT AGCCGTTGGC ACGACAAngG 400

## (2) INFORMATION FOR SEQ ID NO: 3720:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3720:

CGTTACACCT TCCAATAAAT TTGCTGTTGC TGGATAAGGA GAAATATTGA TATATTGTCT 60  
 TAAATTACTA TAATGCCAAT TTAAGTCTGG ATGATTTGTT AAGACACCAA TAGGATTATC 120  
 TTTTATAACC ACTTCACCCT CTTTAAATGA AACTTCGACT GTATGTCCAG TTGCATCGGA 180  
 AACATGATAA TGCAATGGCG GAACTTCACC GATGTCATTT AAATATACAG CTACAACATG 240  
 TATTTGGGAT GCTTGTTGTT TCATATCTTC AATGCTTGTT GTATATCCCA AAATCCATGT 300  
 CACAATTCA TTTTGCCTAA TATTCATCGC GTCCGCTTTG TGTGTTGGAT CCATATGGAA 360  
 CTATAACCTC GGGAAATATT GTGGTTGAAA TGGGCACGCC 400

## (2) INFORMATION FOR SEQ ID NO: 3721:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3721:

AGTCAGTTTA TAGCGATTGC TGGACTGACA GTACTTGTGC CATTATTGCC AATTTATATG	60
GCATCACTAC AAAATCTATC AGTCGTAGAA ATACAGTTGT nGAGTGGTAT AGCGATTGCT	120
GCTCCAGCTG TAACGACGAT GATAGCTTCG CCGATATGGG GGAAGCTAGG TGATAAGATC	180
AGCCGAAAAT GGATGGTGTT AAGAGCGTTA CTTGGTTTGG CCGTATGCTT ATTTTAAATG	240
GCATTGTGTA CGACACCATT ACAGTTTGTG CTTGTGGAGG TTATTGCAGG GACTATTTGG	300
TGGTGTGTGT GATGCATCAA GTGCGTTTGC GAGTGCAGAA GCGGCCACTG AnAGATCGTG	360
GGAAAGGTAT TAGGAAGACT GCAAATTnCA GTTCAGCGCA	400

20

(2) INFORMATION FOR SEQ ID NO: 3722:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3722:

TCTAAAAGTT GAACTACTCC CGCATAAACC TGGAGGCGGC AACCGGATTT GAACCGGTGA	60
TAAAGGTTTT GCAGACCTCT GCCTTACCAC TTGGCTATGC CGCCAATAAC TGGGCTAGCT	120
GGATTCGAAC CAACGAGTGA CGGATAAAGT CCGTTGCCTT ACCGCTTGGC TATAGCCCAT	180
TAATAATAAG GCGGGCTGAA GGGGATCGAA CCCTCGAATG TCGGAACCAC AATCCGATGT	240
GTTAACCACT TCACCACAGC CGCCATGGCA GGGGCAGTAG GAATCGAACC CACACCAAAG	300
GTTTTGGAGA CCTCTATTCT ACCnTTGAAC TATGCCCCCTA TTAAATGAT AAATGGAGGG	360
GGGCAGATTC GAACTGCCGA ACCCGAGGGG CGGATTTTAC	400

45

(2) INFORMATION FOR SEQ ID NO: 3723:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3723:

GGTTCAAGTC CTCTGGCCGG CACCATTtnt GGAGGGGTAG CGAATGGCTA AACGCGGCGG 120  
 ACTGTAAATC CGCTCCTTCG GGTTCGGCAG TTCGAATCTG CCCCCCTCCA TTTATTATTT 180  
 5 TTAATAGGGG CATAGTTCAA CGGTAGAATA GAGGTCTCCA AAACCTTTGG TGTGGGTTCC 240  
 ATTCCTACTG CCCCTGCCAT GCGGGCTGTG GTGAAGTGGT TAACACATCG GATTGTGGTT 300  
 10 CCGACATTCG AGGGTTCGAT CCCCTTCAGC CGCCTTATTA TTAATGGGCT ATAGCCAAGC 360  
 GGTAAGGCAA CGGACTTTGA CTCCGTCACT CGTTGGTTCC 400

## (2) INFORMATION FOR SEQ ID NO: 3724:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3724:

CACTTTAGCA AATGGTGACA AAGTCCGTAT TGCTACAATT TTTGACTTAA TGGCAAGTCA 60  
 25 ATATGGCGTG CGTCGTTTTC ATCATAAATT AGAATCAAAA GGATACGACG ATGCAGAATC 120  
 AAAATATACA CCTGCTTGGC AAGAAGCCAT TTCAGGCGTA AAACAAAGTG TTTGTCAATC 180  
 30 AAGTAGCGAA AGAATTTGCG CAAAACGCTA TCGATACTGA AGGGCGTTCA ATGATTATCA 240  
 TGGGTGCGGG TATTAACCAT TGGTTTAACT CAGATACGAT TTATCGTTCC AATCTTAAAC 300  
 TTAGTTATGT TATGTGGCTG TCAGGTGTGA ATGGTGGCGG TTGGGGCTCA CTATGTGGGG 360  
 35 ACAAGAAAAA TGTCGTCCGA TTGAAGGATG GAGTACTGTC 400

## (2) INFORMATION FOR SEQ ID NO: 3725:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 476 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3725:

CGCTATCTGA ATCTGAATCG CTATCTGAAT CTGAGTCGTT GTCTGAGTCC GAATCGCTAT 60  
 50 CTGAATCTGA GTCGCTATCT GAGTCTGAGT CGCTATCTGA ATCTGAGTCG CTGTCTGAAT 120  
 CTGAATCACT GTCTGAGTCT GAGTCGCTGT CTGAGTCTGA ATCGCTGTCA GAATCTGAGT 180  
 CGCTATCTGA GTCTGAATCT GAATCACTGT CTGAGTCCGA ATCGCTATCT GAATCTGAAT 240

CCGAGTCTGA ATCGCTGTCT GAGTCTGAGT CGCTGTCTGA ATCTGAATCG CTATCTGAGT 360  
 CTGAGTCGCT GTckGAATgC GCTGTCTGAA TCTGAGTCGC TATGCTGAAT GCTGAGTnCG 420  
 CTATGTGAGT CTGAATGCGC TGTGCAGAAT CTGAGTGGCG TCATCTGATG TTTCTT 476

(2) INFORMATION FOR SEQ ID NO: 3726:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3726:

ATACGACCAC TGTTTAATGC GTCCATTAAA TCTGGCCAAT TATTGAATTT AACTAATTCT 60  
 AGTTTATATT TCGGATGATT GTATTGTGAT AATAATTTTT TAGTCATCAT CAAATTAGCT 120  
 GAATGTGTAA TCGGCAAATA TCCAATTTTA ATCACTTGCT GATTTTGGGC ATTTTLAGAC 180  
 CGTTCTTTAG ACGTCCTTTG CCAATCACAT CCTGTAATTA TAAAGATTCC AATGATGACG 240  
 ATTATGCTTA ACCTTTTCAT CGTCACTCAC TCCTTATAAA TAATATTCAG GTTCAACTTG 300  
 ATGATGATTC AATGCAAnGT TTCCATAATT TCATTACGAA TCTTAAGTAG GTGGCTATCA 360  
 TTACGGACTG CGTGGATGTG AnGCTGTAAA TTCCATAnTG 400

(2) INFORMATION FOR SEQ ID NO: 3727:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3727:

ACGACGGATA GGGACCGAAC TGTCTCACGA CGTTCTGAAC CCAGCTCGCG TACCGCTTTA 60  
 ATGGGCGAAC AGCAAACCTT TGGGACCGAC TACAGCCCCA GGATGCGATG AGCCGACATC 120  
 GAGGTGCCAA ACCTCCCCGT CGATGTGAAC TCTTGGGGGA GATAAGCCTG TTATCCCCGG 180  
 GGTAGCTTTT ATCCGTTGAG CGATGGCCCT TCCATGCGGA ACCACCGGAT CACTAAGTCC 240  
 GTCTTTGAC CCTGCTCGAC TTGTAGGTCT CGCAGTCAAG CTCCTTATG CCTTTACACT 300  
 CTATGAATGA TTTCCAACCA TTCTGAGGGA ACTTTGAGCG CCTCCGTTnC CTTTTAGGAG 360  
 GCGAACGGCC CCAGTTCAAA CTGCCCGCCT GAACACTGTC 400

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3728:

TTGAAAAGTC ATATCAAAGC GCACATGTTT TTAAGCGTCG TCGAACACCT ATCGTGAAAG 60  
 GTGTGTCATT TGAGTGTCCA ATCGGTGCCA CGATTGCGAT TATCGGAGAA AGTGGTAGCG 120  
 GTAAATCGAC GTTGAGTCTA TTGATATTAG GTATTGAGAA ACCGGATAAA GGTGTGTGTA 180  
 CCTTAAATGA TCAACCGATG CATAAGAAGA AAGTGAGACG TCATCAAATT GGTGCTGTAT 240  
 TTCAAGATTA TACGTCATCA TTACATCCAT TTCAGACTGT TAGAGAAATC TTATTTGAAG 300  
 TGATGTGTCA ATGTGATGGA CAACCTAAAG AAGTTATGGA AGTCCAAGCA ATTACATTGT 360  
 TGGAGAAGT CGGTCTATCT AAGGCATACA TGGGATAAAT 400

(2) INFORMATION FOR SEQ ID NO: 3729:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3729:

ATCGAACCCC CGACCTCAGC GGTATGAACC GTACGCTCTA GCCAGCTGAG CTACACCGCC 60  
 TTATATAGTT TGTAATAAT ATGGTGGAGA CTAGCGGGAT CGAACCGCTG ACCTCCTGCG 120  
 TGCAAAAGC CGCTCTCCA GCTGAGCTAA GCGCCCATAA TAATTACAGT ATATCGGGAA 180  
 GACAGGTTTC AACCTGCGAC CCCTTGGTCC CAAACCAAGT GCTCTACCAA GCTGAGCTAC 240  
 TTCCCGTATA ATTAACGCGC CCGATAGGAG TCGAACCCAT AACCTCTTGA TCCGTAGTCA 300  
 AACGCTCTAT CCAATTGAGC TACGGGCGCA TATGTTTTTA TTGAAAATGG TGCCGAGGAC 360  
 CGGAATCGAA CCGTAGTGA ATCACTCACC GCAGATTTTA 400

(2) INFORMATION FOR SEQ ID NO: 3730:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3730:

5 ATCTCTGGAT CAAAGCTTAC TTACAGCTCC CCAAAGCATA TCGTCGTTAG TAACGTCCTT 60  
 CATCGGCTTC TAGTGCCAAG GCATCCACCG TCGGCCCTTA ATAACCTAAT CTATGTTTCC 120  
 ACCATTTTTTA TAAGTCAAAC GTTAACATGA AGTTACGTTT TTTTATAAAA AGATTTAAAC 180  
 10 GCGTTATTAA TCTTGTGAGT GTTCTTTTGA AACTAGCGA TTATTTCTTA TGAATTCAAG 240  
 CTTATTTAAA ACTCTTTATT CACTCGGTTT TGCTTGGTAA AATCTATATT TTACTTACTT 300  
 ATCTAGTTTT CAATGTACAA ATAATGGTGG AGACTAGCGG GATCGAACCG CTGACCTCCT 360  
 15 GCGTGCAAAG CAGGCGCTCT CCCAGCTGAG CTAAGCCCCC 400

## (2) INFORMATION FOR SEQ ID NO: 3731:

## (i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 401 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3731:

25 TGATTACAAG TCAGTTGCTC TACCAATTGA GCTAGGCOGG CAATATGTAA GAATAAATGG 60  
 30 TGGAGAATGA CGGGTTGGA CCGCCGACCC TCTGCTTGTA AGGCAGATGC TCTCCAGCT 120  
 GAGCTAATTC TCCGATTTAA AACTGCCTGG CAACGTTCTA CTCTAGCGGA ACGTAAGTTC 180  
 GACTACCATC GACGCTAAGG AGCTTAACTT CTGTGTTCCG CATGGGAACA GGTGTGACCT 240  
 35 CCTTGCTATA GTCACCAGAC ATATGAATGT AATTTATACA TTCAAAACTA GATAGTAAGT 300  
 AAAAGTGATT TTGCTTCGCA AAACATTTAT TTTGATTAA GTCTTCGATC GATTAGTATT 360  
 CGTCAGCTCC ACATGTCACC ATGCTTCCAC CTCGAACCTA T 401

## (2) INFORMATION FOR SEQ ID NO: 3732:

## (i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 397 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3732:

50 CATTATTAAC GGCTATGGTT TAACTGAAGC ACCTCTTGTA CTTGTTAATA CACCGGAAAA 60  
 TTCAAAACGT AAGCCAATGA GTATTGGTAA AGCAGTCATG TTCGTTGATG CACGTATCCT 120

AAATGTCACG CCAGGATATT GGAATAAACC AGCAGAGACT GCCAAAGCAT TTCATGGTCG 240  
 ATATTTATTA ACTGGTGACT TAGCGAGATG GACAACGATG GCGATATATT TATTATTGAC 300  
 5 CGCAAAaAAG AaTTAATCAT AACTGGTGgc GAAAATGTCT TACCATCCGa gTCGAAAtGC 360  
 TTaCtGaGCA TCCACTAGTA GACCGGTGTG TGGTCGT 397

## (2) INFORMATION FOR SEQ ID NO: 3733:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3733:

20 AAGTAACAAT CGTTCACCGT CGTGATGAGT TACGTGCACA GCGTATTTTA CAAGATAGAG 60  
 CATTCAAAAA TGATAAAATC GACTTTATTT GGAGTCATAC TTTGAAATCA ATTAATGAAA 120  
 AAGACGGCAA AGTGGGTCTT GTGACATTAA CGTCTACAAA AGATGGTTCA GAAGAAACAC 180  
 25 ACGAGGCTGA TGGTGTATTC ATCTATATTG GTATGAAACC ATTAACAGCG CCATTTAAAG 240  
 ACTTAGGTAT TACAAATGAT GTTGGTTATA TTGTAACAAA AGATGATATG ACAACATCAG 300  
 TACCAGGTAT TTTTGCAGCA GgGATGTTC GCGACAAAGG TTACGCCAAA TTGTCACTGC 360  
 30 CACGGCGATG GTAGTATGCC AGCGCAAGTG CCACGGAATG 400

## (2) INFORMATION FOR SEQ ID NO: 3734:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3734:

45 GCCGTTTACT GTGGCTTCGA TTCGTAGCTT CGCAGAAGCT AACCACTCCT CTTAACCTTC 60  
 CAGCACCGGG CAGGCGTCAG CCCTATACAT CACCTTACGG TTTAGCAGAG ACCTGTGTTT 120  
 TTGATAAACA GTCGCTTGGG CCTATTCACT GCGGCTCTTC TGGGCGTTAA CCCTAAAGAG 180  
 CACCCCTTCT CCCGAAGTTA CGGGGTCATT TTGCCGAGTT CCTTAACGAG AGTTCGCTCG 240  
 50 CTCACCTTAG AATTCTCATC TTGACTACCT GTGTGCGTTT GCGGTACGGG CACCTATTTT 300  
 CTATCTAGAG GCTTTTCTCG GCAGTGTGAA ATCAACGACT CGAAGACACA ATGTCTTCTC 360



TAGACGTGCA ATCCAATCGG CAACGCTTCG CCTAATCCTA ACTGGCGGTC CCCCCCnAT 480

(2) INFORMATION FOR SEQ ID NO: 3735:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3735:

CGATCCCTTC AGCCGGACTT GGGTATTCTT CCAAATTAT ATGGACCTTG CAGACTCGAA 60  
 CCTGCGACCG AACGGTTATG AGCCGTTAGC TCTAACCAAC TGAGCTAAAG GTCCTAAATA 120  
 TAATTTTACA ACTAATAAAT AGTGGCGGTG GAGGGGATCG AACCCCCGAC CTCACGGGTA 180  
 TGAACCGTAC GCTCTAGCCA GCTGAGCTAC ACCGCCTTAT ATAGTTTGTA AATAATATGG 240  
 TGGAGACTAG CGGGATCGAA CCGCTGGACC TCCTGCGTGC AAACAGnCGC TCTCCAGCT 300  
 GAGCTnAAGC CCCATAATA ATTACAGTAT ATCGGGAAGA CAGGATTCGA ACCTGCGACC 360  
 CCTTGGTCCC CAAACCAAGT GGTnTnACCA AGTTGAGCTA 400

(2) INFORMATION FOR SEQ ID NO: 3736:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3736:

TGAGCCCGAC GAGCTACCGA ACTGCTCCAT CCCGCGATAA TAAAAAATAA TGGCGGAGGA 60  
 AGAGGGATTG GAACCCCCGC GGCCCGTTAA GGCCCTGTCT GTTTTCAAGA CCGATCCCTT 120  
 CAGCCGGACT TGGGTATTCC TCCATTATTA TAGGTAAATC GCTATTAAAT ATAAAAATTAA 180  
 ATGGCGGTCT CGACGGGAAT CGAACCGCG ATCTCCTGCG TGACAGGCAG GCGTGTTAAC 240  
 CGCTACACTA CGAGACCATT AGTAAACGG AGGAAGAGGG ATTCGAACCC CCGCGAGCCG 300  
 TTAAGCCCCCT GTCGGTTTTT AAGACCGATT CCTTCAGCCG GACTTGGGTA nTcnTCCAAA 360  
 ATTATATGGA CCTTGCAGGA CTCGAAGTGC GAnCGAACGG 400

(2) INFORMATION FOR SEQ ID NO: 3737:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3737:

	TAATAATTAC AGTATATCGG GAAGACAGGA TTCGAACCTG CGACCCCTTG GTCCCAAACC	60
10	AAGTGCTCTA CCAAGCTGAG CTACTTCCCG TATAATTAAC GCGCCCGATA GGAGTCGAAC	120
	CCATAACCTC TTGATCCGTA GTCAAACGCT CTATCCAATT GAGCTACGGG CGCATATGTT	180
	TTTATTGAAA ATGGTGCCGA GGACCGGAAT CGAACCGGTA CGTGATCACT CACCGCAGGA	240
15	TTTTAAGTCC TGTGCGTCTG CCAGTTCCGC CACCCCGGCA CTATAAAAAT GGAGCAGAAG	300
	ACGGGATTCTG AACCCGCGAC CCCAACCTTG GCAAGTTGT ATTCTACCGC TGAACTACTT	360
20	CTGCATATGC GGGTGAAGGG AGTCGAACCC CCACGCCGTA	400

(2) INFORMATION FOR SEQ ID NO: 3738:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3738:

	AGAATGACGG GTTCGAACCG CCGACCCTCT GCTTGTAAGG CAGATGCTCT CCCAGCTGAG	60
	CTAATTCTCC GATTTAAAC TGCCTGGCAA CGTTCTACTC TAGCGGAAGT AATCGGAnCT	120
35	ACCATCGACG CTAAGGAGCT TAACTTCTGT GTTCGGCATG GGAACAGGTG TGACCTCCTT	180
	GCTATAGTCA CCAGACATAT GAATGTAATT TATACATTCA AACTAGATA GTAAGTAAAA	240
	GTGATTTTGC TTCGCAAACA TTTATTTTGA TTAAGTCTTC GATCGATTAG TATTCGTCAG	300
40	CTCCACATGT CACCATGCTT CCACCTCGAA CCTATTAACC TCATCATCTT TGAGGGATCT	360
	TATAACCGAA GTTGGGAAAT CTCATCTTGG AGGGGGGCTT	400

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(2) INFORMATION FOR SEQ ID NO: 3739:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3739:

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CACCACCCGA CATATTTTCC ACTTCCGAAC TTAATTGATA ATGTCCCAAA CCGACATCTT 120  
 TAATTAATTG CTnTGACGT TTTCTATCAA ATTTATCATT ACGTGCAAGT GATGGGAATA 180  
 5 TCATGTTATC TTCAATCGTT TCACCAAACA AGTCACTTTG CTGCATCAA TAACTGATTC 240  
 GTTGACGCAA TTCTTCCGGG TCATAATCAT TATAGGGTTT ACCTTTAAAA TAAAGTTCTC 300  
 CACTAGTTGG ACTAAACAAA TTACATATnT GCTTTTGAAA TGTACTTTTA CCACTACCTG 360  
 10 ATGGACCTAT AATGGCAATA CTCTCGCCTT TATCTACTTT 400

(2) INFORMATION FOR SEQ ID NO: 3740:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 413 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3740:

ATCGCTTGCT TCTTTCCTCT CCTTCGGCTC TCGCTTACTC ATTTAGCTCT ACTAAACTCG 60  
 25 TTGCGCTCTT TTCTCGTTTC GTCAGATTCA AACGTTTTCA CTTGCGCAAG CCATTTTTCT 120  
 TTGTGTTTAC TTTTATTTT GACGTTTTAG ACATAAAAAA AAGAGACCTT GCGGTCTCAA 180  
 TGCGGCTCAT CGCATCCaTT TTTGCGCTGG CAACGTTCTA CTCTAGCGGA AnTAATTGGC 240  
 30 TACCATCGAC GCTAAGAACC TTTCTTGACT TGTGACAATC GCTTGCTTCT TTCCTCTTCT 300  
 TCGGCTCTCG CTTACTCATT TAGCTCTACT AAACCTCGTG CGCTCTTTTC TCGTTTCGTC 360  
 35 AGATtCAAAC GTTTTCACTT CGCCAAGCCA tTTTTCTTG TGTTCGCTT TnA 413

(2) INFORMATION FOR SEQ ID NO: 3741:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3741:

CTTAGATGCT TTCAGCACTT ATCCCGTCCA CACATAGCTA CCCAGCTATG CCGTTGGCAC 60  
 GACAACTGGT ACACCAGAGG TATGTCCATC CCGGTCCTCT CGTACTAAGG ACAGCTCCTC 120  
 50 TCAAATTTCC TACGCCCACG ACGGATAGGG ACCGAACTGT CTCACGACGT TCTGAACCCA 180  
 GCTCGGTAC CGCTTTAATG GGCGAACAGC CCAACCCTTG GGACCGACTA CAGCCCCAGG 240

TAAGCTGTTA TCCCCGGGGT AGCTTTTATC CGTTGAGCGA TGGCCCTTCC ATGCGGAACC 360  
 ACCGGATCAN TAAGTCCGTC TnTCGACCCT GnTGGACTTG 400

(2) INFORMATION FOR SEQ ID NO: 3742:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3742:

GTTTTGAATG TATAAATTAC ATTCATATGT CTGGTGACTA TAGCAAGGAG GTCACACCTG 60  
 TTCCCATGCC GAACACAGAA GTTAAGCTCC TTAGCGTCGA TGGTAGTCGA ACTTACGTTT 120  
 CGCTAGAGTA GAACGTTGCC AGGCAGTTTT AAATCGGAGA ATTAGCTCAG CTGGGGAGAG 180  
 CATCTGCCTT ACAAGCAGAG GGTGCGCGGT TCGAACCCGT CATTCTCCAC CATTTATTCT 240  
 TACATATTGC CGGCCTAGCT CAATTGGTAG AGCAACTGGA CTTGTAATCA GTAGGTTGGG 300  
 GGTTCAGTC CTCTGGCCGG CACCATGGGA AGAGCCATTA GCTCAGTTGG TAGAGCATCT 360  
 GACTTTTAAA TCAGAGGGTT CAGAGGTTnC GAATCCGCTA 400

(2) INFORMATION FOR SEQ ID NO: 3743:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3743:

TCGCAATAAC CGCATCAAAT GTATTGCCTA AAAAGGCTGG ATTTTCCAAT GTGTCATCAT 60  
 TACGGATCTC GAAGTTCTCA TAACGCACAT CATGTAATAA CATATTCATG CGTGCTAAGT 120  
 TGTATGTAGT ATTGTTACGT TCTGTCCGA AATAACGATA CACTTGCGTT TCTTTACCAA 180  
 CACGTAACAA CAATGAACCG GAACCACATG TTGGGTCGTA CACGTGACGT AATTTATCTT 240  
 TACCGTCTGT GACAATCTTC GCCAGTATCT TAGATACTTG TTGTGGTGTA TAGAACTCGC 300  
 CTGCTTTTTT ACCCGCTGTC GCCGCAAAGC GCCCGATTAG GAATTCATAT GCATCACCTA 360  
 ACATATCAAT TTCCATGGTC ACTGTGAACG AATGGGTAAG 400

(2) INFORMATION FOR SEQ ID NO: 3744:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3744:

10 CTACTGATT A CAAGTCAGTT GCTCTACCAA TTGAGCTAGG CCGGCAATAT GTAAGAATAA 60  
 ATGGTGGAGA ATGACGGGTT CGAACCGCCG ACCCTCTGCT TGTAAGGCAG ATGCTCTCCC 120  
 AGCTGAGCTA ATTCTCCGAT TTAAACTGCT CTGGCAACGT TCTACTCTAG CGGAACGTAA 180  
 15 GTTCGACTAC CATCGACGCT AAGGAGCTTA ACTTCTGTGT TCGGCATGGG AACAGGTGTG 240  
 ACCTCCTTGC TATAGTCACC AGACATATGA ATGTAATTTA TACATTCAA ACTAGATAGT 300  
 AAGTAAAAGT GATTTGCTTC GCAAAACATT ATTTGATTAA GTCCTCGATC GATAGTATCG 360  
 20 TCAGCTCCAC ATGTCACCAT GCTTCCanCT CGnACCTATT 400

## (2) INFORMATION FOR SEQ ID NO: 3745:

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 386 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3745:

CATAAGTAAA CTCTGCTTTA AAATAATTTA ACTCATTGTC TGCTAAACGT TTTCTTTTAT 60  
 35 AAAAGATTTT AAACGCGTTA TTAATCTTGT GAGTGTTCTT TCGAACACTA GCGATTATTT 120  
 CTTATGAATT CAAGCTTATT TAAACTCTT TATTCACTCG GTTTTGCTTG GTAAAATCTA 180  
 TATTTTACTT ACTTATCTAG TTTTCAATGT ACAATTTCTT TTTAGTCAAG CGCTCGCATA 240  
 40 CTGCTTTATT nTCAAAAAAT CAAATGCTCA TTTACAAAAG TAAACTCCGC TTTAATTTTC 300  
 TTAATGCATT GTCTAACAAC CGCTTGCTTT AAAAAGAATA GATTGnCAAG CGCTCGCATA 360  
 AGCAATATCA CTTTAAACCAA AAAATA 386

45

## (2) INFORMATION FOR SEQ ID NO: 3746:

## (i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 677 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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AAGGTGAAAA GCACCCCGGA AGGATGTTGA AATAGAACCT GAAACCGTGT GCTTACAAGT 60  
 AGTCAGAGCC CGTTAATGGG TGATGGCGTG CCTTTTGTAG AATGAACCGG CGAGTTACGA 120  
 5 TTTGATGCAA GGTTAAGCAG TAAATGTGGA GCCGTAGCAk AACanGGTCT GAATAGGGCG 180  
 TTTAGTATTT GGTCTACCG AnaACCAGGT GATCTACCCT TGGTCAGGTT GAAGTTCAGG 240  
 10 TAACACTGAA TGGAGGACCG AACCGACTTA CGTTGAAAAG TGAGCGGATG AACTGAGGGT 300  
 AGCGGAGAAA TTCCAATCGA ACCTGGAGAT AGCTGGTTCT CTCCGAAATA GCTTTAGGGc 360  
 TAGCCTCAAG TGATGATTAT TGGAGGTAGA GCACTGTTTG GaCGAgGGGC CCCTCTCGGG 420  
 15 tTACCAATTc AGACAACTC CGAATGCCAA TTAATTTAAC TTGGGgAGTC aGAACATGGG 480  
 TGATAAGGTC CGTGTTGAA AGGGAAACAG CCCAGACCAC CAGCTAAGGT CCCAAAATAT 540  
 ATGTTAAGTG GAAAAGGATG TGGCGTTGCC AGACAACTGA GGATGTTGCC TTAGAAGCAG 600  
 20 CCATCATTTT AAAGAGTGGC TAATAGCTCA CTAGTCGAAG TGACACTGCG CCGAAAATGT 660  
 GACCGGGCnT AAACnAT 677

(2) INFORMATION FOR SEQ ID NO: 3747:

25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 417 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3747:

35 GTCCAATGAT TCATATGCTT TATTATCAGC GTATTGCCTT TGAATCGCAT GCACAAAATA 60  
 TGATGCTCAT TCATGAAAAT GGTGGCCTA CACGTATTGC CTTAAAAGAT TTCCATGATG 120  
 GTGTTGTTTT TAAGCGTGAC ATTTAAGTGA AGCTGCTTCA CACCTGACAT TAAAGCCAAT 180  
 40 GCCAGAAGCA CATAAAAAAG TGAATAGTAA TTCATTTATT GAAACAGATG ACGAACGTTT 240  
 AGTACGCGAC TTTTACATG ATGCATTTTT CTTTATTAAT ATCGCCGAAA TCATCTTATT 300  
 TATTGAAAAG CAATATGGTA TCGATGAGGA GCTGCAATGG cAATGGGkTa AAGGCATCAT 360  
 45 CGAGGCGTAT CCAGrAGcAT TTCCaGAGTT kGAATaACTA TCCAACCATT CGGTTTT 417

(2) INFORMATION FOR SEQ ID NO: 3748:

50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 55 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3748:

5 ATGCTCTCCC AGCTGAGCTA ATTCTCCGAT TTAAAACTGC CTGGCAACGT TCTACTCTAG 60  
 CGGAACGTAA GTTCGACTAC CATCGACGCT AAGGAGCTTA ACTTCTGTGT TCGGCATGGG 120  
 AACAGGTGTG ACCTCCTTGC TATAGTCACC AGACATATGA ATGTAATTTA TACATTCAAA 180  
 ACTAGATAGT AAGTAAAAGT GATTTTGCTT CGCAAACAT TTATTTTGAT TAAGTCTTCG 240  
 10 ATCGATTAGT ATTGCTCAGC TCCACATGTC ACCATGCTTC CACCTCGAAC CTATTAACCT 300  
 CATCATCTTT GAGGGATCTT ATAACCGAAG TTGGGAAATC TCATCTTGAG GGGGGCTTCA 360  
 TGCTTAGATG CTTTCAGCAC TTATCCCGTC CACACATAGC 400

## (2) INFORMATION FOR SEQ ID NO: 3749:

## (i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3749:

25 TCGGCTCTCG CTTACTCATT TAGCTCTACT AAACCTCGTTG CGCTCTTTTC TCGTTTCGTC 60  
 AGATTCAAAC GTTTTCACTT CGCCAAGCCA TTTTCTTTTG TGTTTACTTT TTATTTTGAC 120  
 30 GTTTTAGGCA TAAAAAAAAG AGACCTTGCG GTCTCAATGC GGCTCATCGC ATCCATTTTT 180  
 TGCCTGGCAA CGTTCTACTC TAGCGGAAGT AAGTTGGGCT ACCATCGTCG CTAAAGACCT 240  
 35 TTCTTGACTT GTGACAATCG CTTGCTTCTT TCCTCTCCTT CGGCTCTCGC TTAATCATTT 300  
 AGCTCTACTA AACTCGTTGC GCTCTTTTCT CGTTTCGTCA GATTCAAACG TTTTCACTTC 360  
 GCCAAGCCAT TTTTCTTTG TGTTACTTTT TTAATTTTGA 400

## (2) INFORMATION FOR SEQ ID NO: 3750:

## (i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3750:

50 ATAAAAAAA GAGACCTTGC GGTCTCAAAT GCGGCTCATC GCATCCATTT TTGCCTGGC 60  
 AACGTTCTAC TCTAGCGGAA CGTAAGTTGG CTACCATCGT CGCTAAAGAC CTTTCTTGAC 120

TAAACTCGTT GCGCTCTTTT CTCGTTTCGT CAGATTCAAA CGTTTTCACT TCGCCAAGCC 240  
 ATTTTTCTTT GTGTTTACTT TTTATTTTGA CGTTTTAGAC ATAAAAAAAA GAGACCTTGC 300  
 5 GGTCTCAATG CCGCTCATCG CATCCATTTT TTGCCTGGGC AACGTTCTAC TCTAGCGGAA 360  
 nTAAnTTGGG CTACCATCGA CGCTAAGAAC CTTTCTTGGA 400

## (2) INFORMATION FOR SEQ ID NO: 3751:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3751:

CACTCACCGC AGATnTTTAA GTCCTGTGCG TCTGCCAGTT CCGCCACCCC GGCCTATAA 60  
 AAATGGAGCA GAAGACGGGA TTCGAACCCG CGACCCCAAC CTTGGCAAGG TTGTATTCTA 120  
 CCGCTGAACT ACTTCTGCAT ATGCGGGTGA AGGGAGTCGA ACCCCCACGC CGTAAGCTna 180  
 25 GnATTTCCTAA GTCTAGTGCG TCTGCCAATT CCGCCACACC CGCAAATGGT GAGCCATAGA 240  
 GGATTGGAAC CTCTGGACCC TCTGATTAAA AGTCAGATGC TCTACCAACT GGAGCTAATG 300  
 30 GCTCTTTCCA TGGTGCCCGG CCAGAGGACT TGGAACCCCC AACCTACTGA TTACAAGTCA 360  
 GTTGCTCTAA CCAATTGAGC TAAGCCGGGC AATATGTTAn 400

## (2) INFORMATION FOR SEQ ID NO: 3752:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3752:

TTAnAnAnCC GCGACATTAT AGAGCCAATC ACTAGCCTAT CTCAGAATCA CCAACGAATC 60  
 45 CTTCAATTATT AAGGAATCTA GGCATCTTTA CGGCGTGGTT CTAATCGCAT CTTTTTCAAT 120  
 CTAAGTGCGT TTGTGACAAC ACTTACTGAA CTTAGTGCCA TTGCAGCACC AGCAACCCAT 180  
 50 GCGCAAGTA AGCCCAATGC AGCTATAGGG ATACCGGCAA TATTATAGCC GAATGCCCAA 240  
 AATAGATTTT GACGAATATT ACGAATGGTT GCTTTACTTG cATAAATGGC TTTAGGaATA 300  
 AGCATCAAGT cGCCACCAAG AATAGTAATA TCAGCTGCTT CAATGGGCAA CTTCTGTTAC 360  
 55



## (2) INFORMATION FOR SEQ ID NO: 3753:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3753:

CCTTGCGGTC TCAATGGCGG CTCATCGCAT CCATTTTGTG CCTGGCAACG TTCTACTCTA 60  
 GCGGAACGTA AGTTGGCTAC CATCGTCGCT AAAGACCTTT CTGACTTGT GACAATCGCT 120  
 TGCTTCTTTC CTCTCCTTCG GCTCTCGCTT ACTCATTTAG CTCTACTAAA CTCGTTGCGC 180  
 TCTTTTCTCG TTTCGTCAGA TTCAAACGTT TTCACTTCGC CAAGCCATTT TTCTTTGTGT 240  
 TTACTTTTTTA TTTTGACGTT TTAGACATAA AAAAAAGAGA CCTTGCGGTC TCAATGCGGC 300  
 TCATCGCATC CATTTTTTGC CTGGCAACGT TCTACTCTAG CGGAACGTAA GTGGCTACCA 360  
 TCGACGCTAA GAACCTTTCT TGA CTGGTGA CAACGCTTG 400

## (2) INFORMATION FOR SEQ ID NO: 3754:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3754:

CTGAGCTAAG CCCCCAAATA GGTATTAAAT TAATGGTGGG CCTAAGTGA CTCGnACCAC 60  
 CGACCTCAGC CTTATCAGGC GTGCGCTCTA ACCAGCTGAG CTATAGGCCC ATTAATTTGA 120  
 ATGAnCAAAC ATTCAAACT GAATACAATA TGTCACGTTA TTCCGCATCT TCTGAAGAAG 180  
 ATGTTCCGAA TATATCCTTA GAAAGGAnGT GATCCAGCCG CACCTTCCGA TACGGCTACC 240  
 TTGTTACGAC TTCACCCCAA TCATTTGTCC CACCTTCGAC GGCTAGCTCC TAAAAGGTTA 300  
 CTCCACCGGC TTCGGGTGTT ACAAACTCTC GTGGTGTGAC GGGCGGTGTG TACAAAACCC 360  
 GGGAACGTAT TCACCGTAGC A 381

## (2) INFORMATION FOR SEQ ID NO: 3755:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3755:

5 AGCTCCCCAA AGCATATCGT CGTTAGTAAC GTCCTTCATC GGCTTCTAGT GCCAAGGCAT 60  
 CCCC GTGCGC CCTTAATAAC TTAATCTATG TTTCCACCAT TTTTATAAGT CAAACGTTAA 120  
 CATGAAGTTA CGTTCMTTA TAAAAAGATT TAAACGCGTT ATTAATCTTG TGAGTGTCT 180  
 10 TTCGAACATA GCGGATTATT TCTTATGAAT TCAAGCTTAT TTAAACTCT TTATTCATC 240  
 GGTTTTGCTT GTAAAAACn ATATTTTACT TACTTATCTA GTTTTCAATG TACAATTTCT 300  
 TTTTAGTCAA GCGCTCGCAT ACTGCTTTAT TTTCCATAAG CAATAnCACT TTAACCAAAA 360  
 15 AATATTTGGA ATGTnAAAT AAACATnCAA AACTGAATAC 400

## (2) INFORMATION FOR SEQ ID NO: 3756:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3756:

CTACTCACAC CGGCATTCTC ACTTCTAAGC GCTCCACATG TCCTTACGAT CATGCTTCAA 60  
 30 CGCCCTTAGA ACGCTCTCCT ACCATTGTCC AAAGGCATGC GCACAGCTTC GGTAATATGT 120  
 TTAGCCCCGG TACATTTTCG GCGCATGTCA CTCGACTAGT GAGCTATTAC GCACTCTTTA 180  
 AATGGATGGC TGCTTCTAAG CCAACATCCT AGTTGTCTGG GCAACGCCAC ATCCTTTTCC 240  
 35 ACTTAACATA TATTTTGGGA CCTTAGCTGG TGGTCTGGGC TGTTTCCGGn GGGGnACACG 300  
 GACCTTATCA CCCATGTTCT GACTCCCAAG TTAAATTAAT TGGCATTCCG ATTTGTCTGA 360  
 40 ATCGGTAACC CGAGAGGGCC CnTCGTCCAA ACAGTGCTCT 400

## (2) INFORMATION FOR SEQ ID NO: 3757:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 458 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3757:

GGCAGATGCT CTCCCAGCTG AGCTAATTCT CCGATTTAAA ACTGCCTGGC AACGTTCTAC 60

ATGGGAACAG GTGTGACCTC CTTGCTATAG TCACCAGACA TATGAATGTA ATTTATACAT 180  
 TCAAAACTAG ATAGTAAGTA AAAGTGATTT TGCTTCGCAA AACATTTATT TTGATTAGT 240  
 5 CTTGATCGA TTAGTATTCG TCAGCTCCAC ATGTCACCAT GCTTCCACCT CGAACCTATT 300  
 AACCTCATCA TCTTTGAGGG aTCTTATAAC CGAaRtttGG GAAtCTCATC TTGAGGGGGG 360  
 gCTCATGctT AGATGCTTcA GCACTTATCC CGTCCACACA TAGCTAnCCA GCTATGCCGT 420  
 10 TnGCACGACA ACTGGTACAC CAGAnGTATG TCCATCCC 458

## (2) INFORMATION FOR SEQ ID NO: 3758:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3758:

AGCGCTCGCA TACTGCTTTA TTTTCAAAAA ATCAAATGCT CATTTACAAA AGTAAACTCC 60  
 25 GCTTTAATTT TTCTTAATGC ATTGTCTAAC AACCGCTTTC TTTAAAAAGA ATAGATTGTC 120  
 AAGCGCTCGC ATAAGCAATA TCACTTTAAC CAAAAATAT TTGAATGTTA AATAACATT 180  
 30 CAAAACTGAA TACAATATGT CACGTTATTC CGCATCTTCT GAAGAAGATG TTCCGAATAT 240  
 ATCCTTAGAA AGGAGGTGAT CCAGCCGCAC CTTCCGATAC GGCTACCTTG TTACGACTTC 300  
 ACCCCAATCA TTTGTCCAC CTTGACGGC TAGCTCCTAA AAGGTTACTC CACCGGCTTC 360  
 35 GGGTGTTACA AACTCTCGTG GTGTGACGGG CGGTGTGTAC 400

## (2) INFORMATION FOR SEQ ID NO: 3759:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3759:

GACTTGGGTA TTCCTCCAAA ATTATATGGA CTTGCAGGA CTCGAACCTG CGACCGAACC 60  
 50 GTTATGAGCC GTTAGCTCTA ACCAACTGAG CTAAAGGTCC TAAATATAAT TTTACAACTA 120  
 ATAAATAGTG GCGGTGGAGG GGATCGAACC CCCGACCTCA CGGGTATGAA CCGTACGCTC 180  
 TAGCCAGCTG AGCTACACCG CCTTATATAG TTTGTAAATA ATATGGTGA GACTAGCGGG 240

TAATAATTAC AGTATATCGG GAAGACAGGA TTCGAACCTG CGACCCCTTG GTCCCAAACC 360  
AAGTGCTCTA CCAAGCTGAA GCTACTTTCC CGTATAATTA 400

5 (2) INFORMATION FOR SEQ ID NO: 3760:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
10 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3760:

CACTTAATGC CCGTACCACA CATAGCTACC CAGCTATGCC GTTGGCACGA CAACTGGTAC 60  
ACCAGAGGTA TGTCCATCCC GGTCTCTCG TACTAAGGAC AGCTCCTCTC AAATTTCTTA 120  
20 CGCCCACGAC GGATAGGGAC CGAACTGTCT CACGACGTTT TGAACCCAGC TCGCGTACCG 180  
CTTTAATGGG CGAACAGCAA ncccttggga cggactacag ccccaggatg cgatgagccg 240  
ACATCGAGGT GCCAAACCTC CCCGTCGATG TGAAGTCTTG GGGGAGATAA GCCTGTTATC 300  
25 CCCGGGGTAG CTTTTATnCG TTGAGCGATG GncCTTnCAT GCGGAACACC GGATCACTAA 360  
GTCCGTCTTT CGACCCTGCT CGACTTGTAG GTCTCGCAGT 400

(2) INFORMATION FOR SEQ ID NO: 3761:

30 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 623 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3761:

40 TATGTATTTT ATAATGTACA GCTCGTTGAn TChTATTTTT CTTATATTA AGTGCCATTA 60  
ATACAAAACC TAGCTCTCGT TTAACCTTAT TTATTCCTCG AACTGACATT CGAGTGAACC 120  
CAAAATAGCC TTCATAAATC CAAAACAGG CTCTACATCA ATTTTTCTTT GACTATAGAT 180  
45 TTTTTTCGTT TCTGGTTCAG AAAGCTTTTG ATTAATTTGG ACTTTAAAGT ATTCCCAATT 240  
ATAATTCTTC ATGATTTTCT TATTGGATTT CGAATTTGGT TTCATGCATT GATGTCTCAA 300  
AGAACATGAT GAACAGTCAT CACATTCATA TAGTTTGAAG TCTCGTTTAA AACCATATCT 360  
50 ATCATTACGG TATGCATATC TTTTAAACC TATTCTTTTG TTATTAGGAC ATATAAATTC 420  
ATCATTAAAGT TCGTCATATT TCCAATTTTA AGTGTGAAA ATGTCACCTT TAACTTTCT 480

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AATAGCCATA TAGTTTTGCT CACTACCATA ACCGGCATCA GCTACAAATA TACTCCGGTA 600  
 AATAACCGAG GGATTGTTGG AAT 623

5 (2) INFORMATION FOR SEQ ID NO: 3762:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 718 base pairs  
 (B) TYPE: nucleic acid  
 10 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3762:

ATTTTAAAA TAGTTCTTTA AATTATATAC CCACCACATT TGGTGGAGAA CCTAAAAAAA 60  
 AGCACTTCCC AAAAATGGAA AGTGCAAGTA GTGAGCCATA GAGGATTCTGA ACCTCTGACC 120  
 20 CTCTGATTAA AAGTCAGATG CTCTACCAAC TGAGCTAATG GCTCTAATGG CTGGGCCTAG 180  
 CTGGATTCTGA ACCAACGAGT GACGGAGTCA AAGTCCGTTG CCTTACCGCT TGGCTATAGC 240  
 CCAATATATA GATGGTGGAG GGGGGCAGAT TCGAACTGCC GAACCCGAAG GAGCGGATTT 300  
 25 ACAGTCCGCC GCGTTTAGCC ACTTCGCTAC CCCTCCAGCT TATTCATATA ATTTAATAAT 360  
 CAAAATGGTG GaGAATGACG GGTTGGAACC GCCGACCCTC TGCTTGTAAG GCAGATGCTC 420  
 TCCCAGCTGA GCTAATTCTC CAAAATAATG ACTCCTACGG GACTCGAACC CGTGTTACCG 480  
 30 CCGTGAAAGG GCGGTGTCTT AACCCTTGA CCAAGGAGCC ATGGCTCCAC AGGTAGGACT 540  
 CGAACCTTAC GACCGATCGG TTTAACAGCC GATAGCTCTT ACCACTGGAG CTA CTGTGGG 600  
 35 ATTAATATTA TGCTGGGCA ACGTTCTTAC TCTTAGCGGA ACGTTAAGTT CCGACTTACC 660  
 ATCCGACGCT AAGGAGCTTT AACTTTCTnG TGTTCCGGC ATGGGGGGAA CAGGTGGT 718

(2) INFORMATION FOR SEQ ID NO: 3763:

- 40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3763:

50 TnCACTCACC GCAGATTTTT AAGTCCTGTG CGTCTGCCAG TTCCGCCACC CCGGCACTAT 60  
 AAAAATGGAG CAGAAGACGG GATTGGAACC CGCGACCCCA ACCTTGCAA GGTGTATTC 120  
 TACCGCTGAA CTA CTCTGTC ATATGCGGGT GAAGGGAGTC GAACCCCCAC GCCGTAAGCT 180

55

AGGATTCGAA CCTCTGGACC CTCTGATTAA AAGTCAGATG CTCTACCAAC TGGAGCTAAT 300  
 GGCTCTTCCA TGGTGCCGGC CAGAGGACTT GGAACCCCCA ACCTACTGGA TTTACAAGTT 360  
 5 CAATTGCTCT AnCAATTTGA GCTAAGGCCG GGCAATATGT 400

## (2) INFORMATION FOR SEQ ID NO: 3764:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 610 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3764:

TTAAAGTATT CCCAATTATA ATTCTTCATG ATTTTCTTAT TGGATTTCTGA ATTTGGTTTC 60  
 20 ATGCATTGAT GTCTCAAAGA ACATGATGAA CAGTCATCAC ATTCATATAG TTTGAAGTCT 120  
 CGTTTAAAC CATATCTATC ATTACGGTAT GCATATCTTT TAAAACCTAT TCTTTTGTTA 180  
 TTAGGACATA TAAATTCATT ATTAAGTTCG TCATATTTCC AATTTTGAGT GTTGAAAATG 240  
 25 CCACTTTTAA ACTTTCTAGT TTTATCTTTA ATAAACATGC CATACGTAAT AAGTGGCGTT 300  
 TTATTAAAT CATCTATAAT AGCCATATAG TTTTGCTCAC TACCATAACC TGCATCAGCT 360  
 ACAATATACT CTGGTAAATA ACCGAAGGAT TTTGAATCAT TGTAAAAAT GGGATTAATG 420  
 30 TTCTAGTATC TGTTGGGTTT TGAAATAGGT CATAGGATAA AACAAATTG GAATTTGTCT 480  
 CTATTTGgTA AATTGGTATC CTGGCTTAAG TTGGGCCATT TTTCCATATG GGCCTTCCTT 540  
 35 CCATTCTCCA TAAAAGTTGG CATCATGGAT CCAGATCCnG TTTTAGGAAA ACCTAATTCC 600  
 AACCTTTAAG 610

## (2) INFORMATION FOR SEQ ID NO: 3765:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3765:

CTTCTGGTG CTGCATATCC CCTACAATAA TTAACCTTT TTTCTTATTT AAAATGTGTC 60  
 50 TTAATGCCGA TGCATCTATA CTTTTTTGAT AGTGCGGTAA AATCTTCATC TCAGAnGTTA 120  
 ACAATTCTGT TGCATTCAAA TCAGGTGTTA ACGGATCTCT AAATGGCAAG TTAATGAA 180

CACAATGGTC TCTTTACTAT CATCCGCAAT AGGCATATCG AACTCATAnC TTACATAATT 300  
 ATTAAACATA TTTACTTGAT TAATCGCTTG TGGTGCGCCT ACAnTTCTTA ATTCAGCGGA 360  
 5 CGGTCACTTG TTAAACGGT TTAAGGTATT CTACTAATTn 400

## (2) INFORMATION FOR SEQ ID NO: 3766:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 451 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3766:

CnTTTAACCT TTTTAAGGAA TCCTGCTAAT GCGGGTTTTG GCATTTTCGA nTnTTTrGTA 60  
 20 tCTCACGCAA tCTTGTTGGT CATTcAGTTC GTATATGGCA TCCATTAAAG CGCGAAGATC 120  
 AAATGGACTA TTGATGACTT CTGGAATACC ACGATCTATA TTTAGTAATT GATAAACAGC 180  
 TTCCATGGCA GTACGAACCG AATATTCTGT TGTAAATACA GTGTCTCGCT CTGTTTCTGC 240  
 25 AAAGTTACCA ATAAATGCTA AGTTCTGAGA TTGATGCGGG ACGACTAAAG GTCTGTGCGC 300  
 GATAGCACGC GTCATGAAAT AAGATGTGAT ATATGGCATA TAAACAGGgA ATCGTATTAG 360  
 ATGCATGTnT TGCTAAGTCT TCAATTTTGG TCAGTTGATA CACCTAAGTG GATACAGCCA 420  
 30 TTCTTGGCAT ATTTcATTAC CACTACATnC T 451

## (2) INFORMATION FOR SEQ ID NO: 3767:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3767:

ACACGTGAAC GTCTTCAAAT GGAAGTACGT GACGTTCACT ACTCTCACTA TGGCCGTATG 60  
 45 TGTCCAATTG AAACACCTGA GGGACCAAAC ATTGGATTGA TTAACTCATT ATCAAGTTAT 120  
 GCACGTGTAA ATGAATTCGG CTTTATTGAA ACACCATATC GTAAAGTTGA TTTAGATACA 180  
 CATGCTATCA CTGATCAAAT TGAATTTTA ACAGCTGACG AAGAAGATAG CTATGTTGTA 240  
 50 GCACAAGCAA ACTCTAAATT AGATGAAAAT GGTGTTTTCA TGGATGATGA AGTTGTATGT 300  
 CGTTTCCGTG GTAACAATAC AGTTATGGCT AAAGAAAAA TGGATTATAT GGATGTATCG 360

## (2) INFORMATION FOR SEQ ID NO: 3768:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3768:

CCTACGACCG ATCGGTTAAC AGCCGATAGC TCTACCACTG AGCTACTGTG GATTAATATT 60  
 ATGCCTGGCA ACGTTCTACT CTAGCGGAAn TAAGTTCGTA CTACCATCGA CGCTAAGGAG 120  
 CTTAACTTCT GTGTTGGCA TGGGAACAGG TGTGACCTCC TTGCTATAGT CACCAGACAT 180  
 ATGAATGTAA TTTATACATT CAAAAGTAGA TAGTAAGTAA AAGTGATTTT GCTTCGCAAA 240  
 ACATTTATTT TGATTAAGTC TTCGATCGAT TAGTATTCGT CnGCTCCACA TGTCACCATG 300  
 CTTCCACCTC GAACCTATTA ACCTCATCAT CTTTGAGGGA TCTTATAACC GAAGTTGGGG 360  
 AAATCTCATC CTGnAGGGGG CTTCATGCTT AGATGCTTTC 400

## (2) INFORMATION FOR SEQ ID NO: 3769:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3769:

CTTGACCGAA GTTCTTACCT ACATCACCTA AATTAATGAC ATGTCCACCA GTCATATACT 60  
 CTAATCCATG GTCGCCGATA CTTCAACGA CAACATCTAC ACCACTATTT CTAATACAGA 120  
 ATCTTTCTnc TGCACTACCG TTAATAAATG CCTTACCACT TGTCGCACCA TAGAATGAGA 180  
 CGTTACCAGC AATAATTTCA TTTTGTGCTT CTTCAAAGG TGCTTTGACA ATGACCGTAC 240  
 CACCAGATAA TCCTTTACCA ACATAGTCAT TCGCATCTCC AGTATGATGA ATCATTAAAGC 300  
 CTTTCGGTGC ATATGCTGCA GGACTTTGGA CCAGCATGAC CATTCGTATA AACATTAATT 360  
 GTATTTTCAG GGAGGTCCTG CTTCTCCATA TTGTTTCGGA 400

## (2) INFORMATION FOR SEQ ID NO: 3770:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3770:

5 CATTACGTAA TAAAAGATA GTCATTAAGA GAGGnTGATA ACCATGCAAG AAGCATACAT 60  
 TGTAGCTTAT GGGCGTTCAG CGCAGCGAAA CAAAGCAAGG CGCATTATTC CACGAAAGAC 120  
 CTGATGATGT CGCAGCCAAA GTATTACAAG GCGTATTGAA ACGTATTGAC GGAAAATTCA 180  
 10 ATAAGAATAT GATTGAAGAT GTCATTGTTG GTACGGCTTT TCCAGAAGGA TTACAAGGCC 240  
 AAAACATTGC ACGAACGATT GCATTGCGTG CGGGATTATC TGACACGGTA CCGGTCAAAC 300  
 AGTGAATCG CTACTGCTCA TCCAGGnTTT ACAAACCATT CGCGATTGCA GGCCAATCAA 360  
 15 ATTATGGCnG GTCCAAGGAG ATATACTTGT TAGCTGGTGG 400

## (2) INFORMATION FOR SEQ ID NO: 3771:

20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3771:

ACTCTCTTGC AnTAAGGGCA GGAATGACC GATGGGATTA AAAGATCAAG CTGTTACCTG 60  
 30 GGAAGGTAT TTTCATCAAT TTCCAGAACT ATCCGATAAA GAATTTAAGA CTACACAAAA 120  
 AATTAAAGAT ATTTTAACAG AACATCATAT TAGAATATTA GACTTACCAC TTGCGACTGG 180  
 GCTTGTGCT GAAGTGGGAC AAGGTCTGAG TTGTATAGCT GTTCGGGCTG ACATTGATGC 240  
 35 TTTACCGATT CAAGAGCTTG TTGAACAGGA TTTTAAATCT GAAAATGAAG GTGTTATGCA 300  
 TGCGTGTGGT CATGATATTC ACATGGCTAG nATTTTGGCT ACAGCTGGTA AAATTAAAAG 360  
 40 AGATTGAGGG CACTCTTACT GGGCGTGTTA AATCCATTG 400

## (2) INFORMATION FOR SEQ ID NO: 3772:

45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3772:

50 TTTATTTTGA CGTTTTAGAC ATAAAAAAA GAGACCTTGC .GGTCTCAATG CGGCTCATCG 60

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GCTAAGAACC TTTCTTGACT TGTGACAATC GCTTGCTTCT TTCCTCTTCT TCGGCTCTCG 180  
 CTTACTCATT TAGCTCTACT AAACTCGTTG CGCTCTTTTC TCGTTTCGTC AGATTCAAAC 240  
 5 GTTTTCACTT CGCCAAGCCA TTTTCTTTG TGTGTGCTTT TTATTTTGAC GTTTTAGACA 300  
 TAAAAAAAG AGACCTTGCG GTCTCAATGC GGCTCATCGC ATCCATTTTT TGCCTGGGCA 360  
 ACGTTCTACT CTAGCGGGAA CGGTAAGTTC GGACTTACCA 400

(2) INFORMATION FOR SEQ ID NO: 3773:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3773:

TTGATATTCC TGTACCACCT ATAATCGTTT TAATCGATGG GGGGACGCAT AGGnATAGGC 60  
 GACGTGCGAT TGGATTGCAC GTCTAAGCAG TAAGGCTGAG TATTAGGCAA ATCCGGTACT 120  
 25 CGTTAAGGCT GAGCTGTGAT GGGGAGAAGA CATTGTGTCT TCGAGTCGTT GATTTACAC 180  
 TGCCGAGAAA AGCCTCTAGA TAGAAAATAG GTGCCCGTAC CGCAAACCGA CACAGGTAGT 240  
 CAAGATGAGA ATTCTAAGGT GAGCGAGCGA ACTCTCGTTA AGGAACTCGG CAAAATGACC 300  
 30 CCGTAACTTC GGGAGAAGGG TGCTCTTTAA GGTTAACGCC CAGAAGAGCC GCATGGAATA 360  
 GGCCCAACGA nGTTTATTCA AAAACACAGT CTCTGCTAAA 400

(2) INFORMATION FOR SEQ ID NO: 3774:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3774:

TACTTAGACA ATCGAAAGTG TACATTATTA AATTATCATT TCCAGTTCTA CTCTAGCGGA 60  
 ACGTAAGTTG GCTACCATCC TCGCTAAGAA CCTTCTTGA CTTGTGACAA TCGCTTGCTT 120  
 50 CTTTCCTCTC CTTGGGCTCT CACTTACTCA TTTAGCTCTA CTAAACTCGT TCGGTTCTTT 180  
 TCTCGTTTCG TCAGATTCAA ACGTTTTTAC TTCGCCAAGC CATTTTTCTT TGTGTTTGCT 240  
 TTTTATTTTG ACGTTTTAGA CATAAAAAAA AGAGACCTTG CGGTCTCAAA TGCGGCTCAT 300

GACGCTAAGG AGCTTAACT TCTGTGTTTC GGCATGGGGA

400

## (2) INFORMATION FOR SEQ ID NO: 3775:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3775:

CGGTTTATCA AGAATGGAAA GAGTTGTACG TGAAAGAATG TCAATTCAAG ATACTGAGTC 60  
 TATCACACCT CAACAATTAA TTAATATTCG ACCTGTTATT GCATCTATTA AAGAATTCTT 120  
 TGGTAGCTCT CAATTATCAC AATTCATGGA CCAAGCAAAC CCATTAGCTG AGTTAACGCA 180  
 TAAACGTCGT CTATCAGCAT TAGGACCTGG TGGTTTAAACA CGTGAACGGC TCAAATGGAA 240  
 GTACGTGACG TTCACTACTC TCACTATGGC CGGTGTGTCC AATTGAAACA CCTGAGGGAC 300  
 CAAACATTGG ATTGATTAAAC TCATTATCAG TTATGCACGT GTAAATGGAA TTCGGCTTTA 360  
 TTGAAACACC ATATCGTAAA AGTTGATTG GntACACAGC 400

## (2) INFORMATION FOR SEQ ID NO: 3776:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3776:

AGCTTACTTA CAGCTCCCCA AAGCATATCG TCGTTAGTAA CGTCCTTCAT CGGCTTCTAG 60  
 TGCCAAGGCA TCCACCGTGC GCCCTTAATA ACTTAATCTA TGTTTCCACC ATTTTATAAA 120  
 GTCAAACGCT CACATACGGC TTCGTTTTCA TTATTTTAAA TGCTCATTTA CATAAGTAAA 180  
 CTCTGCTTTA AAATAATTTA ACTCATTGTC TGCTAAACGT TTTCTTTTAT AAAAAGATT 240  
 AAACGCGTTA TTAATCTTGT GAGTGTCTT TCGAAGCTAG GCGATTATTT CTTATGGAAT 300  
 TCAAGCTTAT TTAAACTCT TTATTCATC GGTTTTGCCT GGGTAAAATC TAAATTTTAC 360  
 TTACTATCT AGGTTTTCAA TGTACAAATA ATGGTGGGGC 400

## (2) INFORMATION FOR SEQ ID NO: 3777:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3777:

AATTATAAAA TTAAATGGCG GTCTCGACGG GAATCGAACC CGCGATCTCC TCGTGACAG	60
GCAGGCGTGT TAACCTCTAC ACTACGAGAC CATTAGTAAA ACGGAGGAAG AGGGATTCTGA	120
ACCCCGCGA GCCGTTAAGC CCCTGTCGGT TTTCAAGACC GATCCCTTCA GCCGGACTTG	180
GGTATTCCTC CAAAATTATA TGGACCTTGC AGGACTCGAA CCTGCGACCG AACGGTTATG	240
AGCCGTTAGC TCTAACCAAC TGAGCTAAAG GTCCTAAATA TAATTTTACA ACTAATAAAT	300
AGTGGCGGTG GAGGGGATCG AACCCCGAC CTCACGGGTA TGAACCGTAC GCTCTAGCCA	360
GCTGAGCTAC ACCGCCTTAT ATAGTTTGTA AATAATATGG	400

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(2) INFORMATION FOR SEQ ID NO: 3778:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3778:

CAAATCCTGC ACCATCAGAA AGTGGGGCAG ATGTTCTGTC AGTCATAGTG CCGTCAGCTT	60
TAAATACTGT ACGTAATTTG GCTAATGCCT CCATCGTGGT GTCAGGGCGT ATAAATTCAT	120
CTTGGTCAAA GATATTTGTG TGTACTTTTG GTCCTGCGTT TGTATATTCA ACTGAGTTTA	180
CTTGTATTGG AATAATTTCA TCTTTGAACC GACCATCACG TTGTGCGTCA TAGGCACGTT	240
GaTGACTTCT GACAGCATAA GCATCTTGaT CTTGCGGTGA TACGTCAAAT TGGGATGCTA	300
CATTTTtCAG CAGTTAAACC CATAGGATAT GACGCACCTA TATCATCaA TTGTAAGGTT	360
GGATTGTTTG TGGGCTTCGT TnGCCACCnn TTGGTACGGC	400

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(2) INFORMATION FOR SEQ ID NO: 3779:

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(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3779:

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CAATCTAAAT CGTTCAAATT TGGCACAACG ACAAATAAGG CTTCAACACG AATATATTCT 120  
 CTCGGTTGAA ACCTTACTTA TTCATTTTATT TTTTATAAAT TAGTGACATA AACTGTATT 180  
 5 AGCATCTGCA CGATCGGTTG AAATATATGT TACATTTTCT TGCTGCTTAA TAAATGCATC 240  
 ATAGTAATCA TATTGCGACG AATGATATGT GCCATTCGAT GTATCATTG GGTTTAGCAA 300  
 ACAGCCATAA CCTTCGTCAT ATAAATGTTT ACnGAGCATA AGGGGCGTCA TGTTTTAGAA 360  
 10 CCACCTTACC TACATAAAAT TnGCCTCCAT AGGGATCATA 400

## (2) INFORMATION FOR SEQ ID NO: 3780:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3780:

ATGGnCGGTC TCGACGGGAA TCGCAACCCG CGATCTCCTG CGTGACACn CAGGCGTGTT 60  
 25 AACCGCTACA CTACGAGACC ATTAGTAAAA CGGAGGAAGA GGGATTCGAA CCCCCGCGAG 120  
 CCGTTAAGCC CCTGTCGGTT TTCAAGACCG ATCCCTTCAG CCGGACTTGG GTATTCCTCC 180  
 AAAATTATAT GGACCTTGCA GGACTCGAAC CTGCGACCGA ACGGTTATGA GCCGTTAGCT 240  
 30 CTAACCAACT GAGCTAAAGG TCCTAAATAT AATTTTACAA CTAATAAATA GTGGCGGTGG 300  
 AGGGGATCGA ACCCCCGACC TCACGGGTAT GAACCGTACG CTCTAGCCAG CTGAGCTACA 360  
 35 CCGCCTTATA TAGTTTGTAA ATAATATGGT GGAGACTAGC 400

## (2) INFORMATION FOR SEQ ID NO: 3781:

40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3781:

AACCACATCT TTATCAAGTT TCATATTCGG AATACCATAC ATTAATAAAC CGCCTGATTC 60  
 TCTAGCACGT TCATAAATAG TTAAGTTCTT CAGCAGCAGC 120  
 50 TAATCCTGCT GGACCGCTTC CAACGATTGC CACTTTTCA TCTCTACGGC GACTCGGAAC 180  
 TTTCGGCGCT ACCCAACCAT TTTCAAAGC TTCATCAATA ATTGTGCGTT CAATACCTTT 240

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TACACGCCCT GTAAAGTCAG GAAAGTTATT TGTTTCGCTT AAGCGTCATA AGCAGTTTAA 360  
 AAATCTTGAT GATACACCAA GTCGTCCANT CAGGATGGAG 400

(2) INFORMATION FOR SEQ ID NO: 3782:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3782:

ACATGATGCG TGTGGTATTG GTTTTTATGC GAATATGGAT AATAAAAGGT CTCACGACAT 60  
 CATTGATAAA TCGCTTGAAA TGTTGCGACG CTTAGATCAC AGGGGCGGGG TCGGCGCAGA 120  
 TGGCATCACT GGTGATGGCG CAGGTATTAT GACTGAAATA CCTTTTGCAT TTTTCAAACA 180  
 ACATGTAACG GACTTTGATA TCCCAGGTGA AGGTGAATAT GCCGTGGGGT TATTTTTTTC 240  
 CAAAGAACGC ATTTTAGGTT CTGAACATGA AGTAGTTTTT AAAAAATATT TTGGAAGGCG 300  
 AnGGGTTATC AATTCTTGGT TAACGTAATG TACCAGTTAA TAAAAGATGC CATTGCCTAA 360  
 ACCATGTAGC AGATACGATG GCCAGTCATT CCACCAAGTG 400

(2) INFORMATION FOR SEQ ID NO: 3783:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3783:

AATCGGGTGA TGTTGGACGA TGATACGCAG GGAACGTTGC GTTATTCGTA TATGAAATAT 60  
 TGGATAACTG TTTTAACAAT GATGGTAGAG ATATTTTCATC ATTTGTAACA TCGTCAATTT 120  
 TGATATTGTG ATGATTTAAC ATAACGACAT CATCGATATT GAATTGGTAT GAAAAACCTG 180  
 CTGTTGCTGA ATCTGTTAAT TTGGCTCCAA TATTTAAAAT TAAATCGCTG TTGTCCACAT 240  
 AATCTCGTAT TTTATCTTCG GCAATTTTCC CATCGTAAAT ACCCATATAA TATGGATTTT 300  
 CCTCATTAAG AGCACCTTTT CCTAATGAAA GTTGTGCTAC TGGGTATCTG TGTTTGANTT 360  
 ACAAATCTT CnaAGTCCTG GATGGAGGTG AAAACTGTTA 400

(2) INFORMATION FOR SEQ ID NO: 3784:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3784:

10 GGTACTAAGA TGTTTCAGTT CTCGGGGTGT GCCTTCTGAT ATGCTATGTA TTCACATATC 60  
 GATAACATGA CATAACTCAT GCTGGGTTTC CCCATTCGGA AATCTCTGGA TCAAAGCTTA 120  
 CTTACAGCTC CCCAAAGCAT ATCGTCGTTA GTAACGTCCT TCATCGGCTT CTAGTGCCAA 180  
 15 GGCATCCACC GTGCGCCCTT AATAACTTAA TCTATGTTTC CACCATTTTT ATAAGTCAAA 240  
 CGCTCACATA CGGCTTCGTT TTCATTATTT TAAATGCTCA TTTACATAAG TAAACTCTGC 300  
 TTTAAAATAA TTTAACTCAT TGTCTGCAAA ACGTTTTCTT TTATAAAAAG AntTTAAACG 360  
 20 CGTTAATGAA GCTGTGAGTG TTCCTTCGAA CACGAGnnGA 400

## (2) INFORMATION FOR SEQ ID NO: 3785:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3785:

TACTGGAATG ACATCAGATA CATGTGCACC ACCAATCCAT TTCTTTTCAC CATTGATAAC 60  
 35 CCAAGTATCG CCTTGnCGTT CAGCGACTGT TTCAAGACCT CCCGCAACGT CCGAACCGTG 120  
 TTCTGGTTCA GTTAAAGCAA AGCATGTACG CAGTTCATGT GACTGTAATT TAGGTACATA 180  
 TTTGCAATT TGTTCTTTGC TACCTCCGAA ATAGAAAGTG TTATGCCCTA AACCTTGGTG 240  
 40 AACACCGAGT AGGGTAGCTA AGGAAATATC AAATCGCGCG AGTAGGTAAG ACATGAAAAA 300  
 CTGAAATAGT TGACTIONGCA TTTTGCGGTT TGGACGATCC TTGTAAAGTA ATGGATTGTT 360  
 AAAATAATTT AATTCTCCCA GTCTTTAAAT AGTCCTCGGG 400

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## (2) INFORMATION FOR SEQ ID NO: 3786:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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TCATTTGACG AATTTTCATTG TTATTCAAAA TTCTATCTAA TCGTGCTTTT TCAACATTTA 60  
 ATATCTTACC TCGTAATGGT AAAATCGCCT GCGTTCTAGA GTCACGACCA GATTTTGTAG 120  
 5 ACCCCCCGGC AGAGTCCCCT TCGACTAAGA AAATCTCACA TTCTTCAGGA CTTTACTAG 180  
 AGCAATCGGC TAATTTACCT GGAAGCTTGC TACATCTAAC GCTGATTAC GACGTGTTAC 240  
 TTCACGCGCT TTTTTCGCAG CAACACGTGC ACGGCCCGCC ATAATACCTT TTTCAACCAC 300  
 10 TGTACGTGCG ACTTGTGGGA TTTTCATATA AAAATCGTTC AAAGTGCTCT GAGAATAATT 360  
 TATCTACAAC TTGACGCACT TCAGAATTAC CTAATTTTGT 400

(2) INFORMATION FOR SEQ ID NO: 3787:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3787:

25 TCTCTTCCCG TTTCGCTCGC CGCTACTAAG GGAATCGAAn TTCTTTTCTC TTCCTCCGGG 60  
 TACTAAGATG TTTCAGTTCT CCGGGTGTGC CTTCTGATAT GCTATGTATT CACATATCGA 120  
 TAACATGACA TAACTCATGC TGGGTTTCCC CATTCCGAAA TCTCTGGATC AAAGCTTACT 180  
 30 TACAGCTCCC CAAAGCATAT CGTCGTTAGT AACGTCCTTC ATCGGCTTCT AGTGCCAAGG 240  
 CATCCACCGT GCGCCCTTAA TAACTTAATC TATGTTTCCA CCATTTTAT AAGTCAAACG 300  
 TTAACATGAA GTTACGTTCT TTTATAAAAA GATTAAACG CGTTATTAAT CTTGTGAGTG 360  
 35 TTCTTTTCGGA CACTAGCGAT TATTTCTnAT GATnCAAGCT 400

(2) INFORMATION FOR SEQ ID NO: 3788:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3788:

ATTCTCTGCT TTCATCTCAT TTGGTGACTA ATACCCTGAT TTGTCCAAG TAAATGCTTC 60  
 50 ATAAAGTATT CTTGACCTTT TGCAGAACTT GAAATTAAGT TTGAACGCCA TATATAATGA 120  
 TTTTGGATGA TTCTTTTCA AATCAGGATC TCTATTGCAA ATTGTGTTTG TnTTGATTTC 180



TCTTCTGCAA ACAACAACT ATTTTATTAA AATTGTGGAT ATGATGGTAA CCAACCAAGT 300  
 CTAGCTGCTA AnACATTATA ATCAGCTGGA TGTTGATGCT TTAACCTCTC TGTTTTAGCT 360  
 5 AATGGAGATT TTAAACGATC TACATTGAC TCTTCATAAT 400

(2) INFORMATION FOR SEQ ID NO: 3789:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3789:

CGGTTTCTTA ATTATGAACG CAACTATGAA TGGCTTATTA ACTATCACGG GCACATTGGC 60  
 AAAAGATCAG CTTGCACAAA ATGGACAAGG CATGGTGCTC GGTATACAAA CGGTTGAAAC 120  
 CGGTGTTTTT GCGGGGATTA TCACAGGTAT TATGACCGCA ATACTTCACA ACAAATATCA 180  
 CAAAGTGGTA TTACCACCGT ATTTAGGTTT CTTTGGTGGC TCTAGATTTG TCCCTATTGT 240  
 CACAGCATTT GCCGCAATCT TTTTAGGTGT ATTGATGTTT TTCATTGGC CAAGCATACA 300  
 nGCCGGCATT TATCATGTTG GTGGGATTG TAACGAAAAC AGGTGCCATC GGTACTnTTG 360  
 TTTATGGGTT CATCTTTAGG ATTGTTAGGT CCACTCGGTT 400

(2) INFORMATION FOR SEQ ID NO: 3790:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 716 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3790:

ATAATGGACT GTGCCGnGTA ATAATATnGn TCTCTAAAAG TTGTATTTTA AAAATAGTTC 60  
 TTAAATTAT ATACCCACCA CATTTGGTGA kGAACCTAAA AAAAAGCACT TCCC AAAAAT 120  
 GGAAAGTGCA AGTAGTGAGC CATAGAGGAT TCGAACCTCT GACCCTCTGA TTAAAAGTCA 180  
 GATGCTCTAC CAACTGAGCT AATGGCTCTA ATGGCTGGGC TAGCTGGATT CGAACCAACG 240  
 AGTGACGGAT CAAAnGTCCG TTGCCTTACC GCTTGGCTAT AGCCaATATA TAGATGGTGG 300  
 AGGGGGGCAG ATTCGAACTG CCGAACCCGA AGAGCGGATT TACAGTCCGC CGCGTTTACC 360  
 ACTTCGCTAC CCCTCCAGCT TATTCATATA ATTTAATAAT CAAAATGGTG GAGAATGACG 420

CAAAATAATG ACTCCTACGG GACTCGAACC CGTGTTACCG CCGTGAAAGG GCGTgTCTT 540  
 AACCGtTGAC CAAGGAGCCA TGGCTCaCcA GGTAgGACTC GAACCTACGA CCGATCGGTT 600  
 5 TAACAGCCGA TAGCTCTACC ACTGAGCTAC TGTGGGATTA ATATTATGCC TGGCAACGTT 660  
 CTACTCTAGC GGAActAAAG TTnGAACTnA CCATCGACGC TAAAGGAGCT TAACTT 716

## (2) INFORMATION FOR SEQ ID NO: 3791:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3791:

20 TGTCATGACG TTATTTGAAG ATATCGCGCA AGTCTTTTTA AAGGTAACAC TATCATTTAT 60  
 GCAATACGGC GCATTACCAG AGTTGCATGG TCAAAATATA TTGTTGTCAT TTGAAGATGG 120  
 ACGTGACAA AAATGCGTGT TACGTGATCA TGATACTGTC AGAATTTATA AACCATGGCT 180  
 25 AACAGCACAT CAGCTTTTCAT TGCCGAAGTA TGTCGTCAGA GAAGATACAC CTAATACGCT 240  
 AATTAATGAG GATTTGGAAA CATTCTTTGC nTGATTTTCA AACATTAGCT GTGATCGGTA 300  
 AATCTATATG CCATTATTGA TGCAATTCCA AGATTTATTT GGTGTGAAGT GnAGCATGAA 360  
 30 CTTATGTCGT TGTAAAACA AATTTTGAAA AAAGGAAGTG 400

## (2) INFORMATION FOR SEQ ID NO: 3792:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 425 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3792:

TTTTACACA ATACATGGAC ACCATGGTTC AATGCTTCTA TAGAAAGATC AGCATGGAAT 60  
 45 TTATTAGGTG TACAAATGAC CACCGCATCA ACAAGTTTAA ACAGCTCGCT AGGTGTCTCA 120  
 ACTGCATGAG GTATATTAAA GCGCTTCGCA ACATCAATCA TCTGCACTGT ATTAATATCT 180  
 TGTACTGCAA CTAATGAGAC TGTGTCTTTG AGTTTCAGCA ATGCTGGAAT ATGACGGTCT 240  
 50 TGTGCAATAC CACCAACACC TATCACACCA ACTTTTAAAT TTGTCATGAT GTGCCTCCTT 300  
 ACCGTATGAT GTtATTCAA GTAAATTGCT TTGCCTGATT TkGCAGACTG ATaAATyGCT 360

TACCA

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## (2) INFORMATION FOR SEQ ID NO: 3793:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3793:

15 GATGCTCTAC CAACTGAGCT AATGGCTCTA ATGGCTGGGC TAGCTGGATT CGAACCAACG 60  
 AGTGACGGAG NAAAGGTCCG TTGCCTTACC GCTTGGCTAT AGCCCAATAT ATAGATGGTG 120  
 GAGGGGGGCA GATTGGAAT GCCGAACCCG AAGGAGCGGA TTTACAGTCC GCCGCGTTTA 180  
 20 GCCACTTCGC TACCCCTCCA GCTTATTCAT ATAATTTAAT AATCAAAATG GTGGAGAATG 240  
 ACGGGTTTCA ACCGCCGACC CTCTGCTTGT AAGGCAGATG CTCTCCCAGC TGAGCTAATT 300  
 25 CTCCAAAATA ATGACTCCTA CGGGACTCGA ACCCGTGTGA CCGCCGTGAA AGGGCGGTGT 360  
 CTTAACCGCT TTGACCAAGG AGCCATGGCT CCACAGGTAG 400

## (2) INFORMATION FOR SEQ ID NO: 3794:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3794:

40 ATCAGCAGGG TTGAAAGTAC CTGCTGCAAC AGTAATACCA TTATTAGTTC CAGCAATACC 60  
 TGCTACAGTT GCTGCAGATG CTTCTTTCAC CCATGGACTC GTATTATTGC GACGTGTAAA 120  
 TGTTTCACAA CGTTACCATT ACGTTTAAATA ACTAATTTAT CAGCGTATGT CGTTACGTTA 180  
 45 CCGGCATGTG TATTCAGTGT TTGGTTTGCT CCAGGTGCAA TTGTAATCGC TCCTGCCGCT 240  
 GTTTCAGTCA CAGTTGGTTT CGCTGGTTGC ACATCTTTTA CTACAAATTT CGCTGGTAAA 300  
 GATGTTGCAA AAGTATGTCC GTTATAGATG ACGTCCATAT TTTGCGTTAA CGACTTTAGC 360  
 50 CACATTCGGT TTATTCATAG CGGACCAGTT TGCCTCCATT 400

## (2) INFORMATION FOR SEQ ID NO: 3795:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3795:

GCGCCGAAAA TGTACCGGGG CTAAACATAT TACCGAAGCT GTGGATTGTC CTTTGGACAA 60  
10 TGGTAGGAGA GCGTTCTAAG GCGGTTGAAG CATGATCGTA AGGACATGTG GAGCGCTTAG 120  
AAGTGAGAAT GCCGGTGTGA GTAGCGAAAG ACGGGTGAGA ATCCCGTCCA CCGATTGACT 180  
AAGGTTTCCA GAGGAAGGCT CGTCCGCTCT GGGTTAGTCG GGTCCTAAGC TGAGGCCGAC 240  
15 AGGCGTAGGC GATGGATAAC AGGTTGATAT TCCTGTACCA CCTATAATCG TTTAATCGAT 300  
GGGGGGACGC AGTAGGATAG GCGAACGTGC CATTTGATTG CACGTCTAAA GCAGTAAAGC 360  
TGAGTATTAG GCnAATCCGG TACTCGTTnA AGGCTGAACT 400

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(2) INFORMATION FOR SEQ ID NO: 3796:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3796:

GCACATGTTG CCATgCTTGA GCTAAATTAC CTTGCATCAT TGCTAGCTTT TCTTGTATTA 60  
ACTGATATTT ACTAATTGGT TTGCCGAATT GCTTACGCTC AGTGACATAA TCTAATGTGG 120  
35 CACGTAAAGC GCCACCATAC CACCTGTAGC CATATAAGCA ACGsCTGCTC TCGTTGAATA 180  
AAGAATTTTG GCAATATCTT TAAAGCTTGT TATGTTTTGT AAGCGATCCG CTTTCATCTAC 240  
40 TTTGACATTA GTTAATTTAA TTAGGGCGTT AGGAACAATG CGAAGTGCGA TTTTATTATC 300  
AATGACTTCA ATATCGACGC CATCTTGTTT TGGTCTGACT ACAAAGCAAT GGGGTTTGCC 360  
AGTTTCnGTT ATTTACTGCG AATACTGGGG GGGnGnGGTT 400

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(2) INFORMATION FOR SEQ ID NO: 3797:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3797:

GGAACACCAG TGGCGAAGGC GACTTTCTGG TCTGTAACGTG ACGCTGATGT GCGAAACGTG 120  
 GGGATCAAAC AGGATTAGAT ACCCTGGTAG TCCACGCCGT AAACGATGAG TGCTAAGTGT 180  
 5 TAGGGGGTTT CCGCCCCTTA GTGCTGCAGC TAACGCATTA AGCACTCCGC CTGGGGAGTA 240  
 CGACCGCAAG TTGAACTCA AAGGAATTGA CGGGGACCCG CACAACGGTG GGAGCATGTG 300  
 GTTTAATTCTG AAGCAACGnA GAGAACCTTA CCAATCTTTG ACATCCTTTT GACTCTAG 360  
 10 GAGATAGAGC CTTCCCTTCG GGGGGACnAA GTGACAGTTG 400

## (2) INFORMATION FOR SEQ ID NO: 3798:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3798:

CACAAAACAA GCCAAGCAAA ACAACGCAT ATAACGTAAC AACACATGGA AACGGCCAAG 60  
 25 TATCATATGG CGCTCGCCCA ACACAAAACA AGCCAAGCAA AACAAATGCA TACAACGTAA 120  
 CAACACATGC AAACGGTCAA GTGTCATACG GAGCTCGCCC GACATACAAG AAGCCAAGTA 180  
 AAACAAATGC ATACAATGTA ACAACACATG CAGATGGTAC TGCACATAT GGGCCTAGAG 240  
 30 TAACAAAATA AGTTTGTAAC TCTATCCAAA GACATACAGT CAATACAAA CATTACGTAT 300  
 CTTTACAACA GTAATCATGG CATTCTATGG ATGCTTCTAA CTGGAATTAA AGCATCGGAA 360  
 35 CAATCGGGAn GCATATTTCT AAAATTATTT ATTCCATTAT 400

## (2) INFORMATION FOR SEQ ID NO: 3799:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3799:

CTTGCGCGAT ATGGGGGAAG CTAGGTGATA AGATCAGCCG AAAATGGATG GTGTTAAGAG 60  
 50 CGTTACTTGG TTGGCGGTA TGCTTATTTT TAATGGCATT GTGTACGACA CCATTACAGT 120  
 TTGTACTTGT GAGGTTATTG CAGGGACTAT TTGGTGGTGT TGTTGATGCA TCAAGTCCGT 180  
 TTGCGAGTGC AGAGGCGCCA CTGAAGGATC GTGGAAAGGT ATTAGGAAGA CTGCAAAGTT 240

TTTtagTGCg TtactGATGA GTATTGCCGT TATTACTTTT ATTGTCTGtn TTTTCGGTGC 360

CATTAAATG ATTGAAACGA CACATATGGC CAAAnnCACA 400

5 (2) INFORMATION FOR SEQ ID NO: 3800:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3800:

GGAATCTATT ATATTAGATG TAAAAAATTT CGCGCAAAT GTGTtagGTA AAGGTGTCAT 60

TGTCGTCAAT GATGTGCCTG GCTTTGTCGC AAATAGAGTC GGCACGCAA CAATGAATGA 120

20 TATTATGTAT CGCGCCGAGC AACACAAGAT AAGCATTGTA GATGTGGATG CTTTAACTGG 180

GCAAGCGATT GGTGCTCCTA AAACAGGTAC ATATGCGCTA TCTGACCTAG TCGGTTTAgA 240

TATTGCAGTG TCTGTAAATT AAAGGCATGC AACAAgTACC TGAAGAAACA CCTTATTTTC 300

25 ATGATGTCAA AATGTAAATA CGTTGTTTGA CCATGGGCGC ACTCGGACGT TAAnnCGnAA 360

ACCAAGGGTT TTTACCAAAA AGGGTTAAAG GgnAACTTAA 400

30 (2) INFORMATION FOR SEQ ID NO: 3801:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

35 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3801:

40 TGCAGGCGTT TCTGGTCTGC ATAGTTTACG CATACGACCT GCGCGATCCT TATCTGGTAA 60

TAAATTGTAA AACGATAGTT CCCGTTGTTc CTAATAGTTG TATTCTATCT GACGCATAAT 120

GTGAAAAATA ACCTGCCATC TCTAAGCCCG GTCTTGATAT ATCAGCATTt TTAATTGGCT 180

45 TCGATAGTCC TTCTTCACCA GCGATTAAAT CTAACtTTAA TGTTTCAACT AGTTTTTCTG 240

TCGTTAACAT GGGTTcACCT CAATTGTATT TACCCTACTC TTACATCTCT TCTTATCATA 300

50 TCAAAAATAT AACACCAATC TACATTGAAA AGCTAAAnTA AATATTAAATG TTCATTATTG 360

TTATnATTTT ACAAGTCAAT ATCATCATAA TTTATTGCTG 400

(2) INFORMATION FOR SEQ ID NO: 3802:

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- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3802:

10 TTTCACTTTT GAACCATGCG GTTCAAAATG ATTATCCGGT ATTAGCTCCG GTTCCCCGAA 60  
 GTTATCCCAG TCTTATAGGT AGGTTATCCA CGTGTTACTC ACCCGTCCGC CGCTAACATC 120  
 AGAGAAGCAA GCTTCTCGTC CGTTCGCTCG ACTTGCAATG ATTAGGCACG CCGCCAGCGT 180  
 15 TCATCCTGAG CCAGGATCAA ACTCTCCATA AAAATTATGA TGTTTGATTA GCTCATAAAT 240  
 ACTAAATAAT GTTTGTAAC TATAGTTACG TTTTTTGGAA TTAACGTTGA CATATTGTCA 300  
 TTCAGTTTTC AATGTTCAAT TTTCTTACCG ACAAGAATTA ATTATACATT TTATTAACAT 360  
 20 TTAAGTCAAT AACTTTnTTT ATCCTGTCCA TTTnATTTTT 400

## (2) INFORMATION FOR SEQ ID NO: 3803:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3803:

TAGTCACCAG ACATATGAAT GTAATTTATA CATTCAAAAC TAGATAGTAA GTAAAAGTGA 60  
 35 TTTTGCTTCG CAAAACATTT ATTTTGATTA AGTCTTCGAT CGATTAGTAT TCGTCAGCTC 120  
 CACATGTCAC CATGCTTCCA CCTCGAACCT ATTAACCTCA TCATCTTTGA GGGATCTTAT 180  
 AACCGAAGTT GGGAAATCTC ATCTTGAGGG GGGCTTCATG CTTAGATGCT TTCAGCACTT 240  
 40 ATCCCGTCCA CACATAGCTA CCCAGCTATG CCGTTGGCAC GACAACTGGT ACACCAGAGG 300  
 TATGTCCATC CCGGTCCTCT CGTACTAAGG ACAGCTCCTn TCAAATTTCC TACGnCCAnG 360  
 45 ACGGATAGGG ACCGAACTGT TTTACGACG GTnCTGAACC 400

## (2) INFORMATION FOR SEQ ID NO: 3804:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 457 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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AGTnCACTCA CnCCAGATGT TTAAGTCCTG TGCCTCTGCC AGTTCGCGCA CCCCGGCACT 60  
 ATAAAAATGG AGCAGAAGAC GGGATTGAA CCCGCGACCC CAACCTTGGC AAGGTTGTAT 120  
 5 TCTACCGCTG AACTACTTCT GCATATGCGG GTGAAGGGAG TCGAACCCCC ACGCCGTAAG 180  
 TTAGWATCCT AAGTCTAGTG CGTCTGCCAA TTCCGCCACA CCCGCAAATG GTGAGCCATA 240  
 GAGGATTGCA ACCTCTGACC CTCTGATTAA AAGTCAGATG CTCTACCAAC TGAGCTAATG 300  
 10 GCTCTTCCAT GGTGCCGGCC AGAGGACTTG AACCCCAAC CTACTGATTA CAAGTCAGTT 360  
 GCTCTtACCA ATTGaGCTAG GCCGGCAATA TGTaAGAATA AATGGTGGAG AATGACGGGT 420  
 15 TTCGAAACCG CCGnACCCTC TGGCTTGTTA AGGGCAG 457

(2) INFORMATION FOR SEQ ID NO: 3805:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 20 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3805:

ACTTTTTIATT TTGACGTTTT AGACATAAAA AAAGCTCAGG GTCTCAACTT GCCTGGCAAC 60  
 GTTCTACTCT AGCGGAACGT AGTTGGCTAC CATCGTCGCT AAAGACCTTT CTTGACTTGT 120  
 30 GACAATCGCT TGCTTCTTTC CTCTCCTTCG GCTCTCGCTT ACTCATTTAG CTCTACTAAA 180  
 CTCGTTGCGC TCTTTTCTCG TTTCGTCAGA TTCAAACGTT TTCACTTCGC CAAGCCATTT 240  
 35 TTCTTTGTGT TTACTTTTTA TnTTGACGTT TTAGGCATAA AAAAAAGAGA CCTTGC GGTC 300  
 TCAATGCGGC TCATCGCATC CATnTTTTGC CGGCAACGT TCTACTCTTA GCGGAACGTA 360  
 AGTTGGCTAC CATCGTCGCT AAAGACCTTT TTGGACTGTG 400

40 (2) INFORMATION FOR SEQ ID NO: 3806:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 45 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3806:

GTTATGAAAG TCGCGCTTAA AATGCGTTAA TGTGACAAGG ATAATTCAAC ATCGTTTCAT 60  
 TTTACTGAGT CATTGCACTT ATCATACACA TTATATTTAG CATGAGTTAT ATTACTAAAA 120

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TCATTGGCTT AATATTTACA GCGCTTGGTA TTGCAGGTGC CGTATTACCT TTACTGCCAA 240  
 CGACCCCTTT TTTACTCGTA GCAGTTTTTT GCTTGTCTCG AAGTTCAGAT CGCTTTTACA 300  
 5 ATTGGGCnnA TTAATCAAAA AATTTATAAA GAATATGTAG AAAACCTTTn TTTGACATCG 360  
 AGGCTACACG CTACAACAGA AAATTGAAAA TTTAATTAGC 400

## (2) INFORMATION FOR SEQ ID NO: 3807:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 388 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3807:

20 AGGAGAACAT GCTGTTACAT TTGGAGAGCC TGCTATTGCA GTGACCGTTT AACGCAGGTA 60  
 AAATCAAAGT TTTAATAGAA GCCTTAGAGA GCGGGAActA TTCGTCTATT AAAAGCGATG 120  
 TTTACGATGG TATGTTATAT GATGCCCGTG ACCATCTTAA GTCTTTGGTG AACCGTTTTG 180  
 25 TAGAATTAAA TAATATTACA GAGCCGCTAG CAGTGAACGA TCCAAACGAA TTTACCACCA 240  
 TCACGTGGAT TAGGATCGAG TGCCAGCTGT CGCGGTTGCT TTTGTTCTGT CAAGTTATGG 300  
 ATTTTTTAGG GnAAATCATT AACGAAAGnA AGAACTCATT GGAAAAGGCT nATTGGGCCA 360  
 30 GAAGCAAATT GCCACATGGT AAAACCAA 388

## (2) INFORMATION FOR SEQ ID NO: 3808:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 447 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 40 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3808:

45 ATGCGCAGAG TATATGGAGG AACACCACTG TCGAAGCGCA CTTTCTGGTC TGTAAC TGAC 60  
 GCTGATGTGC GAAACGTGkG GGATCAAACA GGATTAGATA CCCTGGTAGT CCACGCCGTA 120  
 AACGATGAGT GCTAAGTGTT AGGGGGTTTC CGCCCCTTAG TGCTGCAGCT AACGCATTAA 180  
 GCACTCCGCC TGGGGAGTAC GACCGCAAGT TgAAAACTCA AAGGrATTGA CGGGGACCCG 240  
 50 CACaAGCGTG GGAGCATGTG GtTTAATTCTG AaGCAACGnn GAGGAACCTT ACCAAATCTT 300  
 GACATCCTTT GACAACTCTA GAGATAGAGC CTTCCCCTTC nGGGAACAAA TGACAGGTGG 360

ACCCTTAAGC TTATTGCCA TCATTAA

447

## (2) INFORMATION FOR SEQ ID NO: 3809:

5

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3809:

15

CCAAC	TGAGC	TACTGA	ACCA	TAATA	AAAAAT	GTAAT	GACTG	GCGGT	CTCGA	CGGGA	ATCGA	60
ACCCG	CGATC	TCCTG	CGTGA	CAGGC	AGGCG	TGTTA	ACCGC	TACAC	TACGA	GACCT	TATAA	120
ATATT	GCGGG	AGGCG	GATTT	GAACC	ACCGA	CCTTC	GCGGT	ATGAG	CCCGA	CGAGC	TACCG	180
AACTG	CTCCA	TCCCG	CGATA	ATAAAA	ATAA	ATGGC	CGAGG	AAGAG	GGGAT	CGAAC	CCCCG	240
CGGCC	CGTTA	AGGCC	TGTC	GGTTT	TCAAG	ACCGA	TCCCT	TCAGC	CGGAC	TTGGG	TATTC	300
CTCCAT	TATT	ATAGG	TAAAT	CGCTA	TTAAT	TATAA	AAATTA	AATGG	CGGTC	TCGAC	GGGAA	360
TCGAAC	CCGC	GATCT	CCTGC	GTGAC	AGGCA	GGCGT	GTAA					400

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## (2) INFORMATION FOR SEQ ID NO: 3810:

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- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3810:

40

TGCTT	GGTAA	AATCT	TATATT	TTACT	TACTT	ATCTA	GTTTT	CAATG	TACAA	ATAAT	GGTGG	60
GCCTA	AGTGG	ACTCG	AACCA	CCGAC	CTCAC	GCTTA	TCAGG	CGTGC	GCTCT	AACCAG	CTGA	120
GCTAT	AGGCC	CATTT	TTTTTG	AATGT	TAAAT	AAACAT	TCAA	AACTGA	AATAC	AATAT	GTCAC	180
GTTAT	TCCGC	ATCTT	CTGAA	GAAGAT	GTTC	CGAAT	TATATC	CTTAG	AAAGG	AGGTG	ATCCA	240
GCCGC	ACCTT	CCGAT	ACGGC	TACCT	TGTTA	CGACT	TACAC	CCAAT	CATTT	GTCCC	ACCTT	300
CGACG	GCTAG	CTCCT	AAAAG	GTTACT	CCAC	CGGCT	TCGGG	TGTTA	CAAAC	TCTCG	TGGTG	360
TGACG	GGCGG	TGTGT	ACAAG	ACCCG	GGAAC	GnATT	CACCG					400

50

## (2) INFORMATION FOR SEQ ID NO: 3811:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 380 base pairs

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(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3811:

GCTTCATGCT TAGATGCTTT CAGCATTAT CCCGTCCACA CATAGCTACC CAGCTATGCC 60  
10 GTTGGCACGA CAACTGGTAC ACCAGAGGTA TGTCATCCC GGTCTCTCG TACTAAGGAC 120  
AGCTCCTCTC AAATTCCTA CGCCCACGAC GGATAGGGAC CGAACTGTCT CACGACGTTC 180  
TGAACCCAGC TCGCGTACCG CTTTAATGGG CGAACAGCCC AACCTTGGG ACCGACTACA 240  
15 GCCCCAGGAT GCGATGAGCC GACATCGAGG TGCCAAACCT CCCCGTCGAT GTGGAAGTCT 300  
TGGGGGAGAT AAGCCTGTTA TnCCCGGGGT AGCTTTTATC CGTTGAGCGA TGGnnCTTCC 360  
ATGCGGGAAC CACCGGGATT 380

20

(2) INFORMATION FOR SEQ ID NO: 3812:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 386 base pairs  
(B) TYPE: nucleic acid  
25 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3812:

GAGGGATCTT ATAACCGAAG TTGGGAAATC TCATCTTGAG GGGGGCTTCA TGCTTAGATG 60  
CTTTCAGCAC TTATCCCGTC CACACATAGC TACCCAGCTA TGCCGTTAGC ACGACAAGTG 120  
35 GTACACCAGA GGTATGTCCA TCCCGGTCCT CTCGTACTAA GGACAGCTCC TCTCAAATTT 180  
CCTACGCCCA CGACGGATAG GGACCGAACT GTCTCAGAC GTTCTGAACC CAGCTCGCGT 240  
ACCGCTTTAA TGGGCGAACA GCAACCCCTT GGGACCGACT ACAGCCCCAG GATGCGATGA 300  
40 GCCGACATCG AGGTGCCAAA CCTCCCGTC GntGTGAACT CTTGGGGGAG ATAAGCTGTT 360  
ATCCCCGGGT GAGnTTTnTC CGTTGA 386

45

(2) INFORMATION FOR SEQ ID NO: 3813:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3813:

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CTTGGTACTT CTGGTGTGG TGGCGTTGGT GTTCCGGCT CACTGGGTAC TTCTGGTGTG 120  
 GGTGGCGTTG GTGGCACGAT TGGAGGTGTT GTATCTTCTT CAATCGTTTG TTGACCTTCA 180  
 5 TTTTGGCCGC TTACTTTTGG AAGTGTATCT TCTTCAAAGT CAACACTATT GTGTCCACCG 240  
 AATTGATAAC TTGGTTTATC TTTATTTGTA TCTTCTTCAA TAATTTTCAGT GTGCTTATTG 300  
 AATCCGTGAA TATGTGGCAC nTGGTCGAAG TCGATATCAA TGATGTTACC GCCATGTTCA 360  
 10 TACTTAGGTT TGTCTTTTTC TGTAnCTTCC TCGAATGACT 400

## (2) INFORMATION FOR SEQ ID NO: 3814:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3814:

TAATTGGGCT ACCATCGTCG CTAAAGACCT TTCTTGACTT GTGACAATCG CTTGCTTCTT 60  
 25 TCCTCTCCTT CGGCTCTCGC TTACTCATTT AGCTCnACTA AACTCGTTGC GChCTTTTCT 120  
 CGTTTCGTCA GATTCAAACG TTTTCACTTC GCCAAGCCAT TTTTCTTTGT GTTTACTTTT 180  
 TATTTTGACG TTTTAGGCAT AAAAAAAGA GACCTTGCGG TCTCAATGCG GCTCATCGCA 240  
 30 TCCATTTTTT GCCTGGCAAC GTTCTACTCT AGCGGAACGT AAGTTGGGCT ACCATCGTCG 300  
 CTAAAGACCT TTCTTGACTT GTGACAATCG CTTGCTTCTT TCCTCTCCTT CGGCTCTCGC 360  
 TTACTCATTT AGCTCTACTA AACTCGGTGC GCTCTTTTCT 400

## (2) INFORMATION FOR SEQ ID NO: 3815:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3815:

TTCTTTCATA TGATTTTTTA GATTTTAGTA AGTCAATAAA GCCAATTTTC TCCAACGATT 60  
 GAATGTAACG TTGATTGATA AATGTATTTT TTGGTAAATC ACCACCCGCT AAAATTGTGG 120  
 50 CGATATTTAA GGCAATATGA TAATCATGGT CGCTAATAAA ATGACCCCGT CTTTGCGCAT 180  
 CTAATTGTCC TTGGATCAAT GCTTTGAAGT CTTACCTTAA AGCGATATAT TGATGTCTAG 240

GTTGTGCTGT ATTGAAAATA ATCGTATCTG GTATCACGTA AATnACCATA ACGACGTGCC 360  
 TCCAAAGGCA TTTGGTAnGA GCCTTCGGCA ATGCCGATAA 400

(2) INFORMATION FOR SEQ ID NO: 3816:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3816:

CCAATATTTA TATTAATGAA AATAAGATGT TATATTCATT GTTAATTTAA CACATAGTAA 60  
 GAnAAACAGT CATAAATTGA TTTCTAATTG AAATCATCTT ATGACTGCTT TTTATTATAC 120  
 TTTACATTTT TCGTTTCGTC AGATTCAAAC GTTTTCACTT CGCCAAGCCA TCTTTCTTTG 180  
 TGTTCGCTTT TATTTTGACG TTTTAGACAT AAAAAAGAG ACCTTGCGGT CTCAATGCGG 240  
 CTCATCGCAT CCACTTTTTG CCTGGCAACG TTCTACTCTA GCGGAAnTAA GTCGGACTAC 300  
 CATCGACGCT AAGGAGCTTA ACTTCTGTGT TCGGCATGGG GAACAGGTGT GACCTCCTTG 360  
 GCTATAGTCA CCAGACATAT GAATGTAAAT TCATACATTC 400

(2) INFORMATION FOR SEQ ID NO: 3817:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3817:

TGTATTGTT CAAAATCATG ATCAAGATCA GTATATCGGG GGGnATTATG AAGCGATGCA 60  
 TACATTATCA CATAATAAGA TTAAATCACA ATTACGTATG ACCTTACCGG AGTACATGAT 120  
 ACCAGTTAAT TTCATGCATA TTGAGCAAAT TCCTATTACT ATTAATGGGA AATTAGATAA 180  
 GAAGGCATTG CCTATCATGG ACTATGTCGA TACGGATGCC TATGTAGCAC CGAGTACAGA 240  
 TACCGAACAC TTGCTATGCC AAATTTTTGC AGATATTTTA CATGTGAATC AAGTAGGTAT 300  
 TCATGATAAT TTCTTTGAAT TAGGTGGCCA TTCATTAAAA GCAACGTTAT GGnTGGAATC 360  
 GGATAGAGGC ATCTACTGGG GAAACGATTA CCAATTGGGG 400

(2) INFORMATION FOR SEQ ID NO: 3818:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3818:

10 TCGGAATCTG GGAGGACCAT CTCCTAAGGC TAAATACTCT CTAGTGACCG ATAGTGAACC 60  
 AGTACCGTGA GGAGAAGGTG AAAAGCACCC CGGAAGGAAG TTGAAATAGA ACCTGAAACC 120  
 GTGTGCTTAC AAGTAGTCAG AGCCCGTTAA TGGGTGATGG CGTGCCTTTT GTAGAATGAA 180  
 15 CCGGCGAGTT ACGATTTGAT GCAAGGTTAA GCAGTAAATG TGGAGCCGTA GCAnAACATG 240  
 TTCTGAATAG GGCCTTTAGT ATTTGGTCGT AGCCGnAAAC CAGGTGATCT ACCCTTGGTC 300  
 CAGGTTGAAG TTCAGGTAAC ACTGGAATGG AGGACCGAAC CGACTTACGT TTGAAAAGTG 360  
 20 AGCGGATGAA CTGAAGGTAG CGGAGAAATT CCAATCGAA 400

## (2) INFORMATION FOR SEQ ID NO: 3819:

- 25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3819:

CAACGAGAGA CTCGGTGAAA TCATAGTACC TGTGAAGATG CAGGTTACCC GCGACAGGAC 60  
 35 GGAAAGACCC CGTGGAGCTT TACTGTAGCC TGATATTGAA ATTCGGCACA GCTTGTACAG 120  
 GATAGGTAGG AGCCTTTGAA ACGTGAGCGC TAnTTACGTG GAGGCGCTGG TGGGATACTA 180  
 CCCTAGCTGT GTTGGCTTTC TAACCCGCAC CACTTATCGT GGTGGGAGAC AGTTTCAGGC 240  
 40 GGGCAGTTTG ACTGGGGCGG TCGCCTCCTA AAAGGTAACG GAGGCGCTCA AAGGTTCCCT 300  
 CAGAATGGTT GGAAATCATT CATAGAGTGT AAAGGCATAA GGGACTTGAC TGCGAGACCT 360  
 45 ACAAGTCGAG CAGGTCCAAA AACGGACnTA GTGATnCGGT 400

## (2) INFORMATION FOR SEQ ID NO: 3820:

- 50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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TGGCTCGAAC CACCGACCTC ACGCTTATCA GGCCTCGCTC TAACCAGCTG AGCTATAGGC 60  
 CATTAAATTTG AATGAACAAA CATTCAAAAC TGAATACAAT ATGTCACGTT ATTCCGCATC 120  
 5 TTCTGAAGAA GATGTTCCGA ATATATCCTT AGAAAGGAGG TGATCCAGCC GCACCTTCCG 180  
 ATACGGCTAC CTGTGTACGA CTTCACCCCA ATCATTGTGTC CCACCTTCGA CGGCTAGCTC 240  
 10 CTAAAAGGTT ACTCCACCGG CTCGGGTGT TACAACTCT CGTGGTGTGA CGGGCGGTGT 300  
 GTACAAGACC CGGAACGTT ATTCACCGTA GCATGCTGAT CTACGATTAC TACGATTCC 360  
 AGCTTCATGT AGTCGAGTTT GCAGACTACA ATnCGAACTG 400

15 (2) INFORMATION FOR SEQ ID NO: 3821:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 20 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3821:

25 TATTAAATTA ATGGTGGGCC TAANTGGACT CGAACCACCG ACCTCACGCT TATCAGGCGT 60  
 GCGCTCTAAC CAGCTGAGCT ATAGGCCCAT TAATTTGAAT GAACAAACAT TCAAACTGA 120  
 30 ATACAATATG TCACGTTATT CCGCATCTTC TGAAGAAGAT GTTCCGAATA TATCCTTAGA 180  
 AAGGAGGTGA TCCAGCCGCA CCTTCCGATA CGGCTACCTT GTTACGACTT CACCCCAATC 240  
 ATTTGTCCCA CCTTCGACGG CTAGCTCCTA AAAGGTTACT CCACCGGCTT CGGGTGTAC 300  
 35 AAATCTCTCGT GGTGTGACGG GCGGTGTGTA CAAGACCCGG GAACGTATTC ACCGTAGCAT 360  
 GCTGATCTAC GATTACTnAG CGnTTCCAGC TTCCATGnTA 400

(2) INFORMATION FOR SEQ ID NO: 3822:

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3822:

50 TCTACCAACT GAGCTAATGG CTCTAATGGC TGGGCTAGCT GGATTCTGAAC CAACGAGTGA 60  
 CGGATAAAGT CCGTTGCCTT ACCGCTTGCC TATAGCCCAA TATATAGATG GnGGAGGGGG 120  
 GCAGATTCTGA ACTGCCGAAC CCGAAGAGCG GATTTACAGT CCGCCGCGTT TACCACTTCG 180

GAACCGCCGA CCCTCTGCTT GTAAGGCAGA TGCTCTCCCA GCTGAGCTAA TTCTCCAAAA 300  
 TAATGACTCC TACGGACTCG AACCCGTGTT ACCGCCGTGA AAGGGCGGTG TCTTAACCGC 360  
 5 TTGACCAAGG AGCCATGCTC CACAGTAGGA TTCGAACTAA 400

(2) INFORMATION FOR SEQ ID NO: 3823:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3823:

AACTTGCCCTC TTTAGGTACA GCATGAGGCC CTAGGAAAGT ATGTTTCATG TCTAAATCAT 60  
 20 ATTTCTCAGC TAAACGATTA GACACTTTCA ATTGCTTCAG TTCATTTTCT CTATCTAATC 120  
 CATAACCACT CTTACTTTCA ACTGCAnGCA CGCCGTGTTT AATCATAGTA AGCAAATCAT 180  
 GCTCTGCTTT TTTAAACAAG TCATCTTCGG ATGTTTCTCT AGTAGCATT ACGGTAGATA 240  
 25 ATATGCCACC ACCCATTTCT AATATTTCAA GGTAAGACTT ACCTGGACGT TTTAATGACA 300  
 TCTCATGTTT TCGAGATCCA CCAAATGThA AATGGGGTAT GTGGCATCTA CTAAGCCGGG 360  
 GGACACTAnC TTTCCCACTA GGCATCAATC G 391

(2) INFORMATION FOR SEQ ID NO: 3824:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3824:

ACATATCGAT AACATGACAT AACTCATGCT GGGTTTCCCC ATTCGGAAAT CTCTGGATCA 60  
 AAGCTTACTT ACAGCTCCCC AAAGCATATC GTCGTTAGTA ACGTCCTTCA TCGGCTTCTA 120  
 45 GTGCCAAGGC ATCCACCGTG CGCCCTTAAT AACTTAATCT ATGTTTCCAT CCTACAGGAA 180  
 ACGCGTTATT AATCTTGTGG AGTGTTCCTT CGAACACTGA GCGATTATTT CTTATGAATT 240  
 CAAGCTTATT TAAAACTCTT TATTCACTCG GTTTTGCTTG GTAAAATCTA TATTTTACTT 300  
 50 AChTATCTAG TTTTCAATGT ACAATTCTTT TTAGTCAAGC GCTCGCATAA GCAATATCAC 360  
 TTTGAACCAA AAAAGATTGG AAGGTGAAAT AAACATTCAA 400



- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3825:

ATCGATAACA TGACATAACT CATGCTGGGT TTCCCCATTC GGAAATCTCT GGATCAAAGC 60  
 TTACTTACAG CTCCCCAAAG CATATCGTCG TTAGTAACGT CCTTCATCGG CTTCTAGTGC 120  
 CAAGGCATCC ACCGTGCGCC CTTAATAACT TAATCTATGT TTCCATCCTA CAGGAAACGC 180  
 GTTATTAATC TTGTGAGTGT TCTTTCGAAC ACTAGCGATT ATTTCTTATG AATTCAAGCT 240  
 TATTTAAAAC TCTTTATTCA CTCGGTTTTG CTTGGTAAAA TCTATATnTT ACTTACTTAT 300  
 CTAGTTTTCA ATGTACAATT TCTTTTTAGT CAAGCGCTCG CATAAGCAAT ATCACTTTAA 360  
 CCAAAAAATA TTTGAATGTn AAATAAACAT TCAAAACTGA 400

(2) INFORMATION FOR SEQ ID NO: 3826:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3826:

TCACTCACCG CAGATTTTTTA AGTCCTGTGC GTCTGCCAGT TCCGCCACCC CGGCACTATA 60  
 AAAATGGAGC AGAAGACGGG ATTCGAACCC GCGACCCCAA CCTTGGCAAG GTTGTATTCT 120  
 ACCGCTGAAC TACTTCTGCA TATGCGGGTG AAGGGAGTCG AACCCCCACG CCGTAAGnCT 180  
 TAGATCCTAA GTCTAGTGCG TCTGCCAATT CCGCCACACC CGCAAATGGT GAGCCATAGA 240  
 GGATTGGAAC CTCTGACCCT CTGATTAAAA GTCAGATGCT CTACCAACTG AGCTAATGGC 300  
 TCTTCCATGG TGCCGGCCAG AGGATTTGAA CCCCCAACCT TATTGGTTAC AAGTCAGTTG 360  
 CTCTTACCAA TTGAGCTAGG nCGGCAATAT GTTAAGATTA 400

(2) INFORMATION FOR SEQ ID NO: 3827:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3827:

5 AGTGGTGGAA TGGTCTTAAA AGTTGGTGGT CTAACCTTAG AGAAGACCAA AAGAAGAAAA 60  
 GTGATAAATA CGCTAAAGAA CAAGAAGAAA CAGCTCGTAG AAACAGAGAA AATATAAAGA 120  
 AATGGTTTGG AAATGCTTGG GACGGCGTAA AACTAAAAAC TGGTGAAGCC TTTAGTAAAA 180  
 10 TGGGCAGAAA TGCTAATCAT TTTGGCGGCG AAATGAAAAA AATGTGGAGT GGAATCAAAG 240  
 GAATTCCAAG CAAATTAAGT TCAAGTTGGA GCTCAGCCAA AAGTTCTGTA GGATATCACA 300  
 CTAAGGCTAT AGCTAATTAG TACTGGTAAA ATGGTTTGA AAAGCTTGGC CAATCTGTTA 360  
 15 AATTCGACTA CAGGAAGTAT TTACATTCAA ACTAGGCAAA 400

## (2) INFORMATION FOR SEQ ID NO: 3828:

## (i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3828:

TCTCAGTTCC AGTGTGGCCG ATCACCCTCT CAGGTCGGCT ATGCATCGTT GCCTTGTTAA 60  
 GCCGTTACCT TACCAACTAG CTAATGCAGC GCGGATCCAT CTATAAGTGA CAGCAAGACC 120  
 30 GTCTTTCACT TTTGAACCAT GCGGTTCAAA ATATTATCCG GTATTAGCTA CGGTTTCCCG 180  
 AAGTTATCCC AGTCTTATAG GTAGGTTATC CACGTGTTAC TCACCCGTCC GCCGCTAACA 240  
 TCAGAGAAGC AAGCTTCTCG TCCGTTGCGT CGACTTGCAT GTATTAGGCA CGCCGCCAGC 300  
 35 GTTCATCCTG AGCCAGGATC AACTCTCCA TAAAAATTAT GATGTTGANT AGCTCATAAA 360  
 TACTAAATAA TGTGTAACT TATAGTACGT TTTTnGAAAT 400

## 40 (2) INFORMATION FOR SEQ ID NO: 3829:

## (i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3829:

CAAGCGCCAT GACATCATAA CTTTCTTGCA CAAGATATGT GAACGGCGGT GTTGATCCTA 60  
 GATTCGTGGC ATGCATACGC AAACCATTTT CTTCAATTAC TTCACCAAGG CGTTTAAAAAT 120

55

ATTGATAAAA CCTTGATGTG TTTCGTGTCA ATGACATACC ATATCGACTA GGTACCTTTT 240  
 TAGAATGTTG ATTAATCACA ACAAATATCA TGGCAAGGTC ATCTTCAAAA TGATTTCGATT 300  
 5 CAAGTGGGAR sGGCATATGA CGTCTCATCA CtATACCCTt TnTnCCCATT CTGCAAATnC 360  
 ACCCATAAAT ACTACGGGAC GGAGAACCCG TACCCATTTT 400

## (2) INFORMATION FOR SEQ ID NO: 3830:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3830:

20 GGGTACTAAG ATGTTTTCAGT TCTCCGGGTG TGCCTTCTGA TATGCTATGT ATTACATAT 60  
 CGATAACATG ACATAACTCA TGCTGGGTTT CCCCATTCGG AAATCTCTGG ATCAAAGCTT 120  
 ACTTACAGCT CCCCAAAGCA TATCnCGTTA GTAACGTCCT TCATCGGCTT CTAGTGCCAA 180  
 25 GGATCCACCG TCGGCCCTTA ATAACCTAAT CTATGTTTCC ACCATTTTTTA TAAGTCAAAC 240  
 GCTCACATAC GGCTTCGTTT TCATTATTTT AAATGCTCAT TTACATAAGT AAACCTCTGCT 300  
 TTAAAATAAT TTAACCTATT GTCTGCTAAA CGTTTTCTTT TATAAAAAGA TTTAAACGCG 360  
 30 TTATTAATCT TGTGAGTGGT CCTTCGAACA CTAGCGATnA 400

## (2) INFORMATION FOR SEQ ID NO: 3831:

- (i) SEQUENCE CHARACTERISTICS:  
 35 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3831:

AAATGCGGCT CATCGCATCC ATTTTTTGCC TGGCAACGTT CTA CTCTAGC GGAACGTAAG 60  
 45 TTGGCTACCA TCGTCGCTAA AGACCTTTCT TGA CTGTGA CAATCGCTTG CTTCTTTCTT 120  
 CTCCTTCGGC TCTCGCTTAC TCATTTAGCT CTA CTAACT CGTTGCGCTC TTTTCTCGTT 180  
 TCGTCAGATT CAAACGTTTT CACTTCGCCA AGCCATTTTT CTTTGTGTTT ACTTTTTATT 240  
 50 TTGACGTTTT AGACATAAAA AAAAGAGACC TTGCGGTCTC AATGCGGCTC ATCGCATCCA 300  
 TTTTTGCCT GGGCAACGTT CTA CTCTAGC GGAACGTAAT TGGGCTACCA TCGACGCTAA 360

## (2) INFORMATION FOR SEQ ID NO: 3832:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3832:

AGCTTATTTT AAAACGTCGT TTATTCACCTC TGGTTTGTCT TGGTAAAATC TATATTTTAC 60  
TTACTTATCT AGTTTTCAAT GTACAATTTT TTTTGTAGTCA AGCGCTCGCA TAAGCAATAT 120  
CACTTTAACC AAAAAATATT TGAATGTAA ATAAACATTC AAAACTGAAT ACAATATGTC 180  
ACATTATTCG GCATCTTCTG AAGAAGATGT TCCGAATATA TCCTTAGAAA GGAGGTGATC 240  
CAGCCGCACC TTCCGATACG GCTACCTTGT TACGACTTCA CCCCAATCAT TTGTCCCACC 300  
TTCGACGGCT AGCTCCTAAA AGGTTACTCC ACCGGCTTCG GGTGTTACAA ACTCTCGTGG 360  
TGTGACGGGC GGTGTGTACA AGACCCGGGA ACGTATTTCA 400

## (2) INFORMATION FOR SEQ ID NO: 3833:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3833:

TTTTCTTCTG GTAAATATC TGCAATAACA GTATCTATGC CTACTTGTTT TGCAATGGCT 60  
TGAGCAGTGT TTTTATTATC GCCAGTTAAC ATGGCAACTT CAATGCCCAT ATCATGCAAT 120  
TGTATTATAG CATCTTTGGC ATGATCTTTG ACAGTATCTG CCACTGCnAT GATACCAGTT 180  
AATGAATAAT TAACAGCAAT GAGCATAGCA GTTTTACCAT CTCGTTTATA ATGTGTTAAA 240  
TCATCAGAAA TATGCTTAGG CAAGCTAATA TCATTGTCAG CCATTAATnT ACGGGTTACC 300  
AACCAATATA TGGTGATGAT CAATCCGTGG CTTCAATACC ATGGCCAGGT ACCGCTTnAA 360  
AGTTGTTGTC TCAGTTAATA TTAATTGCTT TCCTTTTGCA 400

## (2) INFORMATION FOR SEQ ID NO: 3834:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3834:

5 nAATTATATG GACCTTGCAG GACTCGAACC TGCGACCGAA CGGTTATGAG CCGTTAGCTC 60  
 TAACCAACTG AGCTAAAGGT CCTAAATATA ATTTTACAAC TAATAAATAG TnGCGGnnGA 120  
 GGGGATCGAA CCCCCGACCT CACGGGTATG AACCGTACGC TCTAGCCAGC TGAGCTACAC 180  
 10 CGCCTTATAT AGTTTGTAAA TAATATGGTG GAGACTAGCG GGATCGAACC GCTGACCTCC 240  
 TCGTGCAAA GCAGGCGCTC TCCCAGCTGA GCTAAGCCCC CATAATAATT ACAGTATATC 300  
 GGGGAAGACAG GATTCTGAACC TGCGACCCCT TGGTCCCAAA CCAAGTGCTC TACCAAGCTG 360  
 15 AGCTACTTCC CGTATAATTA ACGCGCCCGA TAGGAGTCGA 400

## (2) INFORMATION FOR SEQ ID NO: 3835:

20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3835:

AATAACAATT GCGCCACTAA AACTCAAAAT TTCCACCACC AACATCCAAA TTATCAACAT 60  
 30 CGCAACATAA CCAAATGTTA TAATAAATCT ATTACACAAA GAGATAAATT ACTTATGCAA 120  
 AGGCGGAGGA ATCAGATGTC TATTACTGAA AAACAACGTC AGCAACAAGC TGAATTACAT 180  
 AAAAAATTAT GGTTCGATTGC GAATGATTTA AGAGGGAACA TGGATGCGAG TGAATTCCGT 240  
 35 AATTACATTT TAGGCTTGAT TTTCTATCGC TTCTTATCTG AAAAAGCCGA ACAAGnATAT 300  
 GCAGATGCCT TGTCAGGTGA AGACATCAGC TATCnAGAAG CGTGGGCAGA TGAAGAATAT 360  
 40 CGTGAAGACT TnAAAAGCAG GAATTAATTG GTTCAAGTCG 400

## (2) INFORMATION FOR SEQ ID NO: 3836:

45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3836:

CTAATCGCAT CTTTTTCAAT CTAAGTGCCT TTGTGACAAA CTTACTGAAC TTAGTGCCAT 60  
 55

ATTATAGCCG AATGCCCAAA ATAGATTTTG ACGAATATTA CGAATGGTTG CTTTACTTGC 180  
 ATAAATGGCT TTAGGAATAA GCATCAAGTC GCCACCAAGA ATAGTAATAT CAGCTGCTTC 240  
 5 AATGGCAACT TCTGTACCTG TACCAATGGC GATACCGATA TCAGCTTTAA CTAAATGCAG 300  
 GTGCATCATT TACACCGTCA CCAACCATCG CAACCTTCTT ACCTGTTGGC TGTAGTTTCG 360  
 10 CAATTGTGGC AGCTTTTTTnC TTCCGGnGAA AATATCnGGC 400

## (2) INFORMATION FOR SEQ ID NO: 3837:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3837:

AGAGCGGATT TACAGTCCGC CGCGTTTACC ACTTCGCTAC CCCTCCAGCT TATTCATATA 60  
 ATTTAATAAT CAAAATGGTG GAGAATGACG GGTTCGAACC GCCGACCCTC TGCTTGTAAG 120  
 25 GCAGATGCTC TCCCAGCTGA GCTAATTCTC CAAAATAATG ACTCCTACGG GACTCGAACC 180  
 CGTGTTACCG CCGTGAAAGG GCGTGTCTTA ACCGCTTGGG CCAAGGAGCC ATGGCTCAAC 240  
 30 AGGTAGGACT CGAACCTACG ACCGATCGGT TAACAGCCGA TAGCTCTACC ACTGAGCTAC 300  
 TGTGGGATTA ATATTATGCC TGGCAACGTT CTACTCTAGC GGAAGTAAn TCGGACTACC 360  
 ATCGACGCTA AGGAGCTTAA CTTCTGTGTT CGGCATGGGG 400

## (2) INFORMATION FOR SEQ ID NO: 3838:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3838:

AATCGCTTGC TTCTTTCCTC TCCTTCGGCT CTCGCTTACT CATTAGCTC TACTAAACTC 60  
 GTTGGCGTCT TTTCTCGTTT CGTCAGATTC AAACGTTTTT ACTTCGCCAA GCCATTTTTT 120  
 50 TTTGTGTTTA TTTTATTTT GACGTTTTAG ACATAAAAAA AAGAGACCTT GCGGTCTCAA 180  
 ATGCGGCTCA TCGCATCCAT TTTTGCCTG GCAACGTTCT ACTCTAGCGG AAGTAATTGG 240  
 GCTACCATCG ACGCTAAGAA CCTTCTTGA CTTGTGACAA TCGCTTGCTT CTTTCCTCTT 300

TCAGATCCAA ACGTTTTCA~~n~~ TCGnCCAAGC CAATTTGCCT

400

## (2) INFORMATION FOR SEQ ID NO: 3839:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 416 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3839:

15 TTACGGCCGC CGTTTACTGG GGCTTCGATT CGTAGCTTCG CAGTAGAcrc GACTCCTCTT 60  
AACCTTCCAG CACCGGGCAG GCGTCACCCT gATAcATCAC CTTACGGTTT AGCAGAGACC 120  
TGTGTTTTTG ATAAACAGTC GCTTGGGCCT ATTCACTGCG GCTCTTCTGG GCGTTAACCC 180  
20 TAAAGAGCAC CCCTTCTCCC GAAGTTACGG GGTCATTTTG CCGAGTTCCT TAACGAGAGT 240  
TCGCTCGCTC ACCTTAGAAT TCTCATCTTG ACTACCTGTG TCGGTTTGCG GTAGGGcACC 300  
TATTTTCTAT CTAGAGGCTT TTCTCGGCAG TGTGAAATCA ACGACTcGAg GACACAATGT 360  
25 CTCTCCCCA TCACAGtTCA GCCTTgAACG rGTaCCGGAT TTGnCTAATG ATTCAG 416

## (2) INFORMATION FOR SEQ ID NO: 3840:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3840:

AAGTTAGGCT ACCATCCTCG CTAAGAACCT TTCTTGACTT GTGACAATCG CTTGCTTCTT 60  
40 TCCTCTCCTT CGGCTCTCGC TTA~~CT~~CATTT AGCTCTACTA AACTCGTTGC GCTCTTTTCT 120  
CGTTTCGTCA GATTCAAACG TTTTCACTTC GCCAAGCCAT TTTTCTTTGT GTTTACTTTT 180  
45 TATTTTGACG TTTTAGACAT AAAAAAAGAG ACCTCACGGT CTCAA~~ACT~~TG CCTGGCAACG 240  
TTCTACTCTA GCGGAACGTA AGTTGGCTAC CATCGTCGCT AAAGACCTTT CTTGACTTGT 300  
GACAATCGCT TGCTTCTTTC CTCTCCTTCG GCTCTCGCTT ACTCATTTAG CTCTACTAAA 360  
50 CTCGTTGGnG CTCTTTTCTT CGGTTTnGTC AGAnTTCAAA 400

## (2) INFORMATION FOR SEQ ID NO: 3841:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3841:

	CGCGACTGAn GAATACAATG nCTACGATAA CTAAACCCAA TCAATCTTTT CATTCTATCA	60
10	ATTCTTTTCA AAATCTTCAC TATATATCAT TAATGTCTAC GTATGAATCT AGCTAGAACA	120
	TTCCCTAGCG TTTGAATCAC TTGGACAATA ATGACTAATA CAATAACGGT AATAATAATG	180
	ACCGTCGTAT CAAATCTTTG ATAACCATAC ACTAAAGCTA AGTCTCCTAT ACCACCACCG	240
15	CCAACAGCTC CTGCCATCGC CGTACTTCCA ATAAGTCCAA TAATCGCAGT GGTAATTGCT	300
	AATACTAACG AACCTAAAGC TTCAGGAATT AAAAAATATC TAATGATTG TAGTGGTGAA	360
20	GCGCCCATCG CTTTCGCCGC TTCAATAATC CCCTCGTCTA	400

(2) INFORMATION FOR SEQ ID NO: 3842:

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 400 base pairs
25	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3842:

	TCGCGATTCTG CGTGTTTCTG AATCATCGGC ATCGCGTCAT TCAATGATTCT ATATGCATCT	60
	AAAGCAATAG AAGATAATGT GTCTGGCACA TATACCCATG CCAACGTATC AGTAGACGTA	120
35	TGATGTTCTG CTACCGCAAA AACAGTTGTC TCTGGAATAT ACACACCTGA TTGTTTTAAT	180
	CCTTGTTCTGA CATTTGGACG ATTACATATC ATCGCTAATA ACTTAGCATT AAAACCGCTT	240
40	GATGCGCCAC CACAAGCCCC ACATTCAAGT GATGCATGAT GTGGATTATT GTGAGAATGA	300
	CTAGCATGAC CTGCTAACAC AACGAACGGC GCAAATGCTT CGGkTAAATC CATCAATTTT	360
	AACGCTgTAA CGCGAATCAA TTGCTCTGCT CAGTAAATCC	400

45

(2) INFORMATION FOR SEQ ID NO: 3843:

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 400 base pairs
	(B) TYPE: nucleic acid
50	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3843:

55



5      GCCAACATCC TAGTTGTCTG GGCAACGCCA CATCCTTTTC CACTTAACAT ATATTTTGGG      120  
 ACCTTAGCTG GTGGTCTGGG CTGTTTCCCh GTCGAACACG GACCTTATCA CCCATGTTCT      180  
 GACTCCCAAG TTAAATTAAT TGGACATTCG GAGTTTGTCT GAATTCGGTA ACCCGAGAGG      240  
 GGCCCCCTCGT CCAAACAGTG CTCTACCTCC AATAATCATC ACTTGAGGCT AGCCCTAAAG      300  
 10      CTATTTCCGA GAGAACCAGC TATTTCCAGG TTCGATTGGG AATTCTCCGC TAACCTCAST      360  
 TCATCCGnTC ACTTTCAACG TAATTCGGGT CGGGTCTCCA      400

## (2) INFORMATION FOR SEQ ID NO: 3844:

15      (i) SEQUENCE CHARACTERISTICS:  
          (A) LENGTH: 469 base pairs  
          (B) TYPE: nucleic acid  
          (C) STRANDEDNESS: double  
          (D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3844:

25      ACTTTTACTT GCTGCGCCTC CAGCCAAACC TGCTGTTCCA GCACCGATCG CTGCACCTTT      60  
 TTTGCCATTA TGATGATCTT TAGACTTATC TTGAGACGCT TTATCCTCAG TCGAGTTATT      120  
 CGCCTTGCCA GAATTACTTT TGTTTTGAGC GTCATTTGAA TGTTTCTTAG CTTTAGAAGC      180  
 30      AGCCATTGCA CCAGCTGCAC CTGCAACACC TGCTGTTCCA GCACCAATAG CTGCTGCTTT      240  
 TTTACCATTA TGATGTTCTT TAGGTTTCATC TTGATCTTGT TTTACAGAAT CATTATCATG      300  
 TTCATTTTTT GATGTTTCTG ATTGGTTAGC ACCTGTTGTA AAATATGGTT TAGGTTGCTG      360  
 35      AGATTGTTCA GCTTCACTCT TATCAGAAAC TGTTGAATGC TCAGTGTAT TTTCTGCATT      420  
 TTTAATAGTA TCGTGTITAn CCATTGTCCT CGAATGGGTT CnGGATGTG      469

## (2) INFORMATION FOR SEQ ID NO: 3845:

40      (i) SEQUENCE CHARACTERISTICS:  
          (A) LENGTH: 400 base pairs  
          (B) TYPE: nucleic acid  
          (C) STRANDEDNESS: double  
          (D) TOPOLOGY: linear

45

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3845:

50      GCTTCACTAC CAAGTGAAGA AGTTGCTGAA ACTCCTGCAG CACCTGCAnC AGTAACATTA      60  
 GAAGCGACT TCCCAGAAAC AACTGAAAAA ATCCCTGCTA TCGTAGAGC AATTGCGnAA      120  
 CATGGnTTTA ACTCTAAGCA TACTGCACCT CATGTAACAT TAATGGATGA AATTGATGTT      180

55

TTAACATTCT TACCTTATGT TGTTAAAGCA CTTGTTTCTG CATTGAAAAA ATACCCAGCA 300  
 CTTAACACTT CATTCAATGA AGAAGCTGGT GAAATCGTTC ATAAACATTA CTGGGAATAT 360  
 5 CGGTATTGCA GCAGACACTG ATAGAGGATT ATTAGTACCT 400

## (2) INFORMATION FOR SEQ ID NO: 3846:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3846:

TTAAGCTACC ATCCTCGCTA AGAACCTTTC TTGACTTGTG ACAATCGCTT GCTTCTTTCC 60  
 20 TCTCCTTCGG CTCTCGCTTA CTCATTTAGC TCTACTAAAC TCGTTGCGCT CTTTCTCGT 120  
 TTCGTCAGAT TCAAACGTTT TCACTTCGCC AAGCCATTTT TCTTTGTGTT TACTTTTTAT 180  
 TTTGACGTTT TAGACATAAA AAAAGAGACC TCACGGTCTC AACTTGCCTG GCAACGTTCT 240  
 25 ACTCTAGCGG AACGTAAGTT GGGCTACCAT CGTCGCTAAA GACCTTTCTT GACTTGTGAC 300  
 AATCGCTTGC TTCTTTCCTC TCCTTCGGCT CTCGCTACT CATTAGCTC TACTAAACTC 360  
 30 GTTGCGCTC TTTTCTCGGT TCGTCAGATT CAAACGGTTT 400

## (2) INFORMATION FOR SEQ ID NO: 3847:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3847:

ATCGTCAACT TATTATTAGA CGATGTACAA GTTACATTAG ACAAAAAAGG TATTACGATG 60  
 GACGTTTCTC AAGATGCGAA AGATTGGTTA ATTGAAGAAG GCTATGATGA AGAATTAGGT 120  
 45 GCACGTCCAT TAAGACGTAT TGTGAACAG CAAGTACGTG ACAAATTAC AGATTACTAT 180  
 TTAGATCATA CAGACGTAA ACATGTGGAT ATAGATGTTG AGGGATAACG AATTAGTCGT 240  
 50 AAAAGGTAAA TAACGACACT TTAACATATC GCGCATCAAA AATGAGCATC AGGTCGCCCT 300  
 TGCCTGTGGC TCATTTTTTT GAATTATTC CCTGGGAAAA TGATTCGCTG TGTGCTGTTT 360  
 TGTnCCACA ACAATCACGA TTGAATGTGC ACATGTGACC 400

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3848:

```

TTTAAACTC TTTATTCAC TCGTTTTGCT TGGTAAATC TATATTTTAC TTACTTATCT   60
AGTTTTCAAT GTACAAATAA TGGTGGGCTT AAGTGGACTC GAACCACCGA CCTCACGCTT   120
ATCAGGCGTG CGCTCTAACC AGCTGAGCTA TAGGCCCAT TTTTGAATG TTAAATAAAC   180
ATTCAAAACT GAATACAATA TGTCACGTTA TTCCGCATCT TCTGAAGAAG ATGTTCCGAA   240
TATATCCTTA GAAAGGAGGT GATCCAGCCG CACCTTTCCG ATACGGCTAC CTTGGTnACG   300
ACTTCACCCC AAATCATTTG TCCCACCTTC GACGGCTAGC TCCTAAAAGG TTACTCCACC   360
GGCTTCGGGn GTTACAACT CTCGTGGGTG TGACnGGCGG   400

```

(2) INFORMATION FOR SEQ ID NO: 3849:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3849:

```

GTCTCAACTT GCCTGGCAAC GTTCTACTCT AGCGGAACGT AAGTTGGCTA CCATCGTCGC   60
TAAAGACCTT TCTTGACTTG TGACAATCGC TTGCTTCTTT CCTCTCCTTC GGCTCTCGCT   120
TACTCATTTA GCTCTACTAA ACTCGTTGCG CTCTTTTCTC GTTTCGTCAG ATTCAAACGT   180
TTTCACTTCG CCAAGCCATT TTTCTTTGTG TTTACTTTTT ATTTTGACGT TTTAGGCATA   240
AAAAAAGAG ACCTTGCGGT CTCAATGCGG CTCATCGCAT CCATTTTTTG CCTGGCAACG   300
TTCTACTCTA GCGGAACGTA AGTTGGCTAC CATCGTCGCT AAAGACCTTT CTTGACTTGT   360
GACAATCGCT TGCTTCTTTC CTnTCCTTCG GCTCTCGCTT   400

```

(2) INFORMATION FOR SEQ ID NO: 3850:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 463 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3850:

5 GTCTACTAAT GTTACAACCA CACCTGATTa ATTGCTTTTT TAGCAGTAAT TGCCACATCT 60  
 GTGTGACGAT AATGATATGC GACAGTTAAT AATTTGTGAT TTTTATTAGC CGCTTCAATC 120  
 ATGCGATCAC ACTCTTCCGT CGTCATCGCC ATTGGCTTTT CACACAATAC ATGGACACCA 180  
 10 TGGTTCAATG CTTCTATAGA AAGATCAGCA TGAATTTAT TAGGTGTACA AATGACCACC 240  
 GCATCAACAA GTTTAAACAG CTCGCTAGGT GTCTCAACTG CATGAGGTAT ATTAAAGCGC 300  
 TTCGCAACAT CAATCATCTG CACTGTATTA ATATCTTGTA CTGCAACTAA TGAGACTGTG 360  
 15 TCTTTGAGTT TCAGCAATGC TGAATATGA CGGTCTTG TG CAATACCACC AACAACTATG 420  
 CACACCAACT TTTAAaTTTG TnCATGATGT GCCnGCTTnA CCG 463

## (2) INFORMATION FOR SEQ ID NO: 3851:

20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 628 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 25 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3851:

30 TATGCTCTAA TGCTGGGCTT AGTGGAITCG ACCAACGAGT GACGnAGTCA AAGTCnGTTG 60  
 CTTTACGCTT GGCTATAGCC CCAATATATA GATGTTGGAG GGGGCAGATT CGAACTGCCG 120  
 AACCCGAAGG AGCGGATTTA CAGTCCGCCg CGTTTAGCCA CTTGCTACC CCTCCAGCTT 180  
 35 ATTCATATAA TTTAATAATC AAAATGGTGG AGAATGACGG GTTCGAACCG CCGACCCTCT 240  
 GCTTGTAAGG CAGATGCTCT CCCAGCTGAG CTAATTCTCC AAAATAATGA CTCCTACGGG 300  
 ACTCGAACCC GTGTTACCGC CGTGAAAGGG CGtGTcTTAA CCGCTTGACC AAGGAGCCAT 360  
 40 GGCTCaCAGG TAGGACTCGA ACCTACGACC GATCGGTTAA CAGCCGATAG CTCTACCACT 420  
 GAGCTACTGT GGaTTAATAT TATGCCTGGC AACGTTCTAC TCTAGCGGAA CGTAAGTtCG 480  
 GACTrACCAT CGACGCTgAA GGAGCTTAAa CTTCTGTGTT CgGCATGGGa ACAGGTGTGA 540  
 45 CCTCCTTGCT ATAGTCACCA GACATATGGA ATGTGAATTT GATGACATTG CAAAaNTAGn 600  
 TTAGTAAGTA AAAGTGGATT TTGGnTTn 628

## (2) INFORMATION FOR SEQ ID NO: 3852:

50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 55 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3852:

5 TAAAGATTTA AAAGTAGCTG TTATTGGnAC AGGTGGAATT GGCCGTGTAG TAGCCGATAT 60  
 ATTTGCCAAT GGTATCAAA GTGATGTGGT CGCATACGAC CGTTTCCTAA TGCTAAAATT 120  
 GCAACGTATG TCGATTACAA AGATACGATT GAGGAAGCGG TTGAAGGTGC TGATATCGTG 180  
 10 ACATTACATG TACCTGCAAC GAAATATAAT CATTATCTAT TTAATGCTGA ATTATTTAAA 240  
 CATTTTAAAA AGGGCGCnTA TTTGTCAATT GTGCGAGAGG TTCTTTAGTA GGATACTAAG 300  
 GCGTTATTAG ACGCATTAGA CAATGGTGTG ATTAAAGGTG CAGCACTTgn TTACGTATGG 360  
 15 ATTTGGAACG GCAAACTTTT TCCCAAGTGG TCCAAAGGGG 400

## (2) INFORMATION FOR SEQ ID NO: 3853:

## (i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3853:

TCTTAAACAT TAGCCACAGC TAATTGTGAC TTAAAAATAG GAATACATGA GTAAAACTCA 60  
 30 TCATAAGAAA TACTAATTTT TATAGAAAAA GTATTACTTT ATCGTTGTCC CACCCCAACT 120  
 TGCACATTAT TGTAAGCTGA CTTTCGCCCA GCTTCTGTGT TGGGGCCCCG CCAACTTGCA 180  
 CATTATTGTA AGCTGACTTT TCGTCACTTG CTGTGTTGGG GCCCCGCCAA CTGTCACATT 240  
 35 ATTGTAAGCT GACTTTTCGT CACTTnCTGT GTTGGGGCCC CGCCAAGTGG CATTGTCTGT 300  
 AGAAATTGGG AATCCAATTT CTGCTATGTT GGGGCCCA CAACCAACTnC GCATTGCCTG 360  
 TAGAATTTCT TTTCGAAATT CTCTGTGTTG GGGGCCCA 400

## (2) INFORMATION FOR SEQ ID NO: 3854:

## (i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3854:

50 GTGCAATCTG CGTTAACAAA TGTAATCGT GTCAATGAGC GATTAACGCA AGCAATTAAT 60

5 GAAATCAATA nATCAGTAAC TACTGATGGT ATGACACAAT CATCAATCCA AGCATATGAA 180  
 AATGCTAAAC GTGCGGGTCA AACAGAATCA ACAAATGCAC AAAATGTTAT TAACAATGGT 240  
 5 GATGCGACTG ACCAACAAAT TGCCGCAGAA AAAACAAAAG TAGAAGAAAA ATATAATAGC 300  
 TTAAACAAG CAATTGCTGG ATTAnCTCCA GACTTGGCAC CATTACAAAC TGCAAAAnCT 360  
 10 CAGTTGCAAA TgntATTGTC AGCCACGAGT ACGGCTGGTA 400

(2) INFORMATION FOR SEQ ID NO: 3855:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3855:

TGTGTGAAAA ACCAATGGCT GAAAACGACA GCAGAAGCTC AAAAAATGAT AGATACAGCT 60  
 AAATCAACAG GTAAAAAATT AACAATAGGT TATCAAAATC GTTCCGAGC AGATAGTCAA 120  
 25 TTTTACATC AAGCAGCGCA ACGTGCGCAC TTAGGAGACA TTTACTTCGG AAAGGCACAT 180  
 GCCATTGCTC GTCGAGCAGT ACCAACATGG GGTGTCTTTC TAGACGTAGT AAGCTCAAGG 240  
 TGGAGGACCA TTAATCGATA TCGGTACACA CGCTTTAGAT TTAACGTTAT GGATGATGGA 300  
 30 TAnTTATGGA ACCAGAATCA GTGATGGGTT TCAACATTCC ATAAATTnAA TAAACAGCCT 360  
 CATGCGGGCA AACGCTTGGG GTTTCAGGnG TTCCAGATGG 400

35 (2) INFORMATION FOR SEQ ID NO: 3856:

40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3856:

45 CGTTCTCAAT AGAATGATTT AAATCTTCGA TTTCTTTATC TAAATGACTA CCAATTAAAT 60  
 CTATTTCTTC TATTGTTAAA TCGCTATCTC CATCTTCTTT TATCTCTGGT ATTATTTTTT 120  
 CTTCAACTAA GTCACGATAT AATGTTTTTG AATTTTCGTT CAATTTTCGAT TCGTGATTTT 180  
 50 GAATACTTTT CTTCACACA AATGTATATC TATTGGCATT AGCTTCTACT TTTGTACCAT 240  
 CAATAAAAAT TGAATTATTA TCAATAAGAT TTTGCTTTAA ACATTGACTA TGGAAGTGA 300

55

TATAAGAAGG nGTTGGAnC nTGAGCGAAC CACAnCATCC

400

(2) INFORMATION FOR SEQ ID NO: 3857:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3857:

GGCATACCAT GGTCAAACGC GTGATGATCA AGTAACATCA CATGTTCAAC ATATTTTGA 60  
 AGTTGTGAAT GCACATGGTA AACATTTTGT TGCATTACCA CGTGAAGATG AAGATATTGC 120  
 AAAATGGCAG GCACAAGGTG TACAAACATT TATTTTAGGT GATGATCGCG GAAAAATATA 180  
 TCGCCATTTA AGTGCATCTC TAGCGACGTC TAAACAGAAA GGGGATGAAG GCTAATGCGT 240  
 AAAGTTCAAC CTGTTATTGA ACAATTAAAA GCACAATCTC ATCCAGTTTG TCATTAnATC 300  
 TATGATTTAG TCGGACTGGG ACATCATTTG CAnCATATTA CATCGnCCCT GCCGAGTAAT 360  
 TGTCAARTGT ACTATGCAAT G 381

(2) INFORMATION FOR SEQ ID NO: 3858:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3858:

GCATGAAGCC CCCCTCAAGA TGAGATTTC CAACTTCGGT TATAAGATCC CTCAAAGATG 60  
 ATGAGGTTAA TAGGTTGAG GTGGAAGCAT GGTGACATGT GGAAGCTGAC GAATACTAAT 120  
 CGATCGAAGA CTTAATCAAA ATAAATGTTT TGCACAAATT CACTTTTACT TACTATCTAG 180  
 TTTTGAATGT ATAAATTACA TTCATATGTC TGGTGACTAT AGCAAGGAGG TCACACCTGT 240  
 TCCCATGCCG AACACAGAAG TTAAGCTCCT TAGCGTCGAT GGTAGTCGAA CTTACGTTCC 300  
 GCTAGAGTAG AACGTTGCCA GGCAAAAAAT GGATGCCGAT GGAGCCGCAT TGAGACCGCA 360  
 GGnCTnTTTG TTTTTTATGT CTAAAACGTC CAAATTAAnA 400

(2) INFORMATION FOR SEQ ID NO: 3859:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 573 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3859:

	GTTTATTAAAT CGTGTCATTA GCATCTTTAT AATTGCTTCT AATCGTATTC AAATCACCTA	60
10	ATGTTAAATC TGTTTAAACA TTATTTTGAA TTTCATTCTAT GCATCTGAAT CTGAATCGCT	120
	ATCTGAATCT GAGTCGTTGT CTGAGTCCGA nTCGCTATCT GAnTCTGAGT CGCTGTCTGA	180
	ATCTGAATCG CTATCCGAGT CTGAGTCGCT ATCTGAGTCT GAGTCGCTAT CTGAATCTGA	240
15	ATCGCTGTCT GAGTCTGAAT CGCTATCTGA GTCTGAATCG CTGTCCGAAT CTGAGTCGCT	300
	ATCTGAATCT GAATCGCTAT CTGAATCTGA GTCGTTGTCT GAGTCCGAAT CGCTATCTGA	360
	ATCTGAGTCG CTATCTGAGT CTGAGTCGCT ATCTGAATCT GAGTCGCTGT CTGAATCTGA	420
20	ATCACTGTCT GAGTCTGAGT CGCTGTCTGA AGTCTGAATC GCTGTCAGAA TCTGAGTCGC	480
	CAACTGAGTC TGAATCTGAA TCACTGGTCT GAGTCCGAAT CGCnATCTGA ATCnGAATCG	540
25	CnAACCGAGT CCGAAGCCGC nAATCCGAAT CTG	573

(2) INFORMATION FOR SEQ ID NO: 3860:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3860:

	GAGCTACACC GCCTTATATA GTTTGTAAAT AATATGGTGG AGACTAGCGG GATCGAACCG	60
40	CTGACCTCCT GCGTGCAAAG CAGGCGCTCT CCCAGCTGAG CTAAGCCCCC ATAATAATTA	120
	CAGTATATCG GGAAGACAGG ATTCGAACCT GCGACCCCTT GGTCCCAAAC CAAGTGCTCT	180
	ACCAAGCTGA GCTACTTCCC GTATAATTAA CGCGCCCGAT AGGAGTCGAA CCCATAACCT	240
45	CTTGATCCGT AGTCAAACGC TCTATCCAAT TGAGCTACGG GCGCATATGT TTTTATTGnA	300
	AAATGGTGCC GAGGnACCGG GAATCGGAAC CGGTACGGTT GATnCACTCA CCGGCAGGAT	360
	TTTTAAGTCC TGTGCGTCTG CCAGTTCGCG CACCCCGnGC	400

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(2) INFORMATION FOR SEQ ID NO: 3861:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3861:

5 TGTTCGACT AAACCATTAC CTATCGCACA TATGACGAAA CCAATGATAA CTGCAATGAC 60  
 ATATTGTGAT GCCAATAATT GAGTCATGCT AATAATAGTG ATGCCGATGA CAGGGAACAA 120  
 CGGACCAATG ATGAGCATCA ATTTGCCACC GAAACGTAAT GTTGCTTTTT CACCTAAACG 180  
 10 AATCATCGCA ACTGCCACAA TGGCATATGG CAATGTAACA nGTCCAGATT GCGCACTGAT 240  
 AAACCAAGGT GTGTTTGAGC ATATATGAAA AAGACCACTG TTACGCCTAG ACCGCTATTT 300  
 AAAACAAAGT TATTTAAAAA TGCACCAATG GAACGGACGG TTGCGTAATA CTGGAGAAnt 360  
 15 CAATAAAAGG TACTTCCATG TCCGACGTTT CGATGGATGG 400

## (2) INFORMATION FOR SEQ ID NO: 3862:

## (i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3862:

GTGCGCATGG GAACTATCAA GCTTTGAAGA TGTGGTACTA CATGCGTTGA ATTAGGGATC 60  
 30 GGTACTTTAT ATGAAGACGT GCTGCTTCCA TTAAATGAGT GATGCGATTT TGGCATGAAG 120  
 GTCACCTTAA ATGTACATTG TTGTAATAAA ATTGCCTATA AATTTTTAGC ACATAAAATA 180  
 AGAGGAGCCA ACCATTGTGA GACTATAACA ACGGTTGGCT CTTTAATTGT AAAAAGAAAA 240  
 35 CCATACGCTA TCGGTATGGT TCAGAAAAGG TCTACCATTG TCACCAAAAA TGCATCTCTA 300  
 CGTGCTAGAA TAAATATTGG TCAGCCAACC AAAATAATCC ACACGGGGAG ATGCTATTTA 360  
 ATGTCCTCCT GACACCAACA GTTAGCACCA TACAAAATGG 400

## 40 (2) INFORMATION FOR SEQ ID NO: 3863:

## (i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3863:

TCGGCAAGCC ATTTTCTTT GTGTTTACTT TTTATTTTGA CGTTTTAGAC ATAAAAAAA 60

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CTAGCGGAAC GTAAGTTGGC TACCATCGAC GCTAAGAACC TTTCTTGACT TGTGACAATC 180  
 GCTTGCTTCT TTCCTCTTCT TCGGCTCTCG CTTACTCATT TAGCTCTACT AAACCTGTTG 240  
 5 CGCTCTTTTC TCGTTTCGTC AGATTCAAAC GTTTTCACCT CGCCAAGCCA TTTTCTTTG 300  
 TGTGCTGCTT TTATTTTGAC GTTTTAGACA TAAAAAAAAG AGACCTTGCG GTCTCAAATG 360  
 10 CGGCTCATCG CATnCATtnt TGCCGGCAAC GTTCTACTCT 400

(2) INFORMATION FOR SEQ ID NO: 3864:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 15 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3864:

GTACTATAGA ATTAAAGAAT TATAAAAATA TAATCCTGAT TAGCTTGTTG TCAAGTCATC 60  
 GTTCATAATG AAGATATCAC GTTCAATTGT ATTGTTTGTT TATGGGAAAT GAATTAATGT 120  
 25 AATAGTATAT GTATGCGGTT ACATAAAAAG CGAACATCTA ACCTGATATT TAAATGAACC 180  
 TGACGCTCAA TCAACTAATT TACAACCGTA TTTTATAAT CAACCATAAA GGAGGAGATA 240  
 30 GAAAATGAAT AGTGCAAAAT TGATTGATCA CACTTTATTG AAGCCTGAGT CAACACGTAC 300  
 GCAAATCGAT CCAAATCATC GATGAAGCGA AGCATACCAT TTAAATCTG TATGTGTGAA 360  
 TCCAACGCAT GTTAAAGTG CCAGCAGAGC GACTAGCTGG 400

35 (2) INFORMATION FOR SEQ ID NO: 3865:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 40 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3865:

GCAGCACGTC TTCATATAAA GTACCGATCC CTAATTCAAC GCATGTAGTA CCACATCTTC 60  
 AAAGCTTGAT AGTTCCCATG CGCACACCAC GTTTCATACT AGCTATGCGA GCTCAACTTG 120  
 50 GTTCATAAAC TCTTTAATAT AAGTCAATGT TTCAACCATC GCTGGTGGTC TTGGCACATG 180  
 TCCTTCTGCC ATTTGATAAA ATGTTTCATG CGTGGCACCT TTAACTCTA GTTGGTCCGC 240  
 TAAATAATAC GCATGATGAA TACCAACTTG CTGGTCTTTC CCTCCATGTA CAATTAATAT 300

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TTTTTTCGGA TGACCAATCA TTCTTCGTAG CATGCCTCTT

400

## (2) INFORMATION FOR SEQ ID NO: 3866:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3866:

AAGTCAATAA CTTTTTTTAT CTGTGCCATT TTATTTTTTA ACCAAAATTG GATTAAAAAA 60

CTGCCTGGCA ACGTTCTACT CTAGCGGAAC GTAAGTTCGA nCTACCATCG ACGCTAAGGA 120

GCTTAACTTC TGTGTTCCGC ATGGGAACAG GTGTGACCTC CTTGCTATAG TCACCAGACA 180

TATGAATGTA ATTTATACAT TCAAACTAG ATAGTAAGTA AAAGTGATTT TGCTTCGCAA 240

AACATTTIATT TTGATTAAGT CTTGATCGA TTAGTATTCG TCAGCTCCAC ATGTCACCAT 300

GCTTCCACCT CGGAACCTAT TAACCTCATC ATCTTTGGAG GGGATCTTAT AACCGGAGGT 360

TGGGGnAAAT CTCATCTTGA GGGGGGGCTT CCAGGCTTAG 400

## (2) INFORMATION FOR SEQ ID NO: 3867:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3867:

CACCTATAAT CGTTTTAATC GATGGGGGGA CGCATAGGGA TAGGCGAnGT GnCGATTGGA 60

TTGCACGTCT AAGCAGTAAG GCTGAGTATT AGGCAAATCC GGTACTCGTT AAGGCTGAGC 120

TGTGATGGGG AGAAGACATT GTGTCTTCGA GGTGTTGAT TTCACACTGC CGAGAAAAGC 180

CTCTAGATAG AAAATAGGTG CCCGTACCGC AAACCGACAC AGGTAGTCAA GATGAGAATT 240

CTAAGGTGAG CGAGCGAACT CTCGTAAAGG AACTCGGCAA AATGACCCCG TAAC'TTCGGG 300

AAGAAGGGTG CTC'TTTAAGG TTAACGCCCA GAAGAGCCGC ATGAATAGGC CCAAGCGACT 360

GTTTAnTCAA AACACAGTCT CTGCTAAACC TAAGGATGTA 400

## (2) INFORMATION FOR SEQ ID NO: 3868:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 383 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3868:

TTCTTTGGAA ATAGTAACGT TGAAGTTGTA CTCACTGGTG ATACATTTGA TCACTGTTTA 60  
10 GCTGAAGCTT TAACTTATAC AAGTGAACAT CAAATGAnCT TTATAGATCC ATTCAATAAT 120  
GTTTCATACAA TTTCTGGACA AGGTACGCTT GCTAAAGAAA TGCTAGAACA AGCAAAGTCT 180  
GACAATGTTA ACTTTGATTA TCTATTTGCC GCAATTGGTG GTGGCGGTTT AATTTCAAGT 240  
15 ATTAGTACTT ACTTTAA AAC CTATTCACCT ACCACGnAAA TTATAGGTGT TGAACCTTCA 300  
GGTGCCAACT AGTATGTGAT GGAATCTGTT GTGAAATATT CAGGTAGTCA CATTGCCCTA 360  
AnTCGATAAA TTTGTGGACG GTG 383

20

(2) INFORMATION FOR SEQ ID NO: 3869:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3869:

CTAAGCTTAA GGGTTGCGCT CGTTGCGGGA CTTAACCCAA CATCTCACGA CACGAGCTGA 60  
CGACAACCAC CACCTGTCAC TTTGTCCCCC GAAGAAGnGC TCTATCTCTA GATTGTCAAA 120  
35 GGATGTCAAG ATTTGGTAAG GTTCTTCGCG TTGCTTCGAA TTAAACCACA TGCTCCACCG 180  
nTTGTGCGGT TCCCCGTC AA TTCCTTTGAG TTTCAACCTT GCGGTCGTAC TCCCCAGGCG 240  
GAGTGCTTAA TGC GTTAnTG CCAGCACTAA GGGGCGGAAA CCCCCTAACA CTTAGCACTC 300  
40 ATCGTTTACG GCGTGGACTA CCAGGTATC TAATCCTGTT TGATCCCCAC GGTTTCGCAC 360  
ATCAGCGTCA TTTACAGACC AGAAAGTCGn CTTCGGCAAT 400

45

(2) INFORMATION FOR SEQ ID NO: 3870:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 377 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3870:

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GTGTGCCTTC TGATATGCTA TGTATTCACA TATCGATAAC ATGACATAAC TCATGCTGGG 120  
 TTTCCCCATT CGGAAATCTC TGGATCAAAG CTTACTTACA GCTCCCCAAA GCATATCGTC 180  
 5 GTTAGTAACG TCCTTCATCG GCTTCTAGTG CCAAGGCATC CACCGTGCGC CCTTAATAAC 240  
 TTAATCTATG TTTCCATCCT ACAGGAAACG CGTTATTAAT CTTGTGAGTG TTCTTTTCGAA 300  
 CATGAGCGAT TATTTCTTAT GAATTCAAGC TTATTTAAAA CTCTTTATTC ACTCGGTTTT 360  
 10 GCTTGGTAAA AGCnnGn 377

## (2) INFORMATION FOR SEQ ID NO: 3871:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3871:

ATAACGTTGC CCTCCCCATG TATATCCTAC CCAAACATGA CCATCTTGTA ACATCACTTC 60  
 25 TGTATAATCA CAATACCCAC CAGGTTGGAA CTGATAACCC ACTGGACAAG ATAAGAAATGG 120  
 CCCCACTTTT CTTACTGTGA TTGGTTGATT GCCGTTTGTG AATCTAGCAC TTTCTTCCAT 180  
 GTAGTAAGTA CCATATTTAT TACGTTTCCA TGCACCTGCA ACTGGTTTAA CTGTATTACT 240  
 30 TGAAGCGCTT GACTCATTAG AGACAGTGGC AACCGGTATT TTACCATCCA TGTACGCCCT 300  
 AAATCTGCTT GATAAAGTAG TCTTTTAAGT TGCAACCGCT TGTCTTCTGG GCAATAGACC 360  
 35 GCGAGTTACn GGGGTCCAAA CCCnTGGTGT AAAAnCGAAC 400

## (2) INFORMATION FOR SEQ ID NO: 3872:

40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3872:

CGCTACACTA CGAGACCATT AGTAAAACGC AGGAAGAGGG ATTCTGAACCC CCGCGAGCCC 60  
 TTAAGCCCCT GTCGGTTTTT AAGACCGATC CCTTCAGCCG GACTTGGGTA TTCCTCCAAA 120  
 50 ATTATATGGA CCTTGCAGGA CTCGAACCTG CGACCGAACG TTATGAGCCG TTAGCTCTAA 180  
 CCAACTGAGC TAAAGGTCCT AAATATAATT TTACAACTAA TAAATAGTGG CGGTGGAGGG 240

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GCCTTATATA GTTTGTAAAT AATATGGTGG AGACTAGCGG GGATCGAACC GCTGTACCTC 360  
CTGCGTGCAA ACGGGCGCTC TTCCCAGCTG nAGCTAAAGC 400

(2) INFORMATION FOR SEQ ID NO: 3873:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 584 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3873:

ACAGCTCACG GTCTCAACTT GCCTGGCAAC GTTCTACTCT AGCGGAACGT AAGTTGGCTA 60  
CCATCGTCGC TAAAGACCTT TCTTGACTTG TGACAATCGC TTGCTTCTTT CCTCTCTTCG 120  
GTCTCGCTTA CTCATTTAGC TCTACTAAAC TCGTTGCGCT CTTTCTCGTT TCGTCAGATT 180  
CAAnngTTTT CatTCGCCAA GCCATTTTTC TTTGTGTTTA CTTTTTATTT TGACGTTTTA 240  
GGCATAAAAA AAAGAGACCT TGCGGTCTCA AnTGCGGCTC ATCGCATCCA TTTTTTGCCT 300  
GGCAACGTTT TACTCTAGCG GAAnTAAGTT GGGCTACCAT CGTCGCTAAA GACCTTTCTT 360  
GACTTGTGAC AATCGCTTGC TTCTTTCCTC TCCTTCGGCT CTCGCTTACT CATTTAGCTC 420  
TACTAAACTC GTTGCCTCTT TTTCTCGTTT CGTCAGATTC AAACGTTTTT ACTTCGCCAA 480  
GCCATTTTTC TTTGTGTTTA CTTnTnATTT TGACGTTTTA GACATAAAAA AAAGAGACCT 540  
TGCGGTCCAA ATGCGGGCTC ATCGCATCCA TTTTTTGCCT GGGC 584

(2) INFORMATION FOR SEQ ID NO: 3874:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3874:

TTTGCTGGC AACGTTCTAC TCTAGCGGAA CGTAAnTTGG CTACCATCGT CGCTAAAGAC 60  
CTTCTTGAC TTGTGACAAT CGCTTGCTTC TTCTCTCTCC TTCGGCTCTC GCTTACTCAT 120  
TTAGCTCTAC TAAACTCGTT GCGCTCTTTT CTCGTTTCGT CAGATTCAAA CGTTTTCACT 180  
TCGCCAAGCC ATTTTTCTTT GTGTTTACTT TTTATTTTGA CGTTTTAGAC ATAAAAA 240  
GAGACCTTGC GGTCTCAATG CGGCTCATCG CATCCATTTT TTGCCTGGCA ACGTTCTACT 300

GCTTGCTTCT TTCCTCTTCT TCGGCTCTCG CTTACTCATT

400

(2) INFORMATION FOR SEQ ID NO: 3875:

- 5 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3875:

15 TCTGCTAATT TAAAAATGAT ATTTTCTATC TTTTCTTTAT TATTAACGTC TAATGCACTG 60  
 GTCGATTCAT CTAATAAAAG AATATCCGGT GTATACATCA GTTGGCGCGC TATAGCAATT 120  
 CTTTGCCGCT CACCACCGA CATATTTTCC ACTTCCGAAC TTAATTGATA ATGTCCCAAA 180  
 20 CCGACATCTT TAATTAATTG CTTTGCACGT TTTCTATCAA ATTTATCATT ACGTGCAAGT 240  
 GATGGGAATA TCATGTTATC TTCAATCGGT CACCAAACAA GTCACTTTGC TGCATCAAAT 300  
 AACTGATTCG TTGACGCCAA TTCTTCCGGG GCATAATnCA TATAGGGGTT ACCTTAAAAA 360  
 25 TAAAGGTCCT CCACTAGTTG GCCTAnACnA ATTACATAAn 400

(2) INFORMATION FOR SEQ ID NO: 3876:

- 30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3876:

AGATAGACTT TCTGGTGAAG ATACACGTGA AGGTATGACA GCAATTATAT CTATCAAACA 60  
 40 TGGTGATCCT CAATTCGAAG GTCAAACGAA GACAAAATTA GGTAATTCTG AAGTGCCTCA 120  
 AGTTGTAGAT AAATTATTCT CAGAGCACTT TGAACGATTT TTATATGAAA ATCCACAAGT 180  
 CGCACGTACA GTGTTTGAAA AAGGTATTAT GCGGGCACTG CACGTnTTGC TGCGAAAAAA 240  
 45 GCGCGTGAAG TAACACGTCC GTAAATCAGC GTTAGATGTA GCAAGCCTTC CAGGTAAATT 300  
 AGCCGATTGC TCTAGTAAAA GTCCTGAAGA ATGTGAGATT TCTTAGTCGA AGGGGCTCTG 360  
 CCGGGGGGTC TACAAAATCT GGTGCTGACT CTAGACCGCA 400

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(2) INFORMATION FOR SEQ ID NO: 3877:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs

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(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3877:

ACCAATTTCT CCTTTGTATC CGCCATCTTT AAATAATTTT ACTGCTCTAG CATGAGCCAC 60  
10 CATCATGTTA TGTGATTGGA AACTTTTTTC AAAATCATAT TTAATACCTG GAGGGAATTT 120  
ACCTACTAAA TATTGACCAT CACCAATAGG TCCAATTTCA TTGAATGTAG TCCAATATTT 180  
TACTTCTGGG AATTCTTTAA AACAATATTC AGCATAATCT ACAAAGTAGT CAATCGTTTT 240  
15 ACGnTTTAGA AAATCGCCAT CTTTGGTGGT ACACTTCTGG GnGTATCAAA ATGnTGCAAT 300  
GTTACAAATG GTTCAACATG ACGGTTTATG GnCACTCTGC AAATAACCTT ATGGTAATAC 360  
TCAACACCTT AGGGGTTAAC TTCGGCCATA TCCCTTTTGG 400

20

(2) INFORMATION FOR SEQ ID NO: 3878:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3878:

ATTAAAGCAG TTTCTGGATC TGGTAAAAAT GGTCGTATTA CAAAAGAAGA TG TAGATGCA 60  
TACTTAAATG GTGGTGACC AACAGCTTCA AATGAATCAG CTGCTTCACT AACAAGTGAA 120  
35 GAAGTTGCTG AAACCTCTGC AGCACCTGCa GCAGTTAACA TTAGAAGGCG ACTTCCCAGA 180  
AACAAGTGA AAAAATCCCT GGCTATGCGT AGAGCAATTG CGAnAACATG GGTTTAACTC 240  
40 TAAGCATACT GCACCTCATG TAACATTAAT GGATGAAATT GGATGTTCAA GCATTATGGG 300  
GATCACCGTA AGAAATTTAA AGAAATCGCG GCTGAACAAG GTACTAAGTT AACATTCTTA 360  
CCTTATGTTG TTAAnGCACT GTTTTCGGCA TGGnAAAAAT 400

45

(2) INFORMATION FOR SEQ ID NO: 3879:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3879:



TTGTGTTTAC TTTTATTTT GACGTTTTAG ACATAAAAAA AAGAGACCTT GCGGTCTCAA 120  
 TGCGGCTCAT CGCATCCATT TTTTGCTGG CAACGTTCTA CTCTAGCGGA ACGTAAGTTG 180  
 5 GCTACCATCG ACGCTAAGAA CCTTCTTGA CTTGTGACAA TCGCTTGCTT CTTTCCTCTT 240  
 CTTCGGCTCT CGCTTACTCA TTTAGCTCTA CTAAACTCGT TCGGCTCTTT TCTCGTTTCG 300  
 TCAGATTCAA ACGTTTCACT TCGCAAGCCA TTTTCTTTG TGTGCTTTT ATTTGACGTT 360  
 10 TAGACATAAA AnAAGAnCCT TCGGnCTCA ATCGGCCAT 400

## (2) INFORMATION FOR SEQ ID NO: 3880:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3880:

TAGGTGTAAA TCCTGCGATT CGATCTGGAC CATATTTTTT TATTGTATAC AGTAATTGTG 60  
 25 CTGCGATTAT CTCTGTAACG TCTTTCCAAT TTGAACGCAC GTGCCCTCCC ATACCTCGGG 120  
 CTTGCTTATA TTGTTTGGCT TTGTCTTCAT TTTCAACAAT AGACGCCCAT GCAGCAACGC 180  
 GATTACCATT GTTTCTTCT AATGCTTCAG TCCATAAATC CCAGAGTTTT CCACGAATAT 240  
 30 ATGGATATTG ATTCTAAGCG GACTGTATCA TACCAAGAGA ATGACGCACT CGTGGACATC 300  
 CTCTCGGTCA TATTCAGGCA TATCCGACA CAACTTGGAT AGCAGTTGTG ATTTCCAGG 360  
 35 AATCACACCA TTTCACAAAC TTCCAGACAT GGCTGACAGT 400

## (2) INFORMATION FOR SEQ ID NO: 3881:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3881:

TGAGTAGCGA AAGACGGGTG AGAATCCCGT CCACCGATTG ACTAAGGTTT CCAGAGGAAG 60  
 50 GCTCGTCCGC TCTGGGTTAG TCGGGTCCTA AGCTGAGGCC GACAGnGTAG GCGATGGATA 120  
 ACAGGTTGAT ATTCCTGTAC CACCTATAAT CGTTTTAATC GATGGGGGGA CGCAGTAGGA 180  
 TAGGCGAACG TCGATTGGA TTGCACGTCT AAGCAGTAAG GCTGAGTATT AGGCAAATCC 240

TCACACTGCC GAGAAAAGCC TCTAAGATAA GAAAATTAGG TGCCCGTACC GCAAACCGAC 360  
 ACAGGTAGTC CAAGATGGAG AnTCTnaAGG TGGAGCGAGC 400

5

(2) INFORMATION FOR SEQ ID NO: 3882:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 609 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3882:

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CATCCCCAAC TTGCACATTA TTGTAAGCTG ACTTTTCGTC ACTTCTGTGT TGGGGCCCTC 60  
 ACCCCAACTC GCATTGCCTG TAGAATTTCT TTTCGAAATT CTCTGTGTG GGGCCCCTGA 120  
 CTAGAATTGA AAAAAGCTTG TTACAAGCGC ATTTTCGTTC AGTCAACTAC TGCCAATATA 180  
 ACTTCGTAGA GCATAGAATA TTGATTTATG TCCCAGCCTG AGTTAATTTT CTATAAAAGT 240  
 ATATTTAATT TCGTTTTATA CCGTCAAAC TCACTTTAGC TTTGTCAAAC CCCTTTCTAT 300  
 TAAGTTTTCA GAAATAAACC TATCTTAAAA TATAAAAAA TCGAGAATTC GTAGTTTAAT 360  
 AACGAAATTC TCGTTCTTAT CCTTTTGaAT aTACTCAATT TTCCACAAAA ACAACAAGT 420  
 AGTATATCTG TTCTAGCTAC TAGAATGACA TACTACTTGT TATTAAAATA CTTAACTAAA 480  
 CTTTATTAGT TATCTTTnTT CTCTATATTT CTACGTGGAC TGACGCTTTT CAnGAATGTC 540  
 AGATTCATAA TCTTCTTGGT TGGACTCCTG GATATATTCT TGGTAAGCGG ATGGTTTATT 600  
 CGGAGTCAA 609

35

(2) INFORMATION FOR SEQ ID NO: 3883:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 394 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3883:

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ATATATTGGC GGACATAACG ATGTACTAGC AGGTGTCGTA ACCGTCAAAG ATGAATCACT 60  
 CGCGCAACAG TTGTTTGATT TTCACAACAT GACTGGCGCA ACACTTTCAC CAATAGATAG 120  
 TTATTGTTG TTACGTGGAC TTAAACTTT GCATTACGC ATTGAGCGTG CGCAATCAAA 180  
 CGCTAGAAAA CTTGCTAAAA AATGTCAGTC ACTTCAAGCA ATTGACGAAt ACTaTATAGC 240

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GAAAATTTAG ACATTTGcAT TTTTGCAGAA AGTTTAGGag GTACKGAAAC ATTAGTGACC 360  
 TTCCCTTACA CCCAAACACT GTTGATATGC CAGT 394

5 (2) INFORMATION FOR SEQ ID NO: 3884:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 10 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3884:

CGATTAATGA ATTAACAGAA TACGGACCAG AAACGATAAC ACCAGGTCAT CGAGACGAAT 60  
 TTGATCCGAA GTTACCAACA GGAGAGAAAG AGGAAGTTCC AGGTAAACCA GGAATTAAGA 120  
 20 ATCCAGAAAC AGGAGACGTG TTAGACCACC GGTGATTAG CGTAACAAAA TATGGACCTG 180  
 TAAAAGGAGA CTCGATTGTA GAAAAAGAAG AAATTCCATT CAAGAAAGAA CGTAAATTTA 240  
 ATCCTGATTT AGCACCAGGG ACAGAAAAAG TAACAAGAGA AGGACAAAAA GGTGAGAAGA 300  
 25 CAATAACGAC GCCAACACTA AAAAATCCAT TAACTGGAGA ATTATTAGTA AAGGTGATCG 360  
 AAAGAGGAAT CACAAAAGTT CCnTTTATGA TTAACAGATA 400

30 (2) INFORMATION FOR SEQ ID NO: 3885:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3885:

40 TGAGCGGATT ATTTCTTATG AATTCAAGCT TATTTAAAAC TCTTTATTCA CTCGGTTTTG 60  
 CTTGGTAAAA TCTATATTTT ACTTACTTAT CTAGTTTTCA ATGTACAAAT AATGGTGGGC 120  
 CTAAGTGGAC TCGAACCACC GACCTCACGC TTATCAGGCG TCGCTCTAA CCAGCTGAGC 180  
 45 TATAGGCCCA TTTTTTTGAA TGTAAATAA ACATTCAAAA CTGGAATACA ATATGTCACG 240  
 TTATTCCGCA TCTTCTGAAG AAGATGTTCC GAATATATCC TTAGAAAGGA GGTGATCCAG 300  
 CCGCACCTTC CGATACGGCT ACCTTGTTAC GACTTCACCC CAATCATTTG TCCCACCTTC 360  
 50 GACGGCTAGC TCCCAAAGG GTACTnCCAn CGGGnTTCCG 400

(2) INFORMATION FOR SEQ ID NO: 3886:

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- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3886:

10 TACGGTAGGT GGCAAGCAGT TATCCnGGAA TTATTGGGCG TAAAGCGCGC GTAGGGGTTT 60  
 TTTTAAGTCT GATGTGAAAG CCCACGGCTC AACCGTGGAG GGTCAATTGGA AACTGGAATn 120  
 CTTGAGTGCA GAAGAGGAAA GTGGAATTCC ATGTGTAGCG GTGAAATGCG CAGAGATATG 180  
 15 GAGGAACACC AGTGGCGAAG GCGACTTTCT GGTCTGTAAC TGACGCTGAT GTGCGAAACG 240  
 TGGGGATCAA ACAGGATTAG ATACCCTGGT AGTCCACGCC GTAAACGATG AGTGCTAAGT 300  
 20 GTTAGGGGGT TTCCGCCCCT TTAGTGCTGC AGCTAACGCA TTTAAGCACT CCGCCTGGGG 360  
 GAGTTACGAC CGCAAAGTTT GGAAACTCAA AGGGAATTGG 400

## (2) INFORMATION FOR SEQ ID NO: 3887:

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- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3887:

ATTTTTTAAT TTTTCATGCAA ATTTTAAAGC ACCATATAAT GCCTACCAA TTTCAATAAT 60  
 35 CTTTGTTGCC GTTTAAATAA TGTGAATGTC AATAAATTCT CCAAACCTAGT CGAAAATAAA 120  
 GGGAGTnGGA CATAAATCCC TAAAAAACA GCAGTAAGAT AATTTTCAAT TAGAAAATAT 180  
 40 CTTACTGCTG TTCTCTATTT ATACAATACT TCGTATTGAA TGGCTTCGCT TTCCnAGGGT 240  
 GCCGTCTCAG CCTCGGTCTT CGACTGGCAC TGCTCCCTCA GGAGTCTCGC CATTAACTACT 300  
 ACGTATTAAC ATGGAATTTT ACTTTTACAT ACTTTAAAAA ATAAGnCACT TTGGCCAAC 360  
 45 TACACTACCA TAGGAACCCT GGTAGGAATC CCCCAAATGn 400

## (2) INFORMATION FOR SEQ ID NO: 3888:

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- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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ATACGACAAT CACAGCAATA ATAATTGCTT TAGAAAGTCG TGCCGAACTG GAACTTACAA 60  
 GTCTAGTTTC AACACACACT GATGTGAGTG GTTTTATTTA TTTTAAACAT GAACAATCAG 120  
 5 ATAAGTTACT AGCATTAGCA AATATTATTA AATCAAAGGG CTTTCATTCA TAAAATTAAA 180  
 ACAATGATTA AAATTAGACG TGTAATGTT AAATTCTAAA ACGGAAATAA CCACCATCCC 240  
 10 ATTAAACCAC TTTnATnGTT CAATCACTAT ATTTACACA GCTTCATTAA TAAAACGACT 300  
 TGCTTCAACC CGCTTCAACT TCAACTGGCT TCAACTTCAG CCTACTTCAT TCAATnACAA 360  
 AACGAATCCG CTTTCATCCAA AATCANCCAT TCTAACGCAC 400

15 (2) INFORMATION FOR SEQ ID NO: 3889:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 485 base pairs  
 (B) TYPE: nucleic acid  
 20 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3889:

CCATGChAGA CGCATACATT GTaGCTTATG GgCGTTCAGC gCAGCGAAmG aaAGCAAGGC 60  
 GCATTATTCC ACGAAAGACC TGATGATGTC GCAGCCAAAG TATTACAAGG CGTATTGAAA 120  
 30 CGTATTGACG GAAAATTCAA TAAGAATATG ATTGAAGATG TCATTGTTGG TACGGCTTTT 180  
 CCAGAAGGAT TACAAGGCCA AAACATTGCA CGAACGATTG CATTGCGTGC GGGATTATCT 240  
 GACACGGTAC CGGGTCAAAC AGTGAATCGC TACTGCTCAT CAGGATTACA AACCATCGCG 300  
 35 ATTGCAGCCA ATCAAATTAT GGCTGGTCAA GGAGATATAC TTGTaGCTGG TGGCGTTGAA 360  
 TTGATGAGTG CCGTACCAAT GGGTGGCAAC GAGCCCACAA ACAATCCaAC CTTwACAATA 420  
 tGaTGATATA GGTGCGTCCA TATnCTATG GGTTTnAAAT GCTGGAAT GTTAGCCTnC 480  
 40 CCAAT 485

(2) INFORMATION FOR SEQ ID NO: 3890:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 389 base pairs  
 (B) TYPE: nucleic acid  
 45 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3890:

AGGCAGATGC TCTCCAGCT GAGCTAATTC TCCAAAATAA TGACTCCTAC GGGACTCGAA 60

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AGGTAGGACT CGAACCTACG ACCGATCGGT TAACAGCCGA TAGCTCTACC ACTGAGCTAC 180  
 TGTGGGATTA ATATTATGCC TGGCAACGTT CTACTCTAGC GGAAnTGAAT TCGGACTACC 240  
 5 ATCGACGCTA AGGAGCTTAA CTTCTGTGTT CGGCATGGGA ACAGGTGTGA CCTCCTTGCT 300  
 ATAGTCACCA GACATATGAA TGTAATTTAT ACATTCAAAA CTAGATAGTG AAGTAAAAGT 360  
 10 GGTTTTGCnT CGCAAAACAT TTATTTTGn 389

## (2) INFORMATION FOR SEQ ID NO: 3891:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3891:

CAGATGTTTA AGTCCTGTGC GTCTGCCAGT TCCGCCACCC CGGCACTATA AAAATGGAGC 60  
 AGAAGACGGG ATTCGAACCC GCGACCCCAA CCTTGGCAAG GTTGTATTCT ACCGCTGAAC 120  
 25 TACTTCTGCA TATGCGGGTG AAGGGAGTCG AACCCCCACG CCGTAAGCTn AGATCCTAAG 180  
 TCTAGTGCCT CTGCCAATTC CGCCACACCC GCAAATGGTG AGCCATAGAG GATTGGAACC 240  
 30 TCTGACCCTC TGATTAAAAG TCAGATGCTC TACCAACTGG AGCTAATGGC TCTTCCATGG 300  
 TGCCGGCCAG AGGACTTGAA CCCCCAACCT ACTGGATTTA CAAGTCAGTT TGCTCTACCA 360  
 ATTGAGCTA GGGCCGGGCA ATATGGTAAG AATAAATTGG 400

## (2) INFORMATION FOR SEQ ID NO: 3892:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3892:

CTCTCGGTGG TCGTGCTACA ACTGGTAAAA ATGTACATGT AGGGGCTGGC GCAGTATTAG 60  
 CAGGTGTGAT TGAACCCCTT AGTGCTTCAC CGGTTATAAT CGAGGATGAT GTATTAATCG 120  
 50 GTGCAAATGC AGTTATTTTA GAAGGTGTAC GTGTTGGTAA AGGTGCTATT GTTGCAGCTG 180  
 GCGCGATTGT GACACAAGAT GTACCAGCTG GTGCAGTTGT TGCTGGTACA CCTGCAAAAG 240  
 TGATTAAGCA AGCTTCTGAA GTACAAGATA CTA AAAAAGA GATTGTAGCA GCATTAAGAA 300

CCACChTAAT GGTnTAGCAT TGAATAAACT TATGnnCCCC

400

## (2) INFORMATION FOR SEQ ID NO: 3893:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3893:

GAATGTAGTT GTGGTAAATA CAAACGTGTT CGCTACAAAG GCATGGTCTG TGACAGATGT 60  
 GGAGTTGAAG TAACTAAATC TAAAGTACGT CGTGAAAGAA TGGGTCACAT TGAACCTGCT 120  
 GCTCCAGTTT CTCACATTTG GTATTTCAAA GGTATACCAA GTCGTATGGG TATTATTACT 180  
 TGACATGTCA CCAAGAGCAT TAGAAGAAGT TATTTACTTT GCTTCCTTATG TGTGTGTAGAT 240  
 CCAGGTCCAA CTGGTTTAGA AAAGAAAAC TATTATCTG AAGCTGAATT CAGAGATTAT 300  
 TATGATGAAA TACCCAGGTC AATTCGTTGC CAAAAATGGG TGCCAGAAGG TCATTAAAAG 360  
 ATTTACTTGA AGnnGATTGA TnCTTGACGA GGGAACCTna 400

## (2) INFORMATION FOR SEQ ID NO: 3894:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 485 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3894:

CACGTGAAGT TAGAGATACT TCATTACGTG TACCTCACGG CGCTGGCGGT ATCGTTCCTG 60  
 ATGTAAAAGT ATTCAATCGT GAAGAAGGCG ACGATACATT ATCACCTGGT GTAAACCAAT 120  
 TAGTACGTGT ATATATCGTT CAAAACGTA AAATTCATGT TGGTGATAAG ATGTGTGGTC 180  
 GACATGGTAA CAAAGGTGTC ATTTCTAAGA TTGTTCTGTA AGAAGATATG CCTTACTTAC 240  
 CAGATGGACG TCCGATCGAT ATCATGTTAA ATCCTCTTGG TGTACCATCT CGTATGAACA 300  
 TCGGACAAGT ATTAGAGCTA CACTTAGGTA TGGCTGCTaA AAATCTTGGT ATTCACGTTG 360  
 cATCACCAGT ATTTGaCGGT GCaAACGrTG aCGATGTATG GTCAnCAATT GAAGAAGCTG 420  
 GTATGGCTCG TGATGGTAAA ACTGTACTTT ATCGATGGAC GTACCAGGTG ACCChTCCGA 480  
 TAACC 485

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 507 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3895:

GAACAACATA CCTTTGTTTG TTGATTCTTC TCCACCTGTT TCAAGTAGTT CAGATTTCTT 60  
 AGATTGTGGT TTTTLAGTTG GTGCCACTGc TTTAACCTTT TCATTGATTT CAATAACAGG 120  
 TGTACTACT TTACCTTGTT CCACTGGTTT AGAAGGCTTT TTAGGTTCTT CTTTGGCAGG 180  
 TGGTACTGGT TTACCAngTT CAGCTGGTAC CTCTGGTGTT GCGGGTGTTG GAGTTTCTGG 240  
 CTCACCGGC ACTTCTGGTG TCGGTGGTGT TGGTGTTCCT GGCTCACTTG GTACTTCTGG 300  
 TGTGGTGGc GTTGGTGTTC CCGGCTCACT TGGTACTTCT GGTGTCGGTG GCGTTGGtGG 360  
 CACGATTGGA gGTGTTGTAT CTTCTTCAAT CGTTTGTTGA CCTTCATTTT GGGCCGCTTA 420  
 CTTTTGGGAA GTGTATCTTC TTCAAAGTCA AACTAATGT GGTCCACCGG AATTGATAAC 480  
 TGGGGTTAAC CTAAATTGG AACCTCC 507

## (2) INFORMATION FOR SEQ ID NO: 3896:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3896:

CTAGCGGAAG TAATTGGCTA CCATCGTCGC TAAAGACCTT nGgnGACTTG TGACAATCGC 60  
 TTGCTTCTTT CCTCTCCTTC GGCTCTCGCT TACTCATTTA GCTCTACTAA ACTCGTTGCG 120  
 CTCCTTTCTC GTTTCGTCAG ATTCAAACGT TTTCACCTCG CCAAGCCATT TTTCTTTGTG 180  
 TTTACTTTTT ATTTTGACGT TTTAGGCATA AAAAAAGAG ACCTTGCGGT CTCAATGCGG 240  
 CTCATCGCAT CCATTTTTTG CCTGGCAACG TTCTACTCTA GCGGAAnGTA ATTGGGCTAC 300  
 CATCGTCGCT AAAGACCTTT CTTGACTTGT GACAATCGCT TGCTTCTTTC CTCTCCTTCG 360  
 GCTCTCGCTT ACTCATTAG CTCTACTAAA CTCGTTGCGC 400

## (2) INFORMATION FOR SEQ ID NO: 3897:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs



(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3897:

	TTGAAGAAGA TCGCGATGAC TATACAATCA ATATCGAGTA TAATACCGAT TTATATCACT	60
10	CAGAAACAGT TCGTCACATG GGTAATCAAT GTATGATTAT GATTGATTAT ATTTTGAAGC	120
	ATCAAGATAC ACTACAAATT TGTGATATAC CAAACGGCAC GAGGAACTTC TAAATTGGGT	180
	CAATACGCAT GTTAAACGATC GAATGCTTAA TGTCCTGGGA AATAAATCTA TCATAAGTTA	240
15	CTTTAATGAA GTTGTCTCAC GACAAGGTAA TCATGTTGCG CTAGTCATGA ATGANTTGAC	300
	AATGACGTAT GAAACATTAC GCAACTATGT GGGATGCCAT TGCGCACATG CTCCTATCAA	360
20	ATGGTGTGGG CAATGGTCAA CGGGTTGCCT TGGTGTACAG	400

(2) INFORMATION FOR SEQ ID NO: 3898:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3898:

	GAAATCAGTA TTAAAGCAGT TAATCCACAA GGGAAAGTGG TTAATACAGT TGGCTCTGGT	60
	GATAGTACAG TTGCAGGCAT GGTGGCTGGA ATTGCTTCAG GTTTAACGAT TGAAAAAGCA	120
35	TTCCAACAAG CAGTCGCATG CGGTACTGCC ACGGCATTTG ATGAGGACTT AGCAACACGG	180
	GACGCTATAG AAAAAATAAA ATCACAAGTT ACGATTAGCG TACTTGATGG GGAGTGAAAA	240
	TAATGAGAGT AACAGAGTTA TTAACAAAAG ATACAATAGC AATGGATTTA ATGGCAAATG	300
40	ACAAAAATGG TGTATTGAT GAGTTAGTAA ATCAATTAGA CCAAGCAGGT AAATTAAGTG	360
	ATGTCGCGTC ATTTAAAGGA AGCGATTCAC CATCGnGATC	400

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(2) INFORMATION FOR SEQ ID NO: 3899:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3899:

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CTAGCGGAAC GTAAGTTAGC TACCATCCTC GCTAAGAACC TTTCTTGACT TGTGACAATC 120  
 GCTTGCTTCT TTCCTCTCCT TCGGCTCTCG CTTACTCATT TAGCTCTACT AAACCTCGTTG 180  
 5 CGCTCTTTTC TCGTTTCGTC AGATTCAAAC GTTTTCACTT CGCCAAGCCA TTTTCTTTG 240  
 TGTTTACTTT TTATTTTGAC GTTTGTAGACA TAAAAAAGA nACCTCACGG TCTCAACTTG 300  
 10 CCTGGCAACG TTCTACTTCT AGCGGAACGT AAGTTGGCTA CCATCGTCGC TnAAAGACCT 360  
 TTCTTGGACT TGTGGACAAT CGGCTTGGCA nTCTTnCTC 400

## (2) INFORMATION FOR SEQ ID NO: 3900:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3900:

TGCACGCGTA TCTGATGGTT GCTCAGTTGC ATCTACCCAA GGTAACCATT CCCTAAGTGA 60  
 25 ATTTCTTGAA CGATTGACTA AATTGAAAAG CGCTTCTGTG TCATGAGCTT CTAAAATTTT 120  
 TAATGTTATT TGTTCAATCA CTTTCATTCC AAACATACCA TCACATCCTC ATTCATTTTT 180  
 CATATAATTC TGTAAATTAT CATTATAATA ACATATTAAT GTTACGCATT GTATCTTAAA 240  
 30 TTTGTTGTCC TTCCCCAACT TGCATTGCTT GTAGAATTTT TTTTCGAAAT TCTCTATGTT 300  
 GGGGCCCCGn AACTTGCAAT GTCTGTAGAA ATTACGGACC CAATTTCTCT AGGTGGGGCC 360  
 35 CATCCCCAAC TTGCACATTA ATnGCAAGCn GACTTTCCGT 400

## (2) INFORMATION FOR SEQ ID NO: 3901:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3901:

TACTGCTGTT CACTTTTTAT AATACTTCTG AATGTCTTCA CTTATACTTC TAGTCACAGA 60  
 TTTAAATAAT CAAAAGTGCA CATTATTAAA ATATCAATTT CACACTCAAT GCGGCTCATC 120  
 50 GCATTCAATTT CTTGTCTCAA CGTTCTACTC TAGCGGAAGT AAGTTAGCTA CCATCCTCGC 180  
 TAAGAACCTT TCTTGACTTG TGACAATCGC TTGCTTCTTT CCTCTCCTTC GGCTCTCGCT 240

TTTCACTTCG CCAAGCCATT TTTCCTTGGT GGTTTACCTT TTAATTGGA CGGTTTAGAC 360  
 ATnAAAAAAG GGGACCTCAC GGGCCCAACT TGGCCTGGGC 400

(2) INFORMATION FOR SEQ ID NO: 3902:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3902:

TTATTTTGAC GTTTTAGACA TAAAAAAGA GACCTCACGG TCTCAACTTG CCTGGCAACG 60  
 TTCTACTCTA GCGGAACGTA AGTTGGCTAC CATCGTCGCT AAAGACCTTT CTTGACTTGT 120  
 GACAATCGCT TGCTTCTTTC CTCTCCTTCG GCTCTCGCTT ACTCATTTAG CTCTACTAAA 180  
 CTCGTTGCGC TCTTTTCTCG TTTCGTCAGA TTCAAACGTT TCACTTCGC CAAGCCATTT 240  
 TTCTTTGTGT TTACTTTTAA TTTTGACGTT TTAGGCATAA AAAAAAGAGA CCTTGCGGTC 300  
 TCAATGCGGC TCATCGCATC CATTTTGTGC CTGGGCAACG TTCTACTCTA GCGGGAACGT 360  
 AAGTTGGGCT ACCAnCGGCG GCTAAAGACC TTTCCTGGAC 400

(2) INFORMATION FOR SEQ ID NO: 3903:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3903:

TTGTTATAAC GAAAACCATT AATAGATTTT TATTGGTGA TTCAAATCA TGAGACTGGG 60  
 ACAGAAATGA TGTTTTCATA AAAATTATTT CGTTGTTCCA CTCTCATGAT TTTTGTATG 120  
 AACATAATT ACATGATTGA TTGCATCATT TTGTTAAACA AGTGATTGCA AACCTGCCAT 180  
 TTCACACTGA AAATTACAT AATAAGTGAC GATATTTTAC AAGTCATATA CAAATAACAT 240  
 ATATTGTTAA ATAATTTTAC CTAATCTTAA CATTAAATTT ACAATTATAA GCGATAATCT 300  
 AAATATAAAG CTTATTTGAG GTGAAATAAT GGAAATGTCG GTTACAGAAG TCATTTTCTC 360  
 CTTTTTAGGT GGGTTTAGGG AATTTCnTT ACGGCCTTAA 400

(2) INFORMATION FOR SEQ ID NO: 3904:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3904:

10	CATAAGACAT AATCGCTAGT GTTCGAAAGA GCACTCACAA GATTAATAAC GCGTTTCCTG	60
	TAGGATGGAA ACATAGATTA AGTTATTAAG GGCGCACGGT GGATGCCTTG GCACTAGAAG	120
	CCGATGAAGG ACGTTACTAA CGACGATATG CTTTGGGGAG CTGTAAGTAA GCTTTGATCC	180
15	AGAGATTTCC GAATGGGGAA ACCCAGCATG AGTTATGTCA TGTTATCGAT ATGTGAATAC	240
	ATAGCATATC AGAAGGCACA CCCGAGAnC TGAAACATCT TAGTACCCGG AGGAAGAGAA	300
	AGAAAATTCG ATTCCCTTAG TAGCGGCGAG CGAAACGGGA AGAGCCCCAA CCAnCAAGCT	360
20	TGCTTGTTGG GGTGTAGGG CACTCTATAC GGAGTTACAA	400

(2) INFORMATION FOR SEQ ID NO: 3905:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 399 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3905:

	AACTAACATT ACAACATGCA TGTGAACAAT TAAAAACATA TTTTAAGTAG GTGAATGAAA	60
35	TGgTAAATGA ACAAATCATT GATATTTTCAG GTCCGTTAAA GGGCGAAATA GAAGTGCCGG	120
	GCGATAAGTC AATGACACAC CGTGCAATCA TGTGGCGTC GCTAGCTGAA GGTGTATCTA	180
	CTATATATAA GCCACTACTT GGCGAaTtCG TCGTACgATG GaCATTtTCC gACTGTtTAGG	240
40	TGTAGAAATC AAAGAAGATG ATGAAAAATT AGTTGTGACT TCCCCAGGAT ATCAATCTTT	300
	TAACACGCCA CATCAAGTnt TGtntACAGG TAATTCCGGG TACGACAACA CGATTGATAG	360
	TTTGGTTAAT GGGTTAAGTA TTGAAAGTGT TTTGTCCGG	399

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(2) INFORMATION FOR SEQ ID NO: 3906:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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TTCTTTAAAA ATAAACGCCT ATnCGTTATC GGTGGTGGTG ATTCAGCAGT AGAAGAGGGGA 60  
 ACATTCTAAA CTAAATTTGC TGACAAAGTA ACAATCGTTC ACCGTCGTGA TGAGTTACGT 120  
 5 GCACAGCGTA TTTTACAAGA TAGAGCATTG AAAAATGATA AAATCGACTT TATTTGGAGT 180  
 CATACTTTGA AATCAATTAA TGAAAAAGAC GGCAAAGTGG GTTCTGTGAC ATTAACGTCT 240  
 10 ACAAAAGATG GTTCAGAAGA AACACACGAG GCTGATGGTG TATTCATCTA TATTGGTATG 300  
 AACCATTAAAC AGCGCCATTT AAnGCTTAGG TATTACnAAT GATGTTGGTT ATATTGTGAC 360  
 AAAGGTGGAT TGGCCAC 377

(2) INFORMATION FOR SEQ ID NO: 3907:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 502 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3907:

25 AATTAGGTAA TTCAAAATAA TATTAGCGCG GGATGGAGCA GTTCGGTAGC TCGTCGGGCT 60  
 CATAACCCGA AGTCGGtGGT TCAAATCCGC CTCCCGCAAT ACATAGTTTT TAATTTAATA 120  
 GGTCTCGTAG TGTAGCGrTT AACACGcCTG CCTGTCACGC AGAGATCGCG GGTTCGATTG 180  
 30 CCGTCGAGAC CGCCATTATT ATTACCATTG CGGTTCAGTA GCTCAGTTGG TAGAGCAATG 240  
 GATTGAAGCT CCATGTGTCG GCAGTTCGAC TCTGTcCTGa ACCATTCTTA ATTCATGGCG 300  
 GTTGTGGTGA AGTGGTTAAC ACATCGGATT GTGGTTCCGA CATTGAGGG TCGATCCCC 360  
 35 TTCAGCCGCC CCATAATCGT TTACATTAGC GGGTGTAGTT TAATGGcAAA ACCTCAGCCT 420  
 TCCAAGCTGA TGTTGTGGGk TtCGrTTCCC AtCAmCCnGy TCCaTaATTT CnAAnAATTC 480  
 40 CAACAGTAGC CGCAAGTnGG TA 502

(2) INFORMATION FOR SEQ ID NO: 3908:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 45 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3908:

50 AAAAAATGCA TCTCTACGTG CTAGAATAAA TATTGGTCAG CCAACCAAAA TAATCAACAC 60

TAAGTATCAT ATTGTCTTTG CACCTAAATA CAGAAGACAA GTGATATATG GAAAAATAAA 180  
 AAAAGATATA GGGATTATAT TGCCTCAATT ATGTGAAAGA AAAGGTGTAG AGATAATTGA 240  
 5 AGCAGAGGCA TGTAAGATC ATATCCATAT GTTAGTTAGT ATACCACCCA AACTTGGGGG 300  
 TATCATCATT TGTGGGCTA TTTAAAAGGG AAAAAGTAGT TTAATGGATA TTTGGATAGA 360  
 CATGGCTAAC TTAAAGTATA GATATGGGAA ATAGGAAAGT 400

## (2) INFORMATION FOR SEQ ID NO: 3909:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3909:

GGTTTAACTA TTGAAGAAAA TGTGCCGACA ATTAACAAGA TAAAAAATGC GGTATATTCA 60  
 GCAGATAAAG CTTTACCTAA GATTAATGAC TTTGCGAATA AAATTGTATA TTTGAATAAC 120  
 25 CACCAAGCGG ATTTAGATAA ATATGCCAAT GATTTTAGAA AACTAGGAAA TTATAAAGGT 180  
 GATATTTTAC ATGCTCAGAA AAAATTAAAC GAGTCAATGG TGCTATTCCG CAACTTAATG 240  
 AAAAGGCTAA GTTGGATATT AGCTTTTAAA TAATTATATG CCGGAAAATT GGAAAAAGCG 300  
 30 TTTAAATTTT GCAGCTGGAT GACGTGCCAC GCGTTCCCT AAAATTAATC CAGGGCTTAA 360  
 CATTGCGAGT CCAGGTATTG GntCCAAGCT AATGGGGCCG 400

## (2) INFORMATION FOR SEQ ID NO: 3910:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3910:

TTACCCGATA TCGGGAAGGT ATCCACGAAG GTGAAATTGT AAAATGGTTT GTTAAAGCTG 60  
 GAGATACTAT TGAAGAAGAC GATGTTTTAG CTGAGGTACA AAACGATAAA TCAGTAGTAG 120  
 AAATCCCATC ACCAGCATCT GGTACTGTAG AAGAAGTTAT GGTAGAAGAA GGTACAGTAG 180  
 50 CTGTAGTTGG TGACGTTATT GTTAAAATCG ATGCACCTGA TGCAGAAGAT ATGCAATTTA 240  
 AAGGTCATGA TGATGATTCA TCATCTAAAG AAGAACCCTGC GAAAGAGGGA AGCGCCACAG 300

GCCATGCCTT CCAGTTACGT TAAATACGCA CGTGAAAAAG

400

## (2) INFORMATION FOR SEQ ID NO: 3911:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3911:

CGTGTA~~ACTC~~ AAGTTATGGG TCCTGTAATT GATGTT~~CGAT~~ TTGAACATAA CGAATTCCTA 60

AAATTAATAA CGCCTTGGTT ATTGATGTGC CTAAAGAAGA AGGTACAATA CAACTAACAT 120

TAGAAGTTGC GCTGCAATTA GGTGACGACG TTGTTTCGTAC AATTGCGATG GATTCAACTG 180

ATGGTGTCCA AAGAGGCATG GATGTAAAAG ATACAGGCAA AGAAATTAGT GTACCTGTTG 240

GTGACGAAAC ATTAGGTCGT GATTTTAATG TACTAGGTGA AACAAATTGAC CTTAAAGAAG 300

AAATTAGTGA TTCTGTTTCG CGCGATCCTA TCCATCGTTC AAGCACCAGC ATTCCGATGG 360

AACTTTTCAA CAGAAGTTCC AAATTTTTTAG G~~n~~ACAGGGTA 400

## (2) INFORMATION FOR SEQ ID NO: 3912:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3912:

TTGTACAAGT TGAAGAAAAA TCAACACAAC CAAAAGGTAG AAAATTCAAA GATTTCACTA 60

GTAAATTTAA TATAGCATCA GAAGCTAAAG AAAATGAACC TATATCAGTC ATTGGTTATC 120

CAAATCCTAA TGGAAATAAA CTACAAATGT ATGAATCAAC TGGTAAAGTA TTATCAGTGA 180

ATGGGAATAT AGTGT~~CATCG~~ GATGCAATTA TTCAGCCTGG TAGCTCTGGT TCACCTATAT 240

TAAATAGTAA ACACGANGCT ATTGGTGTA TCTATGCCGG TAATAAGCCA TCAGGTGAAA 300

GCACCAGAGG GATTGCTGT TTATTTCTCT CCTGAAATTA AGAAATTCCA TTGCAGATAA 360

TTTAGATAAA TnATTAAGAC CTAnGACATT CACCCAATCC 400

## (2) INFORMATION FOR SEQ ID NO: 3913:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3913:

ACTCATTAG CTCTACTAAA CTCGTTGCGC TCTTTTCTCG TTTCGTCAGA TTCAAACGTT 60  
TCACTTCGC CAAGCCATTT TTCTTTGTGT TTACTTTTAA TTTTGACGTT TTAGACATAA 120  
AAAAAAGAGA CCTTGCGGTC TCAATGnGGC TCATCGCATC CATTTTTTGC CTGGCAACGT 180  
TCTACTCTAG CGGAAGTAAG TTGGCTACCA TCGACGCTAA GAACCTTTCT TGACTTGTGA 240  
CAATCGCTTG CTTCTTTCCT CTTCTTCGGC TCTCGCTTAC TCATTTAGCT CTAATAAAT 300  
CGTTGCGCTC TTTTCTCGTT TCGTCAGATT CAAACGTTTT CACTTCGCCA AGCCATTTTT 360  
CTTTGGGGTT TGCnnTTTGA ATTTGGACGT TTTAGACATA 400

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(2) INFORMATION FOR SEQ ID NO: 3914:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3914:

TGGAATGAGC GGATATAAGC ATCTTTAGAT AATGCACCAT CAACTAATGG ATATTTATGT 60  
CCAGTTGGAC GCCAGAAATC ATAAACGTCT TCAGTGTAAG CAACAGCATC TTCATTTAAT 120  
GCCAAAATGC TTGGATTATG TGCAATAACC ATCGCAACTG nGCCACACCT TGTGTTGGCT 180  
CGCCGCCTGA ATTCAATCCA TAACGTGCTG TATCTGTAGC AATAACTAAT ACTTTTTCAT 240  
TCGGTCTAGT TGCTAAATAA TCTTTAGCTA ATTGAATTGC TGGTGTGCA GCATAACAAG 300  
CTTCTTTCAT TTCAAAGCAG CGTGCAAAAG GTTGGnATAC CTAATAAGTT GTGGAATTG 360  
nACAGCGGCT GCTTTACGAA TTCCAACGTC TGATTCCAGT 400

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(2) INFORMATION FOR SEQ ID NO: 3915:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 371 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3915:



TCTTTATTTA TCCAGTTTCA TAGTCAATGT TTAAAGCAAA ATCTTATTGA TGGTACAAAA 120  
 GTAGAAGCTA ATGCCAATAG GTATACATTT GTGTGGAAGA AAAGTATTCA AAATCACGAA 180  
 5 TCGAAATTGA ACGAaAATTC AAAAACATTA TATCGTGA CT TAGTTGAAGA AAAAATAATA 240  
 CCAGAGATAA AAGAAGATGG AGATAGCGAT TTAACAATAG AnGAAATAGA TTTAATTGGT 300  
 AGTCATTTAG ATAAAGAAAT CGAGGTTTAA ATCATTCTAT TGAGACGnGA TAGTACTCAA 360  
 10 ATTAGAAACA G 371

## (2) INFORMATION FOR SEQ ID NO: 3916: .

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3916:

ACCATGGACG ACGGTTAGGT TTATGAATGT TATTCCAAAT AGGTTTCATCT ATAAAAATAGC 60  
 25 TTTAGTTGGA AAAGATGAGA AAAAATATAA AGATGGACCT TACGATAATA TCGATGTATT 120  
 TATCGTTTTA GAAGACAATA AATATCAATT GAAAAAATAT TCTGTCGGTG GCATCACGAA 180  
 GACTAATAGT AAAAAAGTTA ATCACAAGT AGAATTAAGC ATTACTAAAA AAGATAATCA 240  
 30 AGGTATGATT TCACGCGATG TTTCAGAATA CATGATTACT AAGGAAGAGA TTTCCTTGAA 300  
 AGAGCTTGAT TTTAAATTGA GAAACAAC TATTGAAAAA CAGATCTTTA CGGTAACATG 360  
 GGTTCAGGAC AATCGTATTA AATGAAAACG GGGGAATATA 400  
 35

## (2) INFORMATION FOR SEQ ID NO: 3917:

40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 412 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3917:

GAGGAAATTA TTAACCTTnC GCATCGTATG GGcCnTGAAG GAATAACAaC CTTTAGACCT 60  
 GGAGATTGAG CTAAAATACC TTCTAAGTTA TCTGCGTGTA ATTCTGGTGT GTGTACGCCA 120  
 50 CCACCAAATG GGCTACGAAT TGTTACAGGT GCAGTTTTAG TACCGCCTGA ACGGAAACGA 180  
 GTACGTGCAA TTTGTCCAGC AATCGCATCA AATACTTCGA ATACGAAACC TAAGAATTGT 240

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GATTCAGCTA AAGGTGTATC GAATACTCTA TCTTCACCAA ATTCTTTTGT TAGTCCTTCA 360  
 GTAACACGGA AAACACCGCC GTTAACACCA ACGTCTTCAC CAnAATnAAA AC 412

(2) INFORMATION FOR SEQ ID NO: 3918:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3918:

ATAGATTGCT GAGTGACAAT ACTTCAGGAn TCGCATATGC AGGCCCAATA CCCATAATTT 60  
 TCGGGTCAAC GCCTACTGCC TTAAACCAA CGAATCGTGC AATAGGTGTC ACGCCGAGTT 120  
 CTTTCACTTT ATCTCCAGAC ATTAAAACTA CAAATCCTGC ACCATCAGAA AGTGGGGCAG 180  
 ATGTTCTGTC AGTCATAGTG CCGTCAGCTT TAAATACTGT ACGTAATTTG GCTAATGCCT 240  
 CCATCGTGGT GTCAGGGCGT ATnAAATTCA TCTTGGTCAA AGATATTTGT GTGTACTTTT 300  
 GGTCTGCGT TTGTATATTC AACTGAGTTT ACTTGTATTG GGATnATTTT ATCTTTGGAA 360  
 CCGACCATCA CGGTGTGCGT TCATAGGCAC GTTGATGnAC 400

(2) INFORMATION FOR SEQ ID NO: 3919:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3919:

CAAGGGCAAC AAGGTGGCAA CGGCAATTAT TTAGAACAAA TTGGTCGTAA CCTTACnAAG 60  
 AAGCACGTGA CGGTTTATTA GATCCAGTCA TTGGTCGTGA TAAAGAAATT CAAGAACTG 120  
 CTGAAGTTTT AAGTAGACGA ACTAAAAACA ATCCTATATT AGTTGGAGAA GCTGGTGTG 180  
 GTAAACTGTC GATTGTTGAA GGTTTAGCAC AGGCAATCGT TGAAGGAAAT GTACCAGCAG 240  
 CAATCAAAGA CAAAGAAATT ATTTCTGTAG ACATTTTCATC ATTAGAAGCT GGAACGCAAT 300  
 ATCGTGGTGC TTTTGAGGAA AATATTCCAA AATTAATCGA GGTGTTAAnC TTCACAAATG 360  
 CCGTACTATC TTTGATGAAn CCATCAATTA TCGGTTCAGT 400

(2) INFORMATION FOR SEQ ID NO: 3920:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3920:

10 CTTATCCCGT CCACACATAG CTACCCAGCT ATGCCGTTGG CACGACAACT GGTACACCAG 60  
 AGGTATGTCC ATCCCGGTCC TCTCGTACTA AGGACAGCTC CTCTCAAATT TCCTACGCCC 120  
 ACGACGGATA GGGACCGAAC TGTCTCACGA CGTTCTGAAC CCAGCTCGCG TACCGCTTTA 180  
 15 ATGGGCGAAC AGCCAAGnCC TTGGGACCGA CTACAGCCCC AGGATGCGAT GAGCCGACAT 240  
 CGAGGTGCCA AACCTCCCCG TCGATGTGAA CTCTTGGGGG AGATAAGCCT GTTATCCCCG 300  
 GGGTAGCTTT TATCCGTTGA GCGATGGCCC TTCCATGCGG GAAnCAACGG ATTCACTAAA 360  
 20 GTCCGTCTTT TCGAACCTGG CTCGGACTTG TAGGTCTCGG 400

## (2) INFORMATION FOR SEQ ID NO: 3921:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3921:

CGGGTTGGGC AGGTATGTTG TATTACCGTT CACAGCAGCA TCACTTTGAA CAACATTTGT 60  
 35 TAACGGATTA TTTGGCAATT CGGTTAGTTG TCGAACAATT GCTAGTTGGT GATGAGTTTA 120  
 AGTCAGTCGC TAAAGATTGT GAAAGTAGAT CGGAAAATTG GTTTAAGCAA ACTGTTGCAT 180  
 CATGGTGTTA CTACAGTGGA TATGCCTAGC GATGTATTAC TACAACATGA CGTCAATGAA 240  
 40 ATTCAAACGT TTATTCATTT TGGCAGCAAC TATGGAATAA AAATGTATTT AAAATTTATG 300  
 GCTnAATTGC CnGGGGAAAT GACATACGGG ATCTCAGTTT AAAACAAAAA TTAAAGCAGG 360  
 45 TCATGGAAAG TGTGGCGGGC GCCTTAGGTG TnAACCCAGT 400

## (2) INFORMATION FOR SEQ ID NO: 3922:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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GTGCGCTCTA ACCAGCTGAG CTATAGGCCC ATTTTTTTGA ATGTTAAATA AACATTCAAA 60  
 ACTGAATACA ATATGTCACG TTATTCCGCA TCTTCTGAAG AAGATGTTCC GAATATATCC 120  
 5 TTAGAAAGGA GGTGATCCAG CCGCACCTTC CGATACGGCT ACCTTGTTAC GACTTCACCC 180  
 CAATCATTTG TCCCACCTTC GACGGCTAGC TCCTAAAAGG TTACTIONACC GGCTTCGGGT 240  
 10 GTTACAACT CTCGTGGTGT GACGGGCGGT GTGTACAAGA CCCGGGAACG TATTCACCGT 300  
 AGCATGCTGT ATCTACGTTT ACTAGCGATT CCAGCTTCAT GTAGTCGAGT TGCAGACTAC 360  
 AATnCGAACT GAGGAACAAC TTTTATGGGG TTTGnTTGn 400

15 (2) INFORMATION FOR SEQ ID NO: 3923:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 20 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3923:

AGTAAGTAAA ATATAGATTT TACCAAGCAA AACCGAGTGA ATAAAGAGTT TTAAATAAGC 60  
 TTGAATTCAT AAGAAATAAT CGCTAGTGTT CGAAGAACTC CACAAGATTA ATAACGCGTT 120  
 30 TCCTGTAGGA TGGAAACATA GATTAAGTTA TTAAGGGCGC ACGGTGGATG CCTTGGCACT 180  
 AGAAGCCGAT GAAGGACGTT ACTAACGACG ATATGCTTTG GGGAGCTGTA AGTAAGCTTT 240  
 GATCCAGAGA TTTCCGAATG GGGAAACCCA GCATGAGTTA TGTGATGTTA TCGATATGTG 300  
 35 AATACATAGC ATATCAGAAG GCACACCCGG AGAACTGAAA CATCTTAGTA CCCGGAGAAG 360  
 AGAAAGAAAT TCGnTCCCTA GTACCGCGAn CGAAACGGGA 400

40 (2) INFORMATION FOR SEQ ID NO: 3924:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 45 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3924:

ATGCGATACG TAGCACAGCT GCAACAATCC ATGCTAGTAA AATCGGAGAC ATCTCTGTAC 60  
 CTTCAAATA GCAATTGTAT TTCCGACACC GCCGTCAATT AATACTTGTT TAATGTACC 120  
 CCACCGCCAA TAATCAATAA CATCATTCGG ATTGGATAAA TCGCATTCGT CACTGATTCC 180

GCTATTAGCA TGGCTGTCCC TGCTGTTCTT ATCATATAAA TGATAGATTC AAATAGATTT 300  
 GTAGGGTTGT CATGCCCACT TACAAGTTGC GTTGATCGTn GACACTAACA TTAATATGAC 360  
 5 TGGTAATGTT GCTGTTAATA AACTCATACC AantCCGGGC 400

(2) INFORMATION FOR SEQ ID NO: 3925:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 525 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3925:

GGCTGGGCTA GCTGGATTCT AACCAACGAG TGACGGAnAn AGGTCCGTTG CCTTACCGCT 60  
 20 TGGCTATAGC CCAATATATA GATGGTGGAG GGGGGCAGAT TCGAACTGCC GAACCCGAAG 120  
 AGCCGGATTT ACAGTCCGCC GCGTTTACCA CTTCGCTACC CCTCCAGCTT ATTCATATAA 180  
 TTTAATAATC AAAATGGTGG AGAATGACGG GTTCGAACCG CCGACCCTCT GCTTGTAAAG 240  
 25 CAGATGCTCT CCCAGCTGAG CTAATTCTCC AAAATAATGA CTCCTACGGG ACTCGAACCC 300  
 GTGTTACCGC CGTGaaAGGG CGTGtgCTTA ACCcTTGGAC CAAGGAGCCA TGGCTCaCAG 360  
 GTAGGACTCG AACCTACGAC CGATCGGTTA AcAGCCGATA GCTCTACCAC TGGAGCTGAC 420  
 30 TGTGGATTAA TATTATGCCT GGCAACGTTT TGAnnCTAGC GGAantGAAT TCGGACTGAC 480  
 CATCGACGCh AAGGAGCTGA ACTTCTGTGT TCGGGCATGG GGAAC 525

(2) INFORMATION FOR SEQ ID NO: 3926:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3926:

TGTTATTGTT CAAATCATG ATCAAGATCA GTATATCGTT GCTTATTATG AAGCGATGCA 60  
 TACATTATCA CATAATAAGA TTAAATCACA ATTACGTATG ACCTTACCGG AGTACATGAT 120  
 ACCAGTTAAT TTCATGCATA TTGAGCAAAT TCCTATTACT ATTAATGGGA AATTAGATAA 180  
 50 GAAGGCATTG CCTATCATGG ACTATGTCGA TACGGATGCC TATGTAGCAC CGAGTACAGA 240  
 TACCGnACAC TTGCTATGCC AAATTTTTGC AGATATTTTA CATGTGAATC AAGTAGGTAT 300

TCCGGATAGA GGCATCCACT GGGGAACGGT TACCAATTGG

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(2) INFORMATION FOR SEQ ID NO: 3927:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3927:

TATCGATCAA TTTCTATCGA GTTGGACAAT GCCGAACGTG ACAAAGTTTT TACCATGCAT 60  
 GGTTGCATTT AGCGCAACAT GACCATAGTT TTAATAAAGC ACAGCGCGCA AGTGATTAAA 120  
 GGCTTACCCA ATGATCCTGA AATGACGATA GAGTCAGTAT TAACTCATT TTCAATAGAT 180  
 CAGGAAGACT ACCAAGCTTA TGTGAAGGA CATCTTTTGG CGTTACCGGG TTGGGCAGGT 240  
 ATGTTGTATT ACCGTTTACA ACAGCATCAC TTTGGAACAA CATTTGTTAA CGGATTATTT 300  
 GGCAATTCGG TTAGTTGTCG AACAATTGCT AGTTGGTGGG TGAGTTTAAG TCCATCGCTA 360  
 AAGATGTGGA AATAGnCCGG AAAATGGTTT TAAGCAAAC 400

(2) INFORMATION FOR SEQ ID NO: 3928:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3928:

GTGCACCTAA CGCTGAAATA TCGCCTTCTC GTGTATAGCA GACGGAATCA TTTTTTGTGC 60  
 AnTTTGTAA ATATAGGCCC TGCAATGAGT GTACTGGAAT GGCAATAATC ATACCATA 120  
 GTAATACATC TCCAACATTT GCCTTTAATT CTTTGGCGAT GACTACCGGT CCTGGATGTG 180  
 GTGGTAAAAA GCCATGTGTC ACTGATAAAG CTGTTACCAT AGGTAGTCCT AGTTTAAACA 240  
 CTGAAACATT TCGCGTTTTT GCTACTGTAA ATACTAATGG AATCAGTAAG ACTAAACCTA 300  
 CTTCAAAGAA CAATGCAATA CCGACGATAA ATGCTGGCAA CAAGCATTGC CCCATTGGTA 360  
 CATGGTTTTT GGACCAAATT TTTGGAATCA ACGTGTCTGG 400

(2) INFORMATION FOR SEQ ID NO: 3929:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3929:

	CTCAAGGTGT TGCCTATACA GCTAAAAAAC TTAATTTTAA CGCTGTTATC TTTATGCCAG	60
10	TCACTACACC TTTACAAAAG GTAAATCAAG TAAAGTTCTT TGGAAATAGT AACGTTGAAG	120
	TTGTACTCAC TGGTGATACA TTGATCACT GTTTAGCTGA AGCTTTAACT TATACAAGTG	180
	AACATCAAAT GAACTTTATA GATCCATTCA ATAATGTTCA TACAATTTCT GGACAAGTA	240
15	CGCTTGCTAA AGAAATGCTA GAACAAGCAA nGTCTGACAA TGTTAACTTT GCATTATCTA	300
	TTTGCCGCAA TTGGTGGTGG CGGTTTAATT TCAGGTATTT CGTACTTACT nTTAAACCT	360
	ATTCACTAC CACGnAAATT ATAGGTGTTG AACCCnAGT	400

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(2) INFORMATION FOR SEQ ID NO: 3930:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 374 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3930:

	ATATGATCCT ATGAAGCAAT TTTATGTAGT AAGTGGTTCT AAACATGACG CCCTTATGCT	60
	CTGTGAACAT TTATATGACG AGGTTATGGC TGTTTGCTAA nCCCCAATGA TACATCGAAT	120
35	GGCACATATC ATTCGTCGCA ATATGATTAC TATGATGCAT TTATTAAGCA GCAAGAAAAT	180
	GTAACATATA TTTCAACCGA TCGTGCAGAT GCTAATACAG TGTTATGTCA CTAATTTATA	240
	AAAAATAAAT GAATAAGTAA GGTTTCAACC GAGAGAATAT ATTCGTGTTG AAGCCTTATT	300
40	TGTCGTTGTG CCAAATTTGA ACGnTTTAGA TGGCAATAAG CATGACCATA CAGATTGTGT	360
	ATTATTTCCA TGnA	374

45

(2) INFORMATION FOR SEQ ID NO: 3931:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 387 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3931:

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TGCTTCTTTC GCTAGCCTCG TATGGGCATC TTTATCAATA ATATACTCGC CATGACTATC 120  
 TTTCGCTTTT AAGTCAATTT CATCAAATC TTTCCACCT GTTAACGGTG CACCACTATG 180  
 5 TCGTTTCCGA CCAAATGTAG CCTCTTGTTT TTCCAGCGCA GTACGATCCC ACGTTTCAAT 240  
 GTGTATTTGA ATACGTCTGA CAACGCAATA AGTTCCATGT TTCGCCCATC CGTCATCAAT 300  
 AAACACATAA TCTTTAAGTT GATTATTCTT CCTAGGATTA ATTGTTCCAC TTTAAAATGC 360  
 10 CATTnAAATT CTAGGTGTTT CCnTAnC 387

## (2) INFORMATION FOR SEQ ID NO: 3932:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3932:

AAGGTAATAA TCCTGTAGTC GAAAATGTTG TCTCTCTGA GTGGATCCTG AGTACGACGG 60  
 25 AGCACGTGAA ATTCCGTCGG AATCTGGGAG GACCATCTCC TAAGGCTAAA TACTCTCTAG 120  
 TGACCGATAG TGAACAGTA CCGTGAGGAG AAGGTGAAAA GCACCCCGGA AGGTAGnTGA 180  
 AATAGAACCT GAAACCGTGT GCTTACAAGT AGTCAGAGCC CGTTAATGGG TGATGGCGTG 240  
 30 CCTTTTGTAG AATGAACCGG CGAGTTACGA TTTGATGCAA GGTAAAGCAG TAAATGTGGA 300  
 GCCGTAGCnG AAGnAnGTTT TGAATAGGGC GTTTAGTATT TGGTCGTAGC CGATAACCAG 360  
 GTGATTCTAC CCTTTGGTCA GGTGAAGTT CAAGTAACAT 400

35

## (2) INFORMATION FOR SEQ ID NO: 3933:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 40 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3933:

45 GCGATGGTTG AAACATTGAC TTATATTAAA GAGTTTATGA ACCAAGTTGA GTCGCATAGC 60  
 TAGTATGAAA CGTGGTGTGC GCATGGGAAC TATCAAGCTT TGAAGATGTG GTACTACATG 120  
 50 CGTTGAATTA GGGATCGGTA CTTTATATGA AGACGTGCTG CTTCCATTAA ATGAGTGATG 180  
 CGATTTTGGC ATGAAGGTCA CCTTAAATGT ACATTGTTGT AATAAAATTG CCTATAAATT 240

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AATTGTAAAA AGAAAACCAT ACGCTATGTG nTGCCAAGGA AAAGGTTCTA CCATTGTCAC 360  
 nAAAAATGCA TCTCTACGTG CTAGGAATAA ATATTGGGTC 400

(2) INFORMATION FOR SEQ ID NO: 3934:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3934:

TTTGACGTTT TAGACATAAA AAAAGAGACC TTGCGGTCCA GATGGGGCTC ATCGCATCCA 60  
 CTTTTTGCCT GGCAACGTTT TACTCTAGCG GAANTAAATCG AACTACCATC GACGCTAAGG 120  
 AGCTTAACTT CTGTGTTCCG CATGGGAACA GGTGTGACCT CCTTGCTATA GTCACCAGAC 180  
 ATATGAATGT AAATTATACA TTCAAAACTA GATAGTAAGT AAAAGTGATT TTGCTTCGCA 240  
 AACATTTATT TTGATTAAGT CTTGATCGA TTAGTATTCG TCAGCTCCAC ATGTCACCAT 300  
 GGCTTCCACC TCGAACCTAT TAACCTCATC ATCTTTGAnG GATCTTATAA CCGAATTGGG 360  
 AAnCTCATCT GAAGGGGGCT CAGCTAGATG CTTCAAnCTT 400

(2) INFORMATION FOR SEQ ID NO: 3935:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3935:

TGTTCTTTTT GGGCAGTGGG ACACAAATGG ATATTTTCGG CAAAATTAT TTCGTTCGnT 60  
 CCCACCCCAA CTTGGCACAC TATTGTAAGC TGACTTTTCG CCAGCTTCG TGTGGGGCC 120  
 CCGCCAACCTT GCCATTGTCT GTAGAAATG AGGAGCTAAT TTCTCTGTGT CGGGGCTCCA 180  
 CCCCACCTTG CACACTATTG TAAGCTGACT TTCCGCCAGC CTCTGTGTTG GGGCCCCGCC 240  
 AACTTGCACA CTATTGTAAG CTGACTTTCC ACCAGCCTCT GTGTTGGGCC CCGACTATTT 300  
 TTGAAAAGAG CGTGTACAC GGGCATTGTT TTACAGTCAA CTACTGCTAA AATAAAATTA 360  
 ACGAGCTTAA GGCTTTGGnT TCTGTCCCAA GCC 393

(2) INFORMATION FOR SEQ ID NO: 3936:

(A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3936:

10 AAAAAGAAGA CAACCAAGCC CAATAATGGA CTGGCCGCGT AATAATnGTG GCTCTAAAAG 60  
 TTGTATTTTA AAAATAGTTC TTAAATTAT ATACCCACCA CATTGGGTGG AGAACCTAAA 120  
 AAAAAGCACT TCCCAAAAAT GGAAAGTGCA AGTAGTGAGC CATAGAGGAT TCGAACCTCT 180  
 15 GACCCTCTGA TTAAAGTCA GATGCTCTAC CAACTGAGCT AATGGCTCTA ATGGCTGGGC 240  
 TAGCTGGATT CGAACCAACG AGTGACGGAn TCAAAAGTCC GTTGCCTTAC CGCTTGGCTA 300  
 TAGCCCAATA TATAGATGGT GGAAGGGGGC AGATCGAACT GCCGAACCCG AGGAGCGGAT 360  
 20 TTACAGTCCG CCGCGTTTtag CACTTCGCTA CCTCCAGCT 400

## (2) INFORMATION FOR SEQ ID NO: 3937:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 609 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3937:

GGTTTAACAC GCCTGCCTGT CACGCAGGAG ATCGCGGGTT CGATTCCCTG TCGAGACCGC 60  
 35 CATTATTATT ACCATTACGG TTCAGTAGCT CAGTTGGTAG AGCAATGGAT TGAAGCTCCA 120  
 TGTGTCGGCA GTTCGACTCT GTCCTGAACC ATTCTTAATT CATGGCGGTT GTGGTGAAGT 180  
 40 GGTTAACACA TCGGATTGTG GTTCCGACAT TCGAGGGTTC GATCCCCCTC AGCCGCCCCA 240  
 TAATCGTTTA CATTAGCGGG TGTAGTTTAA TGGCAAACC TCAGCCTTCC AAGCTGATGT 300  
 TGTGGGTTTC ATTCCCATCA CCCGCTCCAT TATTTTCTAT TATTCCACAG TAGCTCAGTG 360  
 45 GTAGAGCTAT CGGCTGTTAA CCGATCGGTC GTAGGTTTCA GTCCTACCTG TGGAGCCATG 420  
 GCTCyTTGGt CAAGCGGTTA AGACACCGCC CTTTCACGGC GGTAACACGG GTTCGAGTCC 480  
 CGTAGaGTyC ATACAAGCAG AAGTGnAAAT ATCGCTTCTG TTTTTTTaTT ACATAwTTAA 540  
 50 TkGTTGgAGG aAGtTGtCG AgCyGGGCGG AAGGaGCACG CCTGGAAATG TGTAAGCGTT 600  
 CACAAGCTT 609

## (2) INFORMATION FOR SEQ ID NO: 3938:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3938:

10 TAAAGTTGTT CTCAGTTCGG ATTGTAGTCT GCAACTCGAC TACATGAAGC TGAATCGCT 60  
 AGTAATCGTA GTCAGCATGC TACGGTGAAT ACGTTCCCGG GTCTTGTACA CACCGCCCGT 120  
 CACACCACGA GAGTTTGTA CACCCGAAGC CGGTGGAGTA ACCTTTTAGG AGCTAGCCGT 180  
 15 CGAAGTGGGA CAAATGATTG GGGTGAAGTC GTAACAAGGT AGCCGTATCG GAAGGTGCGG 240  
 CTGGATCACC TCCTTTCTAA GGATATATTC GGAACATCTT CTTCAGAAGA GCGGAATAAC 300  
 GTGACATATT GTATTCAGTT TTGAATGTTT GTTCATTCAA ATTAATGGGC CTATAGCTCA 360  
 20 GnGGTTAnAG CGCACCTGA TnAACGTGAA GTCGGTGGTT 400

## (2) INFORMATION FOR SEQ ID NO: 3939:

- 25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3939:

AGTTTTGAAT GTATAAATTA CATTATATG TCTGGTGACT ATAGCAAGGA GGTCCACCTG 60  
 35 TTCCCATGCC GAACACAGAA GTTAAGCTCC TTAGCGTCGA TGGTAGTCGA ACTTACGTTT 120  
 CGCTAGAGTA GAACGTTGCC AGGCATAATA TTAATCCACA GTAGCTCAGT GGTAGAGCTA 180  
 40 TCGGCTGTTA ACCGATCGGT CGTAGGTTTC AGTCCTACCT GTGGAGCCAT GGCTCTTGGT 240  
 CAAGCGGTTA AGGACACCGC CCTTTCACGG CGGTAACAGG GGTTTCGAGTC CCGTAGAGTT 300  
 CATTATTTTG GAGAATTAGC TCAGTAGGGA GAGCATCTGC CTTACAAGCA GAGGGTCGGC 360  
 45 GGTTTCGAAC CCTnCATTTT CCACCATTG GTTATTAAAn 400

## (2) INFORMATION FOR SEQ ID NO: 3940:

- 50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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ACACAACAGC TGTTTCAAAA ATGATTGGTA CAACTGCTGG TTATGTTGGT TATGATGACA 60  
 ATTCAAATAC GTTAACTGAA AAAGTACGCC GTAATCCATA CTCAGTCATT CTATTTGATG 120  
 5 AAATCGAAAA AGCAAATCCA CAAATTTTAA CATTGTTATT ACAAGTAATG GATGATGGTA 180  
 ATTTGACTGA TGGTCAAGGT AATGTCATCA ACTTTAAAAA TACAATTATT ATTTGTACAT 240  
 CAAATGCTGG CTTTGGCAAT GGCAATGACG CTGAAGAAAA AGATATTATG CACGAAATGA 300  
 10 AAAAATTCTT CCGCCCTGAA TTCCTTAACC GCTTCAACGG CATCGTGAAT TnCTTACATT 360  
 TAGATAAGGT GCCnTGCAGG TATCGTCCAA CTATTATTAG 400

15 (2) INFORMATION FOR SEQ ID NO: 3941:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3941:

25 ATACAATTTT AAATCTGTAT GTGTGAATCC AACACATGTT AAATATGCAG CAGAGCGnCT 60  
 AGCTGATTCA GAGGTGCTCG TTTGTACGGT AATAGGATTC CCATTAGGTG CGTCGACAAC 120  
 30 TGCAACGAAA GCATTTGAAA CAGAAGATGC AATTCAAAT GGTGCAGATG AAATTGACAT 180  
 GGTCATCAAC ATCGGCGCAT TAAAGATGG ACGTTTTGAT GATGTACAAC AAGACATTGA 240  
 AGCAGTGGTT AAAGCTGCGA AAGGTCACAC AGTAAAGTG ATTATTGAGA CGGTATTGTT 300  
 35 GGACCATGAC GAAATTGTAA AAGCGAGTGA TTAACAAAAG CGGCTGGTGC GGACTTCGTT 360  
 AAAAACTTCA GCAGGTTTTG CCAGTGGCnG TGCGACTGCA 400

(2) INFORMATION FOR SEQ ID NO: 3942:

40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3942:

50 CTCTGGATCA AAGCTTACTT ACAGCTCCCC AAAGCATATC GTCGTTAGTA ACGTCCTTCA 60  
 TCGGCTTCTA GTGCAAGGC ATCCACCGTG CGCCCTTAAT AACTTAATCT ATGTTTCCAC 120  
 CATTTTTATA AGTCAAACGT TAACATGAAG TTACGTTCTT TTATAAAAAG ATTTAAACGC 180

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TATTTAAAAC TCTTTATTCA CTCGGTTTTG CTTGGTAAAA TCTATATTTT ACTTACTnAT 300  
 CTAGTTTTCA ATGTACAAAT AATGGTGGAG ACTAGCGGGA TCCGAACCCG CTGACCCnAC 360  
 CnGCGTGCAA AGCAGGCGCT CTACCCAGCT TGAGCTAAGG 400

## (2) INFORMATION FOR SEQ ID NO: 3943:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3943:

CGCTACACTA CGAGACCATT AGTAAAACGG AGGAAGAGGG ATTCTGAACCC CCGCGAGCCG 60  
 TTAAGCCCCT GTCGGTTTTT AAGACCGATC CCTTCAGCCG GACTTGGGTA TTCCTCCAAA 120  
 ATTATATGGA CCTTGCAGGA CTCGAACCTG CGACCGAACG GTTATGGAGC CGTTAGCTCT 180  
 GAACCAACTG AGCTAAAGGT CCTAAATATA ATTTTACAAC TAATAAATAG TGGCGGTGGA 240  
 GGGGATCGAA CCCCCGACCT CACGGGTATG AACCGTACGC TCTAGCCAGC TGAGCTACAC 300  
 CGCCTTATAT AGTTTGTAAG TnAnnATGGT GGGGAGCTAG CGGGGTTCGA ACCGCTGGAC 360  
 CTCCTGCGTG CCAAAGCAGG CGGCTTCTAC CCAGCTGGAG 400

## (2) INFORMATION FOR SEQ ID NO: 3944:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 406 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3944:

CCAAAATTGC ACCTTGTCGT TTATTCGGAA AATCAATATn GnTAGGGGGT ATAAGATGCA 60  
 CCTACTTTAA CTGTCGCCAA CATCGCCGCA ATCATTTCAA AACTACGTTC TGTAACAAG 120  
 GCAACCCGTT GACCATTGCC CACACCATTG GATAGGAGCA TGTGCGCAAT GGCATCCACA 180  
 TAGTTGCGTA ATGTTTCATA CGTCATTGTC AAATCATTCA TGA TAGCGC AACATGATTA 240  
 CCTTGTCGTG AGAAACTTCA TTAAAGTAAC TTATGATAGA TTTATTTCCC GGGACATTAA 300  
 GCATTCGATC GTTAACATGC GTATTGACCC AATTTAGAAG TTCCTCCGTG CCGTTTGGTA 360  
 TATCACAAAT TTGTAGTGTA wCtTGaTGCT TCmAAATAtC AATCAn 406

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3945:

CAATGACAAC AGCAACTGAG ACAGTGTCAA ACGCTTAATA ATAATGATGT AGTGTGCAAT 60  
 AATACCGCAT TAAATGTACC AACTAAAACA AATGAAAATG GTTCAGGAGG ACATCTAACT 120  
 TTAAAGGAAA TTCAAGAAGA TGTTTCGTCAT TCTTCAAATA AACCAGAGCT AGTTGCAATT 180  
 GCTGGAACCA GCATCTGAAT AGACCGAAAA AGAGAAGTTA GACGTGCGGC ACCGGCAGAT 240  
 CCTGAATGCC AACTCCAGCA GATCCAGCGG CTGCAGCGGT TAGGAAACGG TGGTGCACCA 300  
 GTTGCAATTA CAGCGCCATA TACGCCAACA ACTGATCCTA ATGCCATGAN GCCAGGACAA 360  
 ATGGCACCTA ACGAnGCTTG TTCATTTGAT GGACAnGGTA 400

## (2) INFORMATION FOR SEQ ID NO: 3946:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3946:

CTCGCTGCGA TAAAGTACCA GTTCATAGCA ACGTTTGTnT TAATAGGnTC TGAAACGATA 60  
 CGTGTTGCCG GTTCTGTAAA TGAATAGACC AAAGCATCTT GCATACCAAC AACTATATTT 120  
 GCTGCAAATC CTCCAACAGC GGAAnATATG CCATCGTTAG TCCAGCGATA GGGTGATAGC 180  
 CAATTTTAAT AAAAAGCATT GCTGCAACGG CCGGCAAGAT AATTGTGCGA GCATCGCCGG 240  
 CTGTACTACC TAAAATACCA ATTAATATAA TAGTCGGTAA AATTAAGAAA CGTGGTGCGC 300  
 GATTCACAAC AGAAATCATT AACTTATCGA AGTATCCTGT TTTCTCTGCA ACACCAATAC 360  
 CAATCATCAC TGCTAGGTAC TAAGCCTAAT GCTGGGnACT 400

## (2) INFORMATION FOR SEQ ID NO: 3947:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3947:

5 GCGGGCCAGA GGACTTGGAA CCCCCAACCT ACTGATTACA AGTCAGTTGC TCTACCAATT 60  
 GAGCTAGGCC GGCAATATGT AAGAATAAAT GGTGGAGAAT GACGGGTTTCG AACCGCCGAC 120  
 CCTCTGCTTG TAAGGCAGAT GCTCTCCCAG CTGAGCTAAT TCTCCGATTT AAAACTGCCT 180  
 10 GGCAACGTTT TACTCTAGCG GAANTAAATC GNACTACCAT CGACGCTAAG GAGCTTAACT 240  
 TCTGTGTTTC GCATGGGAAC AGGTGTGACC TCCTTGCTAT AGTCACCAGA CATATGAATG 300  
 TAATTTATAC ATTCAAACT AGATAGTAAG TAAAAGTGAT TTTGCnTTTCG CAAAACATTT 360  
 15 A 361

## (2) INFORMATION FOR SEQ ID NO: 3948:

## (i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 382 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3948:

25 TTCCGTCAGA CCCTGACATG GTTCATGGGT TCATATTGCA TAGGACCGAA ATCTTCAAAC 60  
 30 ACTACGTGCT TTGGGCAGAC TTCGCAAAA TACGGCCTCA ACAAAGGAAT TAAGCCTCGC 120  
 ATAAAGCGGA TTTCGAGTAC AGGGAACCGC TACCTCCCCA CCTAGCACGG CAAGATATAT 180  
 ATTACTATAT TTTAATAGTT AATTGCAAGT ATAAATCATT TATATCATTG TTTACTTTAT 240  
 35 ACGACGTCTT GAGAAGTCAT TAATTTAAAT TCATTTGCAA GATGTTTTGA AATATTATAT 300  
 TGAAACGGCA TTGTATTTTC TAAATACACA nTACTTCGAA CTGTTGCnGA ATAGGCCACC 360  
 GATACATCAC CAACAATTGG na 382

## (2) INFORMATION FOR SEQ ID NO: 3949:

## (i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3949:

50 GCCAAGCCAT TTTCTTTGT GTTTACTTTT TATTTGACG TTTTAGACAT AAAAAAAGA 60  
 GACCTTGCGG TCTCAATGCG GTCATCGCA TCCATTTTTT GCCTGGCAAC GTTCTACTCT 120

TTGCTTCTTT CCTCTTCTTC GGCTCTCGCT TACTCATTTA GCTCTACTAA ACTCGTTGCG 240  
 CTCTTTTCTC GTTTCGTCAG ATTCAAACGT TTTCACCTCG CCAAGCCATT TTTCTTTGTG 300  
 5 TTTGCTTTTT AnTTTGACGT TTTAGACATA AAAAAAGAG ACCTTGCGGn CTCAATGnGG 360  
 GCTCATCGCA TCCAATTTTT GGCCTGGCAA CGGTTCTACT 400

## (2) INFORMATION FOR SEQ ID NO: 3950:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3950:

20 ACTCGGTTTT GCTTGAAAA TCTATATTTA CTTACTTATC TAGTTTTCAA TGTACAATTT 60  
 CTTTTTAGTC AAGCGCTCGC ATACTGCTTT ATTTTCATAA GCAATATCAC TTTAACCAAA 120  
 AAATATTTGA ATGTTAAATA AACATTCAAA ACTGAATACA ATATGTCACG TTATTCCGCA 180  
 25 TCTTCTGAAG AAGATGTTCC GAATATATCC TTAGAAAGGA GGTGATCCAG CCGCACCTTC 240  
 CGATACGGCT ACCTTGTTAC GACTTCACCC CAATCATTTG TCCCACCTTC GACGGCTAGC 300  
 TCCTAAAAGG nTACnCCACC GGCTTCGGGT GTTACAAACT CTCGTGGTGT GACGGGCGGT 360  
 30 GTGTACAAGA CCCGGGAACG nATTCACCG 389

## (2) INFORMATION FOR SEQ ID NO: 3951:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 40 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3951:

45 AAAGCTCGAC TTGTTTACGA TGTGAAAAA CAAGATTATG TACCTGTATC GCAACCACAA 60  
 TTACCAATTT TAAATGAATT TAATAAAGAC TTAGTGCATA ACCTTGATAC CATATTCAAT 120  
 GCGCAAGACG AnCGGGACTA TTTTATGGG AGACATTACG TAATAATTTT TATTACTCTG 180  
 50 CTATCAATGT ACCTAAAGCT ACCGATGATT TCCGAGACAT AGACCGTGCG CTTGTCTGGG 240  
 GGTTCAACTG GAAACTTGGT CCATTCCAAT TATGGGATGC AATGGGATAC GAACGTGTTA 300  
 AAACAnTGAT GGAAGACGA ACTTGGGAGA CTTACCACAA TGGGATTAGT GAnTTAGATG 360



## (2) INFORMATION FOR SEQ ID NO: 3952:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3952:

CAAAGGGCAG CGAAACCGCG AGTCCAGAGC AAATCCCAT AAGTTGTTCT CAGTTCGGAT 60  
 TGTAGTCTGC AACTCGACTA CATGAAGCTG GAATCGCTAG TAATCGTAGA TCAGCATGCT 120  
 ACGGTGAATA CGTTCCCGGG TCTTGACAC ACCGCCGTC ACACCACGAG AGTTTGTAAC 180  
 ACCCGAAGCC GGTGGAGTAA CCTTTAGGA GCTAGCCGTC GAAGTGGGAC AAATGATTGG 240  
 GGTGAAGTCG TAACAAGGTA GCCGTATCGG AAGGTGCGGC TGGGATCACC TCCTTTCTGA 300  
 AGGATATATT CGGGAACATC TTCTTCAGAA GAGCGGGAAT AACGTGACAT ATTGTATTCA 360  
 GNTTTGGAAT GTTTnTTAA CATTnCAAAA AAATGGGGCC 400

## (2) INFORMATION FOR SEQ ID NO: 3953:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3953:

TGATTTTGAC GTTTTAGACA TAAAAAAG AGACCTTGCG GTCTCAAATG CGGCTCATCG 60  
 CATCCATTTT TTGCCTGGCA ACGTTCTACT CTAGCGGAAC GTAATTGGCT ACCATCGACG 120  
 CTAAGAACCT TTCTTGACTT GTGACAATCG CTGCTTCTT TCCTCTTCTT CGGCTCTCGC 180  
 TTACTCATTT AGCTCTACTA AACTCGTTGC GCTCTTTTCT CGTTTCGTCA GATTCAAACG 240  
 TTTTCACTTC GCCAAGCCAT TTTTCTTTGT GTTTGCTTTT TATTTTGACG TTTTAGACAT 300  
 AAAAAAAGA GACCTTGCGG TCTCAATGCG GGCTCATCGC ATCCATTTT TGCCTGGCAA 360  
 CGTTCTACTC nAGCGGGAAG TGAAGnCGGA CTGACCAAGC 400

## (2) INFORMATION FOR SEQ ID NO: 3954:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3954:

AAACTACATA ATGAAAATGC CGTTTTAATC GGTAAATTAA ATATGGATGA GTTTGCAATG 60  
 5 GGTGGTTCAA CAGAAACATC TTATTTCAAA AAAACAGTTA ACCCATTGA CCATAAAGCA 120  
 GTGCCAGGTG GTTCATCAGG TGGATCTGCA GCAGCAGTTG CAGCTGGCTT AGTACCATTT 180  
 AGCTTAGGTT CAGACACAGG TGGTTCAATT AGACAACCGG CTGCATATTG TGGCGTTGTC 240  
 10 GGTATGAAAC CAACATACGG TCGTGTATCT CGATTGGAT TAGTGCTTTG CATCTTCATA 300  
 GACCAAATTG GGCCATGACT CGAATGTAAA GTAATGCCAT CGTATTAGAA GCTATTCTGG 360  
 15 TGCAGATGnT AATGACTCTA CCAGTGCACC AGTGATGAGG 400

## (2) INFORMATION FOR SEQ ID NO: 3955:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3955:

TCGATTGGCA TTTCTCCGCT ACCCTCAGTT CATCCGCTCA CTTTTCAACG TAATCGGTTT 60  
 GGTCTCCAT TCAGTGTTAC CTGAAGTTCA ACCTGACCAA GGGTAGATCA CCTGGTTTCG 120  
 30 GGTCTACGAC AAATACTAAA CGCCCTATTC AGACTCGCTT TCGCTACGGC TCCACATTTA 180  
 CTGCTTAACC TTGCATCAAA TCGTAACTCG CCGGTTCAAT CTACAAAAGG CACGCCATCA 240  
 CCCATTAACG GGCTCTGACT ACTTGTAAGC ACACGGTTTC AGGTTCTATT TCACTCCCCT 300  
 35 TCCGGGGGTG CTTTTCACTT TTCTCTTCAA GGTATGGGTT CACTATCGGT nACTAGAGAG 360  
 TAATTAGCTT AGGnGATGGT CCTCCCAGAT TCGGAAGGGA 400

## (2) INFORMATION FOR SEQ ID NO: 3956:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3956:

GCTACGGGCG CATATGTTTT TATTGAAAT GGTGCCGAGG ACCGGAATCG AACCGGTAGT 60

5 ATAAAAATGG AGCAGAAGAC GGGATTGCGAA CCCGCGACCC CAACCTTGGC AAGGTTGTAT 180  
 TCTACCGCTG AACTACTTCT GCATATGCGG GTGAAGGGAG TCGAACCCCC ACGCCGTAAG 240  
 CTTAGGATCC TAAGTCTAGT GCGTCTGCCA ATTCCGCCAC ACCCGCAAAT GGTGAGCCAT 300  
 AGAGGATTCG AACCTCTGGA CCCTCTGGAT TAAAAGTCAG ATGCTCTACC AACTGGAGCT 360  
 10 AATGGCTCTT TCCATGGTGC CGGGCCAGAG GACTTTGAAa 400

## (2) INFORMATION FOR SEQ ID NO: 3957:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 379 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## 20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3957:

CAGACATGTG TTATACGGGA AATTGGGCGA ACCGCAACTA TTATACATTG ATTTACACCT 60  
 TATACATGAA GTTACTTCTC CTCAAGCATT TGAAGGACTT AGGCTTCAAA ACAGAAAATT 120  
 25 AAGACGCCCA GATTTAACAT TTGCAACACT CGATCACAAT GTTCCTACTA TTGATATATT 180  
 CAATATTAAA GATGAAATTG CAAACAAACA AATCACAACA TTACAAAAAA ACGCCATAGA 240  
 TTTTGGGGTG CATATTTTGT ATATGGGTTC TGATGAACAA GGTATTGTTC ACATGGTAGG 300  
 30 ACCTGAGACA GGAATTACAC AGCCTGGCnA GACCATCCGT nTGTGGGTGA CTCTCACACA 360  
 GCCACACATG GnGCCTTTT 379

## 35 (2) INFORMATION FOR SEQ ID NO: 3958:

40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3958:

TGTTAAAATA CGGTACATCT AAATTAATGT TAACTGATTT TCAAAAAGAG AATTAAATAA 60  
 ATATATTCAA GGTGAGnAC AACGCGTGAT ATTTGAAAAT GGCCATTTTG TCTAATTGAT 120  
 AGTGAATATA ATTAGAGTAA GAGGCTGGGA CATAAATCCC TAAAAACAG CAGTAAGATA 180  
 50 ATTTTCAATT AGAAAATATC TTAAGTCTGT TCTCTATTTA TACAATACTT CGTATTGAAT 240  
 GGCTTCGCTT TCCTAGGGTG CCGTCTCAGC CTCGGTCTTC GACTGGCACT GCTCCCTCAG 300

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AATAAGACAT TTGnCCAAC TGA CACTACC ATTAAAACT

400

## (2) INFORMATION FOR SEQ ID NO: 3959:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3959:

GAGCCGCAGT GGAATGAGGC CCAAGCGACT GTTTATCAAA AACACAGGTC TCTGCTAAAC 60  
 CGTAAGGATG TGTTATAGGG GCTGACGGCT GCCCGGTGCT GGAAGGTAA GAGGAGTGGT 120  
 TAGCTTCTGC GACGTACrGA ATCGAAGCCC CAGTAAACGG CGGCCGTAAC TATAACGGTC 180  
 CTAAGGTAGC GAAATTCCTT GTCGGGTAAG TTCCGACCCG CACGAAAGGC GTAACGATTT 240  
 GGGCACTGTC TCAACGAGAG ACTCGGTGAA AATCATAGTA CCTGTGAAGA TGCAGGTTAC 300  
 CCGCGTACAG GACGGAAAGn CCCCTGGAGC TTTACTGTAG CCTGATATTG AAATnCGGCA 360  
 CAGTTTGTAC AGGATAGGTT AGGAGCCTTG GAAACGTGTG 400

## (2) INFORMATION FOR SEQ ID NO: 3960:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3960:

TGGTCCCAAA CCAAGTGCTC TACCAAGCTG AGCTACTTCC CGTATAATTA ACGCGCCCGA 60  
 TAGGAGTCGA ACCCATAACC TCTTGATCCG TAGTCAAACG CTCTATCCAA TTGAGCTACG 120  
 GGCGCATATG TTTTATTGA AAATGGTGCC GAGGACCGGA ATCGAACCGG TAGTGAnTnC 180  
 ACTCACCGCA GATTTTAAGT CCTGTGCGTC TGCCAGTTCC GCCACCCCGG CACTATAAAA 240  
 ATGGAGCAGA AGACGGGATT CGAACCCGCG ACCCCAACCT TGGCAAGTTG TTATTCTTAC 300  
 CGCTGGAAC TACTTCTGGCA TATGCGGGTT GAAGGGGAGT CGAACCCCA CGCCGTAGGC 360  
 TTAAGATTCC TGAAGTCTAG TCGTCTGGC CAATTTCCGG 400

## (2) INFORMATION FOR SEQ ID NO: 3961:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3961:

	TTTTGATACA TAATCTAAAT TTCTCAAAGC GCCAATAACA GAGGACCATC TCCTAAGGCT	60
10	AAATACTCTC TAGTGACCGA TAGTGAACCA GTACCGTGAG GGAAAGGTGA AAAGCACCCC	120
	GGAAGGGAGT GAAATAGAAC CTGAAACCGT GTGCTTACAA GTAGTCAGAG CCCGTTAATG	180
	GGTGATGGCG TGCCTTTTGT AGAATGAACC GGCGAGTTAC GATTTGATGC AAGGTTAAGC	240
15	AGTAAATGTG GAGCCGTAGC GAAAGCGAG TCTGAATAGG GCGTTTAGTA TTTGGTCGTA	300
	GACCGGAAAC CAGGTGATCT ACCCTTGGTC AGGTTGAAGT TCAGGTAACA CTGAATGGAG	360
	GACCGAACCG ACTTACGTTG AAAAGTGAGC GGATGAACTG	400

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(2) INFORMATION FOR SEQ ID NO: 3962:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 361 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3962:

	TAATAATTAC AGTATATCGG GAAGACAGGA TTCGAACCTn CGACCCCTTG GTCCCAAACC	60
	AAGTGCTCTA CCAAGCTGAG CTACTTCCCG TATAnTTAAC GCGCCCGATA GGAGTCGAAC	120
35	CCATAACCTC TTGATCCGTA GTCAAACGCT CTATCCAATT GAGCTACGGG CGCATATGTG	180
	TTTATTGAAA ATGGTGCCGA GGACCGGAAT CGAACCGGTA CGTGATCACT CACCGCAGGA	240
	TTTTAAGTCC TGTGCGTCTG CCAGTTCCGC CACCCCGGCA CTATAnAAAT GGATCAGAAG	300
40	ACGGGATTCTG AACCCGCGAC CCCAACCTTG GCAAGGTTGT ATTCTACCGC TGAACACTT	360
	C	361

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(2) INFORMATION FOR SEQ ID NO: 3963:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 375 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3963:

AAGTGTCTTA TTTTTTTAA GTATTTCAAA GTAAAATTAC ATGTTAATAC GTAGATTAAT 120  
 GGCGAGACTC CTGAGGGAGC AGTGCCAGTC GAAGCCGTAG GCTGAGACGG CACCCTAGGA 180  
 5 AAGCGAACCA TTCAATACGA AGATnTnATn AAATAGAGAA CAGCAGTAAG ATATTTTCTA 240  
 ATTGAAAATT ATCTTACTGC TGTTTTTTAG GGATTTATGT CCCAGCCTCT TACTCTAATT 300  
 ATATTCAC TAATTAGAC AAAATGGCCA TTTTCAAATA TCACGCGTTG GTTTCTGACC 360  
 10 TTGGAATATA TTTAT 375

## (2) INFORMATION FOR SEQ ID NO: 3964:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3964:

AAAATGGCCT TGATAGACTT GCTCAATGCA GGGTTGCCAC AAACCAATGA TGCACCTTACA 60  
 25 ATTTTAAATA GATTTTAAAG ACCTTGTTGG TTTGTACAA TTAATGTGAC ATGACTAGGT 120  
 CTGACGTT TATATGCATC TTCATTACTG AGTTTTTGT TGATTTCGTT ATGATTTAAT 180  
 30 ACGCCTAATT CTTTCATTG TTGAACCATT TTTATGAAAA TGTAAGCTGT TGCTTCTGTA 240  
 TCATAAATGG CACGGTGATG TTGCGTTAAT TCTACGCCAT ATTTTTTAGC CAAGAAATTC 300  
 AAACCATGTT TACCATATTC AGTATTAATC GTACGAGGAT AATTCTAAAG TATCGATAAC 360  
 35 ACCATTCGTT GGATGGTCCA AACCCAAGAC GTTCATATCC 400

## (2) INFORMATION FOR SEQ ID NO: 3965:

40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 391 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3965:

ACTTTTAATT TTGTCATGAT GTGCCTCCTT ACCGTATGAT GTTATTCAAA GTAAATTGCT 60  
 50 TTGCCTGATT TTGCAGACTG ATAAATCGCT TCAAGAATTT TTGTAAC TAC CATGCTTGT 120  
 TCCGGTTTCA CAACTGGTTC AGTATCATTT ACAACTGCAT CAATCCAAGC TTTTGCTTCT 180  
 55 TCTTCAGCTT CATCCACTTC ATTACCTTCA TAAAAGTCGA CGCCTTTGTT TTCCAATTCA 240

TCAGCACCTG CTTTAGGTTT CTGATAATGA ACATTTTGGC CTCATCCACT TCTAAAGAA 360  
TTAATCGCCC AAGnGGGATT CCAAAAAGGA n 391

5 (2) INFORMATION FOR SEQ ID NO: 3966:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 398 base pairs  
(B) TYPE: nucleic acid  
10 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3966:

CGCTATCAGG TATTGTTTCA ACAATTTTCAT TAACATATCG TGAAATATCA TTTTGAGGGA 60  
TTCTAACAGA AGTTTCTATT GGTAGTGTAG TTGGGGCATG TTATAATTTT TATACATAAG 120  
20 GCACCTCGTT AATTTAGTTT AGTGGTATTT ATTAAATTAT AAGAAGGGAC CCAACACAGA 180  
AAATTCATTT TATTGAATTT TACATTTATG TGCAAGTTGG GCAAAGTGTC TTATTTTTTA 240  
AAAGTATTTT AAAGTAAAAT TACATGTTAA TACGTATATA ATGGcGAGAC TCCTGAGGGA 300  
25 GCAGTGCCAG TCGAAGcCAA GGCTGAGACG GCACCctAGG AAAGCGAcnC ATTcAATACG 360  
AAGATTGTAT AAATAGAGAA CAGCAGTAAG ATATTTTC 398

30 (2) INFORMATION FOR SEQ ID NO: 3967:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 base pairs  
(B) TYPE: nucleic acid  
35 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3967:

40 GCTATAGAAA AAATAAAATC ACAAGTTACG ATTAGCGTAC TTGATGGGGA GTGAAAATAA 60  
TGAGAGTAAC AGAGTTATTA ACAAAGATA CAATAGCAAT GGATTTAATG GCAAATGACA 120  
45 AAAATGGTGT TATTGATGAG TTAGTAAATC AATTAGACAA AGCAGGTAAA TTAAGTGATG 180  
TCGCGTCATT TAAGGAAGCG ATTCACAATC GAGAATCACA AAGTACAAC TGGTATCGGCG 240  
AGGTATTGCC ATTCCACATG CCAAAGTGGC CGCAGTTGAA GTCACCAGCT ATTGCGTTTG 300  
50 GTAAATCTAA AGCAGGCGTG GATTATCAAn TTTGGnTATG CAACCAGCAC ACTTnTTCTT 360  
TGTGGTTGGC AGCG 374

(2) INFORMATION FOR SEQ ID NO: 3968:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3968:

10 ACCCCGGCAC TATAAAATG GAGCAGAAGA CGGGATTCTGA ACCCGCGACC CCAACCTTGG 60  
 CAAGGTTGTA TTCTACCGCT GAACTACTTC TGCATATGCG GGTGAAGGGA GTCGAACCCC 120  
 CACGCCGTAA nCTGAGGATC CTAAGTCTAG TCGCTCTGCC AATTCCGCCA CACCCGCAAA 180  
 15 TGGTGAGCCA TAGAGGATTC GAACCTCTGG ACCCTCTGAT TAAAAGTCAG ATGCTCTACC 240  
 AACTGAGCTG AATGGCTCTT CCATGGTGCC GGCCAGAGGA CTTGAACCCC CAACCTGACT 300  
 GGATTACAAG TCAATTGCTC TACCAATTGA GCTAAGGCCG GGCAATATGT AAGAATAAAT 360  
 20 GGTGGAGAAT GACGGGTTTC GAAnCGCCGA CCCTCTGCTT 400

## (2) INFORMATION FOR SEQ ID NO: 3969:

- 25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3969:

GCGAGTTGGG GTGTGGGCCC CAACATAGAG AAATTGGATT CCCAATTTCT ACAGACAATG 60  
 35 CAAGTTGGCG GGGCCCCAAC ACAGAAGCTG ACGAAAAGTC ATTAnCAATA ATGTGCAAGT 120  
 TGGCGGGGCC CCAACACAGA AGCTGACGAA AAGTCATTAn CAATAATGTG CAAGTTGGCG 180  
 40 GGGCCCCAAC ACAGAAGCTG GCGGAAAGTC AGCTTACAAT AATGTGCAAG TTGGGGTGGG 240  
 ACAACGATAA AGTAATACTT TTTCTATAGA AATTAGTATT TCTTATGCAT GAGTTTTACT 300  
 CATGTATTCC TATTTTTAAG TACACATTAG CTGTGGCTAA TGTTTAAGAC CCACTACATA 360  
 45 ATAAATCATT AGTGGCTCTn TATCATTTCT GTCCCACTCC 400

## (2) INFORMATION FOR SEQ ID NO: 3970:

- 50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 419 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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GATAAGATCA GCCGAAAATG GATGGTGTGA AGAGCGTTAC TTGGTTTGGC GGTATGCTTA 60  
 TTTTAAATGG CATTGTGTAC GACACCATTG CAGTTTGTAC TTGTGAGGTT ATTGCAGGGA 120  
 5 CTATTTGGTG GTGTTGTTGA TGCATCAAGT GCGTTTCCGA GTGCAGAGGC GCCACTGAKA 180  
 GATCGTGGAA AGtATTAGGA gACTGCAAAT TCAGTCAGCG CAGGtCTCTT GTGGGGCCAT 240  
 10 TAATTGGCGG TGTTACAGCT TCGATATTAG GTTTTAGTGC GTTACTGATG AGTATTGCCG 300  
 TTATTACTTT TATTGTCTGT ATTTTCGGTG CATTAAAATg ATTGAAACGA CACATATGCC 360  
 AAaATCACAA ACACCAAATA TTAATAAAGG TnTTCGCCGT TCCAnTtnCA ATGTCTAAT 419

15 (2) INFORMATION FOR SEQ ID NO: 3971:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 381 base pairs  
 (B) TYPE: nucleic acid  
 20 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3971:

AAACITGGGA GACTTCAATA ACAGATTTAG GTTATCTAA AAATCAGGCA TATAATTTCT 60  
 TAATTACATC TAGTCAAAGA TGGGGCCTTA ATCAAGGGAT AAATGCAAAT GGCTGGATGA 120  
 30 GAACTGACTT GAAAGGTTCA GAGTTTACTT TTACACCAGA AGCGCCAAAA ACAATAACAG 180  
 AATTAGAAAA AAAAGTTGAA GAGATTCCAT TCAAGAAAGA ACGTAAATTT AATCCGGATT 240  
 TAGCACCAGG GACAGAAAAA GTAACAAGAG AAGGACAAAA AGGTGAGAAG ACAATAACGA 300  
 35 CACCAACACT AAAAATCCA TTAAGTGGAG TAATTATTAG TAAAGGTGAA CCnnAAGGAG 360  
 GGGTTTCCAn AGTCCGTTAT G 381

40 (2) INFORMATION FOR SEQ ID NO: 3972:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 45 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3972:

GGGTTCAGAA CGTCGTGAGA CAGTTCGGTC CCTATCCGTC GTGGGCGTAG GAAATTTGAG 60  
 AGGAGCTGTC CTTAGTACGA GAGGACCGGG ATGGACATAC CTCTGGTGTA CCAGTTGTCC 120  
 55 TGCCAACGGC ATAGCTGGGT AGCTATGTGT GGACGGGATA AGTGCTGAAA GCATCTAAGC 180

GAnGTTAATA GGTTCGAGGT GGAAGCATGG TGACATGTGG AGCTGACGAA TACTAATCGn 300  
 TCGAnGACTT AATCAAAATA AATGTTTTGC GACCAAATCA CTTTACTTAC TATCTAGTTT 360  
 5 GAATGATAAA TACATCATAT GCTGGnGCCA TACCAAGGGG 400

## (2) INFORMATION FOR SEQ ID NO: 3973:

- 10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3973:

TCTTTTAATT ACGTAATGGC TTACCAGTTT TTAACATATG TGCAATTCTT TCATATGATT 60  
 20 TTTTAGATTT TAGTAAGTCA ATAAAGCCAA TTTTCTCCAA CGATTGAATG TAACGTTGAT 120  
 TGATAAATGT ATTTCTTGGT AAATCACCAC CCGCTAAAAT TGTGGCGATA TTTAAGGCAA 180  
 TATGATAATC ATGGTCGCTA ATAAATGAC CCCGTCTTTG CGCATCTAAT TGTCCCTTGA 240  
 25 TCAATGCTTT GAAGTCTTCA CCTAAAGCGA TATATTGATG TCTAGGATTC GGAATATACT 300  
 TTGTTTCTGC TTCATATTTC GCACGTGTGA GCGCAACTTC GACACGnTGG TGCCTGGATT 360  
 30 nGAAAATAAA CCGGAnCCnG GGATCCACGG GAAATAACCC 400

## (2) INFORMATION FOR SEQ ID NO: 3974:

- 35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3974:

TGCCATGTTT ACCTTGTTTA AAATCAAGGT TTGTAATGTT TCCTTGTGTC ACGATAATAG 60  
 45 GCGTAATATC ACTCTTTGCA TGATTGCGGA TGTAGTCTAA ATCAAAGTTG ATTAATAAAT 120  
 CACCTTGTTT AACTTCTTGA CCTTCCTCAA CATGTAAAGT AAAGCCTTCT CCGTTTAATT 180  
 TAACAGTGTC TAAACCGATG TGGATTAATA GTTCTAAACC ACTATCTGAA TACAAGACCA 240  
 50 ATTGCATGTT TTGTTGGGAA AATCATTTGT TACTTTACCG TTGAAATGGT GCACGAACT 300  
 TCACCTTGTC AnGTTTTTGG ATAGCGATAC CGTCACCCCA TCCATTTTTT TCGCTGAAA 360  
 CACTTGATC AnGGCACTTC TGAATAAATG GTGGTTAACT 400

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3975:

CCTTTGCAGC GCCTCCGTTA CCTTTTAGGA GGCGACCGCC CCAGTCAAAC TGCCCGCCTG 60  
 ACACTGTCTC CCACCACGAT AAGnGCGGGn GTTTAGAAAG CCAACACAGC TAGGGTAGTA 120  
 TCCCACCAGC GCCTCCACGT AAGCTAGCGC TCACGTTTCA AAGGCTCCTA CCTATCCTGT 180  
 ACAAGCTGTG CCGAATTTCA ATATCAGGCT ACAGTAAAGC TCCACGGGGT CTTTCCGTCC 240  
 TGTGCGGGGT AACCTGCATC TTCACAGGTA CTATGATTTC ACCGAGTCTC TCGTTGAGAC 300  
 AGTGCCCAAA TCGTTAACGC CTTTCGTGCG GGTCGGAACT TACCCGACAA GGAnTTTCGC 360  
 TAACTTAGGA CC 372

## (2) INFORMATION FOR SEQ ID NO: 3976:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 395 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3976:

AGGGAATCGA ATTTTCTTTC TCTTCCTnCG GGTACTAAGA TGTTTCAGTT CTCCGGGTGT 60  
 GCCTTCTGAT ATGCTATGTA TTCACATATC GATAACATGA CATAACTCAT GCTGGGTTTC 120  
 CCCATTGCGA AATCTCTGGA TCAAAGCTTA CTTACAGCTC CCCAAAGCAT ATCGTCGTTA 180  
 GTAACGTCCT TCATCGGCTT CTAGTGCCAA GGCATCCACC GTGCGCCCTT AAATAACTTA 240  
 ATCTATGTTT CCACCATTTT TATAAGTCAA ACGCTCACAT ACGGCTTCGT TTTCATTATT 300  
 TTAAAGCTCA TTTACATAAG TAAACTCTGC TTAAATGAT TAACTCATT GTCTGCTAAA 360  
 ACGGTTTnTT TTATGAAAAG GTTTGAAACG GGTTn 395

## (2) INFORMATION FOR SEQ ID NO: 3977:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3977:

TTGGTCCCAA ACCAAGTGCT CTACCAAGCT GAGCTACTTC CCGTATAATT AACGCGCCCG 60  
 5 ATAGAGTCGA ACCCATAACC TCTTGATCCG TAGTCAAACG CTCTATCCAA TTGAGCTACG 120  
 GGCGCATATG TTTTATTGA AAATGGTGCC GAGGACCGGA ATCGAACCGG TAGTnnTTCA 180  
 10 CTCACGCAGA TTTTAAGTCC TGTGCGTCTG CCAGTTCCGC CACCCCGGCA CTATAAAAAT 240  
 GGAGCAGAAG ACGGGATTCTG AACCCGCGAC CCCAACCTTG GCAAGTTGTT ATTCTACCGC 300  
 TGAACTACTT CTGCATATGC GGGTGAAGGG AGTCGAACCC CCACGCCGTA GGCTTAGATC 360  
 15 CTTAAGTCTA AGTGCGTCTG GCCAATTTCC GCCAnACCCG 400

## (2) INFORMATION FOR SEQ ID NO: 3978:

## (i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 387 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3978:

AAGTGGTTAA ATATTATAGA AACATCAAA GGATGTTAAG AAATACAATT TATTACCCAG 60  
 30 CATTTAATAA TGGTGCTATA GAAGGAATTA ATAATAAGAT AAAATTAATC AAGTGAATTT 120  
 CTTTTGGTTA CAGAAATTTT AACAACTTTA AAGCACGTAT AATGATGATT TTCAGCTTGT 180  
 ACAAGGAGA AAAAAAGAAG ACAACCAAGC CCAATAATGG ACTGGCCGCC TAATAATAAA 240  
 35 AGCTCTAAAA GTTGATTTTT AAAAATAGTT CTTTAAATTA TATACCCACC ACATTTGGTG 300  
 GAGGAACCTA AAAAAAGCA CTTCCCAAAA ATGGGAAAGT GCAGTnAGTG GAGCCATAGA 360  
 40 GGATTCCGAA CCTCGGACCC TCnGAnT 387

## (2) INFORMATION FOR SEQ ID NO: 3979:

## (i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3979:

TGGAGCAGAA GACGGGATTC GAACCCGCGA CCCCAACCTT GGCAAGGTTG TATTCTACCG 60  
 55 CTGAACTACT TCTGCATATG CGGGTGAAGG GAGTCGAACC CCCACGCCGT AAnTTAGCAT 120

CGAACCTCTG GACCTCTGA TTAAAAGTCA GATGCTCTAC CAACTGAGCT AATGGCTCTT 240  
 CCATGGTGCC GGCCAGAGGA CTTGAACCCC CAACCTACTG ATTACAAGTT CAGTTGCTCT 300  
 5 ACCAATTGAG CTAGGCCGGn CAATATGTAA GAATAAATGG TGGAGAATGA CGGGTTTCGA 360  
 ACCGCCGAAC CCTCTGCTTG TnAAGGGCAG ATGGCTCnTC 400

## (2) INFORMATION FOR SEQ ID NO: 3980:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3980:

20 TTACCACGTA TTTAGGTTTC TTTGGTGGCT CTAGATTTGT CCCTATTGTC ACAGCATTTC 60  
 CCGCAATCTT TTTAGGTGTA TTGATGTTTT TCATTGGCC AAGCATACAA GCCGGCATT 120  
 ATCATGTTGG TGGATTTGTA ACGAAAACAG GTGCCATCGG TACTTTTGT TATGGCTTCA 180  
 25 TCTTAAGATT GTTAGGTCCA CTCGGTTTAC ACCATATTTT TTACTTACCG TTTTGGCAGA 240  
 CGGCACTTGG TGGTACTTTA GAAGTCAAAG GGCACCTAGT TCAAGGTACG CAGAACATCT 300  
 TCTTTGCTCA ACTTGGTGAT CCAGATGTGA CGAnTATTAT TCCAGGTGTG TCACGCTTTA 360  
 30 nGTCAGCCGT TTTAATACGA GGATGTTCCG CTAnGTGGTG 400

## (2) INFORMATION FOR SEQ ID NO: 3981:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3981:

45 CGACATACGC TGATAAATTA GTTATTAAAC GTAATGGTAA CGTTGTGACG ACATTACAC 60  
 GTCGCAATAA TACGAGTCCA TGGGTGAAAG AAGCATCTGC AGCAACTGTA GCAGGTATTG 120  
 CTGGAATAA TAATGGTATT ACTGTTGCAG CAGGTACTTT CAACCCTGCT GATACAATTC 180  
 50 AAGTTGTTGC AACGCAAGGG AAGCGGAGAG ACAGTGTAGT GGATGGAGCA ACGTATAGTT 240  
 GGATTCACA GTTGTGCGAC CACAACCGAA CCAAGCGACT GACTGAAGAT TTGGCAAAAT 300  
 GGCATATTG ATATCACGCC TAATGAnTCC ATTcAGGACA TTTAATTAAT CCAACTCAAG 360

## (2) INFORMATION FOR SEQ ID NO: 3982:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3982:

TTTAGCTGAA GCTTTAACTT ATACAAGTGA ACATCAAATG AACTTTTATAG ATCCATTCAA 60  
 TAATGTTTCAT ACAATTTCTG GACAAGGTAC GCTTGCTAAA GAAATGCTAG AACAAAGCAAA 120  
 GTCTGACAAT GTTAACTTTG ATTATCTATT TGCCGCAATT GGTGGTGGCG GTTTAATTTT 180  
 AGGTATTAGT ACTTACTTTA AAACCTATTC ACCTACCACG AAAATTATAG GTGTTGAACC 240  
 TTCAGTGCAA GTAGTATGTA TGAATCTGTT GTGGTAAATA ATCAGGTAGT CACATTGCCT 300  
 AATATCGATA AATTTGTGGG ACGGTGCATC TGTAGCTAGA GTTGGCGATA TTACATTGGA 360  
 AATTGCCAAA GAAAAGTAGA GGATTACGTT CCAGTAGAGn 400

## (2) INFORMATION FOR SEQ ID NO: 3983:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3983:

CCACCATTAT TTGTACATTG AAAACTAGAT AAGTAAGTAA AATATAGATT TTACCAAGCA 60  
 AAACCGAGTG AATAAAGAGT TTAAATAAG CTTGAATTCA TAAGAAATAA TCGCTAGTGT 120  
 TCGAAAGACG CGACAAGATT AATAACGCGT TTAAATCTTT TTATAAAAGA AAACGTTTAG 180  
 CAGACAATGA GTTAAATTAT TTAAAGCAG AGTTTACTTA TGTAATGAG CATTTAAAT 240  
 AATGAAAACG AGGCCGTATG TGGAGCGTTT GACTTATnAA AAATGGTGGG AAACATAGAT 300  
 TCAAGTTATT GAAGGGCGCA CGGTGGGATG CCTTGGGCAC TAGnAAGCCG nTGGAAGGAC 360  
 GTTACTAACG ACGATATGCC TTGGGGGAGC 390

## (2) INFORMATION FOR SEQ ID NO: 3984:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3984:

5 GGGCTCTAAC ATATTCTTAA ATTGATCAAA TAGTTCTTGC CTTGTATCTG CAAATGTTTT 60  
 GTAGTCTGCA TGCAATGTGA GTGCTTGATG AATTTTGACC ACAAATTCAA ATGTATCAGG 120  
 10 CGTTTCTTTT ATCCATTTC AATATTTCT TTCCGGTTGT ATCGCATAGT ATGTCGCATC 180  
 TAATTCGACA ACCGGAAAAT GTCCAGCATA TGTTTTAAGT TTATCGGTTT GCGCTTCTAA 240  
 ATCTTCATAT AATGAATAGT GATCACCCCA ACCTGTTAAT CCGATGTTTT ATCATATATA 300  
 15 TCACCAATGT CATCATACCA TATAACTTTT ATCATnATCA TTTCAGCGAA CTTTAGGTTT 360  
 GnAGGTTTTT TGGCCTGGAT TAAAnATCTT TCGGGCGGAT 400

## (2) INFORMATION FOR SEQ ID NO: 3985:

20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 25 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3985:

30 GCATTTGCTT ATATCTTTAA AAAAGATTTT GAAGATATTG AAAGAAAAAC TAAAGAAATT 60  
 ATTTCTGATA TTGAAAGTAA AAATACTAA TAACATTTAG AGGCTGGGAC ATAAATCCCT 120  
 AAAAAnCAGC AGTAAGATAA TTTTCAATTA GAAATATCT TACTGCTGTT CTCTATTTAT 180  
 35 ACAATACTTC GTATTGAAAT GGCTTCGCTT TCCTAGGGTG CCGTCTCAGC CTGGTCTTC 240  
 GACTGGCACT GCTCCCTCAG GAGTCTCGCC ATTGAATACT ACGTATTAAAC ATGThAATTT 300  
 TACTTTGGAA ATACTTTTAA AAAATAAGAC ACTTTGCCCA ACTTGGCACA TAAATGTTAA 360  
 40 AATnCAATGA AATGAATTTT CTGTGTTGGG TCCCTnCTA 400

## (2) INFORMATION FOR SEQ ID NO: 3986:

45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 50 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3986:

55 TTCGTTCAAA GTCATCTAGG TCACATTATT CTATTTGGGA TTCTTAGTGC TGTTCATTAT 60

ATGACAATAC AAAACGTAAA AAAGTCGCAG TGATCGGTAG TATTTTAGTA TTTATCATT 180  
 GTATTCCAGC AACCTTATCT TTTGGTATCT TAAAAGATGT AAGATTCCGT GCGGGAACGA 240  
 5 TTTTGTATAA TATGGATTTC ATCGTTTCGA ATGTATTGAT GCCATTAGGC GCATTAGGTA 300  
 CTACGCTTGT CGTAGGnCAA TTATTAGnTA AAAAATTATT ACAnCAATAT TTTGGTAAAG 360  
 AnCGATTTAG GATTATTCAG TGGTTGGTAT TACTTAATTA 400

(2) INFORMATION FOR SEQ ID NO: 3987:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3987:

GGATTCTGAAC CCCCCTGAGC CGTTAAGCCC CTGTCGGTTT TCAAGACCGA TCCCTTCAGC 60  
 CGGACTTGGG TATTCCTCCA AAATTATATG GACCTTGCAG GACTCGAACC TGCGACCGAA 120  
 25 CGGTTATGAG CCGTTAGCTC TAACCAACTG AGCTAAAGGT CCTAAATATA ATTTTACAAC 180  
 TAATAAATAG TGGCGGTGGA GGGATCGAA CCCCCTGACCT CACGGGTATG AACCGTACGC 240  
 30 TCTAGCCAGC TGAGCTACAC CGCCTTATAT AGTTTGTAAG TAATATGGTG GGGACTAnCG 300  
 GGATCGGAAC CGCTGGACCT CCTGCGTGGC AAAGCAGGCC GCTCTCCCAG CTGGAGCTAA 360  
 GnCCCCCATA ATAATnACAG TATATCnGGG AAGACAGGAT 400

(2) INFORMATION FOR SEQ ID NO: 3988:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3988:

CAGCTGATAA ACAAGTTGAT CTGGTCCCGA TTTGTTGGGT AAACGGTTGA TTAATGnAAA 60  
 ATGTTGCGCCG AAGGATTCAT AATCCGAGAG GTCTAATTCA ACGTATCATT AATCAAGATG 120  
 50 CGCCTATTTA TCAATCTGAA ACAAATTATC ATTTCGAAAGA TCGCGGTAAG TCTAAAAATG 180  
 GTATTCAAAT GGTGTATCAA CATTTAATGA ACGGTGTATC GTTTATGGnT CCTTTTATCG 240  
 TAGTTGGTGG ACTCCTTATC GCCATCGCGC TGACTCCTAG GCGGTGAACG ACCATCCAAA 300



CCTTTAAATT AATGGTCCCA TACCAGnCGG GATAAACGCT

400

## (2) INFORMATION FOR SEQ ID NO: 3989:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 363 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3989:

15	CCAGAGATTT CCGAATGGGG GAAACCCAGC CATGAGTTAT GTCATGTTAT CGATATGTGA	60
	ATACATAGCA TATCAGAAGG CACACCCGGA GAACTGAAAC ATCTTAGTAC CCGGAGAAGA	120
	GAAAGAAAAT TCGATTCCCT TAGTAGCGGC GAGCAAACGG GAAGAGCCCA AACCAACAAG	180
20	CTTGCTTnGn GGTnTG TAGG AACTCTATA CGGATTACAA AGGACGACAT TAGACGAATC	240
	ATCTGGAAAG ATGAATCAAA GAAGTAATA ATCTGTAGT CGAAAATGTT GTCTCTCTTG	300
	AGTGGATCCT GAGTACGACG GAGCACGTGG AAATTCCGTC GGAATCTGGG AGGACCATCT	360
25	CCT	363

## (2) INFORMATION FOR SEQ ID NO: 3990:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3990:

40	TTTCCAAGAA CATGAGCCTG TACAGTTAAC ACCATGTnTG nTTCTTACTT CTTTATCGTG	60
	GCTCCAACGT TCTCTGTACA TTTTTTCCCA TTCTCTACTT TTACTTTCTA GGATCGACCA	120
	ATTCCCATTA AATTTTTCTG TTGGCTTAAA GAAATTCAAT CCAAATTTTC CCATATTTAT	180
45	ATCCTCCTAC GTATAAAAAT ACGATGTGTA GATGTCGTGT TTTTAAATAC TTTAAATGC	240
	CCAAGACTAT TGCTTTAATT AGATTGTACA TTTTTTCACA AACATAAAAT ATTAGGGAAT	300
	CACCTAATTA CTTAAGGnAT TCCCTATCAA TAACGGGATT TCATTGAAAT AATACACAAT	360
50	CAGTAnGGTC AGCCTAATGC CAGGCTAAAT CGTTCAAATT	400

## (2) INFORMATION FOR SEQ ID NO: 3991:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3991:

	AAAGTGGTTA AATATTATAG AAAACATCAA AGGATGTTAA GAAATACAAT TTATTACCCA	60
10	GCATTTAATA ATGGTGCTAT AGAAGGAATT AATAATAAGA TAAATTAAT CAAGTGAATT	120
	TCTTTTGGTT ACAGAAATTT CAACAACCTT AAAGCAGTA TAATGATGAT TTTCAGCTTG	180
	TACAAAGGAG AAAAAAGAA GACAACCAAG CCCAATAATG GACTGGCCGC CTAATAATnn	240
15	GAGCTCTAAA AGTTGTATTT TAAAAATAGT TCTTTAAATT ATATACCCAC CACATTGGT	300
	GGAGAACCTA AAAAAAGCA CTTCCCAAAA ATGGAAAGTG CAAGTAGTGA GCCATAGAGG	360
	ATTGGAACCT CTGACCCTCT GATTAAAAGT CAGATGCTCT	400

20

(2) INFORMATION FOR SEQ ID NO: 3992:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3992:

	AGTGTATGGT TATCAAAGAT TTGATACGAC GGTCATTATT ATTACCGTTA TTGTATTAGT	60
	CATTATTGTC CAAGTGATTC AAACGCTAGG GAATGTTCTA GCTAGATTCA TACGThGACA	120
35	TTAATGATAT ATAGTGAAGA TTTTGAAAGG AATTGATAGA ATGAAAAGAT TGATTGGGTT	180
	AGTTATCGTA GCACTTGTAT TAATTAGCAG CGTGTGGTGG TAACAATGAT AAAAAAGTAA	240
	CAATTGGTGT CGCATCAAAT GACACTAAGG CTTGGGGAGA AGGTTAAAAG AATTAGCTAA	300
40	AAAAAGATGG ATnTTGATGT GGGAGATTAA GCACTTCCTC nGGATTACAA TTTACCGGAT	360
	TAAAGCCTTh AAATGGATGG TGATATTGAT AATGAATGCC	400

45

(2) INFORMATION FOR SEQ ID NO: 3993:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 383 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3993:

55

TTATCAGAAG AACAAATTCGA CATTTTACTG AATCATCCAT TAATCGATGA AGAAGTAGCC 120  
 AATAGTTTAA TTGAAAATGT CATCGCGCAA GGNGCATTAC CCGTTGGATT ATTACCGAAT 180  
 5 ATCATTGTGG ACGATAAGGC ATATGTTGTA CCTATGATGG TGAAGAGGCC TTCAGTTGTC 240  
 GCTGCAGCTA GTTATGGTGC AAAGCTAGTG AATCAGACTG GCGGATTTAA AACGGTATCT 300  
 10 TCTGAACGTA TTATGATAGG TCAAATCGTC TTTGATGGCG TTGACGATAC TGAAAAAnTnT 360  
 CCGCCGGCAT TGAGAGCCTT AGA 383

## (2) INFORMATION FOR SEQ ID NO: 3994:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 366 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3994:

GGTACTATGA TTTACCGAG TCTCTCGTTG AGACAGTGCC CAAATCGTTA CGCCTTTCGT 60  
 25 GCGGGTCGGA ACTTACCCGA CAAGGAATTT CGCTACCTTA GGACCGTTAT AGTTACGGCC 120  
 GCCTTTACTG GGGCTTCGAT TCGTAGCTTC GCAGnnAAAC CnACTCCTCT TAACCTTCCA 180  
 30 GCACCGGGCA GGCCTCACCC TGATACATCA CCTTACGGTT TAGCAGAGAC CTGTGTTTTT 240  
 GATAAACAGT CGCTTGGGCC TATTCAGTGC GGCTCTTCTG GGCCTTAACC CTGAAAGAGC 300  
 ACCCTTCTC CCGAATTACG GGGTCATTG CCGATTCCTT AACGAGATTC GCTCGCTCAC 360  
 35 CTTAGA 366

## (2) INFORMATION FOR SEQ ID NO: 3995:

40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 359 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3995:

AGATATTTTA CATGTGAATC AAGTAGGTAT TCATGATAAT TTCTTTGAAT TAGGTGGCCA 60  
 50 TTCATTAAAA GCAACGTTAT GntGAATCGG ATAGAGGCAT CTAAGGGAA ACGATTACAA 120  
 ATTGGTGATT TATTACAAAA GCCAACTGTA TTTGAACTAG CACAAGCGAT TGCTAAGGTT 180  
 CAAGAACAAA ACTATGAAGT GATTCCAGAA ACTATAGTTA AAGATGATTA TGTGCTGAGC 240

55

GTACCTTTTT TATGGCGGTT ATnCATCAGA ACTTAATGTA GCTCantGCG ACAAGCATG

359

(2) INFORMATION FOR SEQ ID NO: 3996:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3996:

CAATTATTGG TATTCAACTT AAAGATCATG ATGATTTAAT ACAACTCAAA CAACGTTnAA	60
ATCATTTCGA TCCTTCCAAT ATTTATATTA ATGAAAATAA GATGTTATAT TCATTGTTAA	120
TTTAACACAT AGTAAGAAAA ACAGTCATAA ATTGATTCTT AATTGAAATC ATCTTATGAC	180
TGCTTTTTTAT TATACTTTAC ATTTCTCGTT TCGTCAGATT CAAACGTTTT CACTTCGCCA	240
AGCCATCTTT CTTTGTGTTT GCTTTTATTT TGACGTTTnA GACATAAAAA AAGAGACCTT	300
GCGGTCTCAA ATGCGGCTCA TCGCATCCAC TTTTTCCTG GGCAACGTTT TACTCTAGGC	360
GGAAnGTAAG TGGGACTTAC CATCGACGn TAAGGGGCTT	400

(2) INFORMATION FOR SEQ ID NO: 3997:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 358 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3997:

GATACTACCC TAGCTGTGTT GGCTTTCTAA CCCGCACCAC TTATCGTGGT GGGAGACAGT	60
GTCAnGCGGG CAGTTTGACT GGGGCGGTCG CTCCTAAAAG GTAACGGAGG CGCTCAAAGG	120
TTCCCTCAGA TGTTTGAAA TCATTCATAG AGTGTAAGG CATAAGGGAG CTTGACTGCG	180
AGACCTACAA GTCGAGCAGG GTCGAAAnCG GACTTAGTGA TCCGGTGGTT CCGCATTGAA	240
GGGCCATCGC TCAACGGATA AAAGCTACCC CGGGGATAAC AGGCTTATCT CCCCCAAGAG	300
TTCACACGAC GGGGAGGTTT GGCACCTCGA TGTCnCTCA TCGCATCCTG GGGCTGTA	358

(2) INFORMATION FOR SEQ ID NO: 3998:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3998:

5 TAGGAGGAAT TTATATGACA TTTGAAAAAG AAACGGTCTT AAAACATTA TTCCTGAAG 60  
 ATGTACTTAG TATTGCTAAA GGTTTAACAG ACGGTGAAGT CGAATTTTTA CAACAAGTAG 120  
 ATTCATTGCT AGAAAGTAAG TACCGTGAAA ATATTAATCA ACATTGGATA GACGCTACTG 180  
 10 TACCCGAGGA CTATTTTAAA GATCTGGGAG AATTAAATTA TTTTAACAT CCATTACTTT 240  
 ACAAGGATCG TCCAAACGCC AAAATGCCTA GTCANCTATT TCAGTTTTTC ATGTCTTACC 300  
 TACTCGCGCG ATTTGATATT TCCTTAGCTA CCCTACTCGG TGTTCACCAA GGTTAGGGCA 360  
 15 TAACACTTTC TATTTCCGAG GTAGCAAAGA CAAATTGCGA 400

## (2) INFORMATION FOR SEQ ID NO: 3999:

20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 398 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3999:

CGCCCCCTTAG TGCTGCAC TA ACGCATTAA G CACTCCGsCT GGGGAGTACG ACCGCAAGTg 60  
 30 AAAC TCAAAG GAATTGACGG GGACCCGCAC AAGnGTGGAG CATGTGGTTT AATTCGAGGC 120  
 AACGG:AGAA CCTTACCAA TCTTGACATC CTTTGACAAC TCTAGAGATA GAGCTTTCCC 180  
 CTTCGGGGAC CAAAGTGACA GGTGGTGCAT GGTGTGCGTC AGCTCGTGTC GTGAGATGTT 240  
 35 GGGTTAAGTC CCGCAACGAG CGCAACCCCTT AAGCTTAGTT GCCATCATT A GTTGGGCAC 300  
 TCTAAGTTGA CTGCCGGTGA CAAACCCAGG AAGGTTGGGG ATGACGTCAA ATCATCATGC 360  
 40 CCCTTATGGn TTTGGGTTAC ACAAGTGGTT ACAATGGG 398

## (2) INFORMATION FOR SEQ ID NO: 4000:

45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 377 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4000:

TGTTCTTGCA ACGCTATTTA GTATCAGGTT TAACAACAGG TGCGACAAAA GGTTAGTTTG 60

55

GACGTTATGA TGACGATTAA AGTTGGAATC ATTGGGTGTG GTGGTATTGC GAATGGCAAG 180  
CACATGCCAA GTTTACAAA AGTTGAAAAT GTTGAAATGA TCGCATTTTG TGACGTAGAC 240  
5 ATTCGAAAG CAGCGaGTGC GGCAGAAGCA TACGGAAGT ACAATGsCAA aGtTTATGAT 300  
GATTACMaAG CaTTGTTAAA AGATGACACG ATTGATGTTA TCCATGTTTT GTACCCCCAA 360  
TGGACCCCGC ATTGTGG 377

(2) INFORMATION FOR SEQ ID NO: 4001:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4001:

TCGGGTTCTC AAATCATCGA ACATAACAAA AGAAGCTAAG CAACATGTAG GCCGTTGTCA 60  
CTTAACTTCT TGTTCCTCCG ATGACAGCTT CTATTAGAG AATGTCATGA TTATTTTATA 120  
25 TTCACCTCAA TGTTATCAAT ATTAGTGCCA TCTATGACAT CTGCCATGCG ATTTTCTTGT 180  
AATTTTTTGT GCAATTCAAA CGTGTACTTT CCACCGTTTT TCATTTTAAT AACAAATTTA 240  
CCTGAACCAA CGTTACCGTA CAGATTATTT TTTTCAATAA GTGTTTTCTC AATTTAAAT 300  
30 CAAGTCTTT CAAGGAAATC TGTTCTTAG TAATCTTGAA TTCTGAAACA TCATGGGnGA 360  
TTGTACCGTA TnATCTTnCC TAGTAAT 387

(2) INFORMATION FOR SEQ ID NO: 4002:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4002:

CTATTACGAT TGCTGCGAAA GAAGGTATTA AAAATATACA AATAGGCATG GCTCACCGTG 60  
GACGTTTAAA CGTTTAAACG CATGCTTAG AAAAACCGTA CGAAATGATG ATTTCAGAAT 120  
TTATGCATAC AGATCCAATG AAATCTTAC CTGAAGATGG TAGCTTGCAG TTAAGTCTG 180  
50 GATGGACTGG TGATGTGAAA TATCACTTGG TGGGCATTAA AACTACTGAT TCATACGGTA 240  
CAATGCAGCG TATTGCACTG GCTAACAATC CAAGTCACTT GGAAATTGTT GCACCTGTTG 300

TCCATCATAA AnGCAATGnC CATTGTTGAT ACATGGCGAT

400

## (2) INFORMATION FOR SEQ ID NO: 4003:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4003:

AGAAATATAT GCATTTTCGGA TATCATGGTA AAGAGAATGG ATTAAGCGGT AAATCACGTG 60

ATGAAGTGCG AGCGAAATGA AACAAAATTT AGATGTCATG CGAGACGATA ATCAAAGGGA 120

CGACAGGTGA TGGGGTTGAA AGTGTAAcGn GCTACACTGG TCATGATGCT GCTAAACTAC 180

GTGATTATAA TGAAACACAT CATGCTTTGT CTGGATATGA AATGATTGAC GCAGCAAAGG 240

TGCCATTGCA ACAAATGAAG TCAATGCTGC GATGGGTATT ATTTGTGCAC GCCAACAGCT 300

GGTTCCTCGG GTACCATTCC CGGTGCACTT TTAAATTAG GAAAAACAC ATGATTTAAC 360

AGAAGAGCAA ATGATTTGAT TTCTTATTCA CTTCAGCATT 400

## (2) INFORMATION FOR SEQ ID NO: 4004:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4004:

TGAAATAGAA CCTGAAACCG TGTGCTTACA AGTAGTCAGA GCGCGTTAAT GGGTGATGGC 60

GTGCCTTTTG TAGAATGAAC CGGCGAGTTA CGATTTGATG CAAGGTTAAG CAGTAAATGT 120

GGAGCCGTAG CGAAAGCGAG TCTGAATAGG GCGTTTAGTA TTTGGTCGTA GACCGAAACC 180

AGGTGATCTA CCCTTGGTCA GGTGAAGTT CAGGTAACAC TGAATGGAGG ACCGAACCGA 240

CTTACGTTGA AAAAGTGAGC GGATGAACTG AGGGTAGCGG AGAAATTCCA ATCGACCTGG 300

AGGATANTGG TTCTCTCCGA ATAGTTTAGG GCTAGCCTCA AGTGTGATTA TTGAGGTAGA 360

NACTGTTTGA CGAGGGGCCC TCTCGGGTAC CGAATTCAGG 400

## (2) INFORMATION FOR SEQ ID NO: 4005:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 415 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4005:

	ATACTAAGGC GTTATTAGAC GaTTAGACAA TGGTGTGATT AAAGGTGCAG CACTTGATAC	60
10	GTATGAATTT GAACGCAAAC TTTTCCCAAG TGATCAAAGG GGCAAAACAC TGAACGATCC	120
	ATTGTTAGAA TCGTTGATTG ACAGGGAAGA TGTCATATTA ACACCACATA TTGCGTTMTA	180
	TACTGAAGCT GCAGTTAAAA ATCTAATTGT CGATGCATTA GATGCAACAT TAGATGTATT	240
15	GGCAGACTGG AGATACTAGG TTACGAGTAA ATTAAAAATC GAACTGATGA GATAATTTGG	300
	ATTGTTGGGG ATTCTGCATC CAGTTCGATT TTTTTAATTT GGTGTTGGAT GACGTTGnAA	360
20	TGTTGCCTAA TTAAACGAC ATCGTAAACC nTGGATCCTC CAATGGCGTC CTTnC	415

(2) INFORMATION FOR SEQ ID NO: 4006:

(i) SEQUENCE CHARACTERISTICS:

25	(A) LENGTH: 444 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4006:

	CTAACAGAAG CTAGTATAGG AAATCGGTAC TCGTTAAGGC TGATCTGTGA TGGGGAGAAG	60
35	ACATTGTGTC TTCGAGTCGT TGATTTTACA CTGCCGAGAA AAGCCTCTAG ATAGAAAATA	120
	GGTGCCCGTA CCGCAAACCG ACACAGGTAG TCAAGATGAG AATTCTAAGG TGAGCGAGCG	180
	AACTCTCGTT AAGGAACTCG GCAAAATGAC CCCGTAACTT CGGGAGAAGG GGTGCTCTTT	240
40	AGGGTTAACG CCCAGAAGAG CCGCAGTGAA TAGGCCCAAG CGACTGTTTA TCAAAAACAC	300
	AGGTCTCTGC TAAACCCGTA AGTGATGTAT AGGGGCTGAC GCTGCCCGGT GCTGGAAAGT	360
	TAAAGAGAGT GGGTTACTTC TTGCGACTTA nCGAAATCGA GnCCCCAGTA AACGGCGGGC	420
45	CGTAACTATA ACnGTCCTAA GGTA	444

(2) INFORMATION FOR SEQ ID NO: 4007:

(i) SEQUENCE CHARACTERISTICS:

50	(A) LENGTH: 400 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

55



TTTGAACTCT ATCAAAGCAT CAGCAATCAA AACATACGTA TCTTTACAAC AGTAATCATG 60  
 CATTCTATGA TGCTTCTAAC TGAATTAAAG CATCGAACAA TCGGAAGCAT ATTTCTAAAT 120  
 5 TATTTATTCA TTATAGTCTT AAACATAACA TGACCTAATA TATTACTAAC CTATTAAAT 180  
 AAACCACGCA CATCTAAGTG ATATACGACA ATCACAGCAA TAATAATTGC TTTAGAAAGT 240  
 10 CGTGCCGAAC TGGAACCTAC AAGTCTAGTT CGAACACACA CTGATGTGAG TGGTTTTCTT 300  
 TATTTTAAAC ATGAACAATC AGATAAGTTA CTAGCATTAG CAAATATTAT TAAATCAAGG 360  
 GCTTCGnTTT ATAAATTTAA AACATGTTAA ATTAGACGTG 400

(2) INFORMATION FOR SEQ ID NO: 4008:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 20 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4008:

TATACTTGTT TTTACAAACC ACAAAAAGCT CTAACATTA GTTTAAACCA ATGCTTAGAG 60  
 CTTTCTAATT ATTTTATGCT TTAAAAGATA CTGTGTTATC TACGATGACC TTACCGTCTT 120  
 30 TAATAACTTT TTCTGCGTGA TTGATACCAA AATGATATGG AATATATTCA TGATTTGGTG 180  
 CATCCCAAAT TACTAAATTA GCCTTATCAC CTGTGTTAAT TGTACCCGCG TTAATGTCTA 240  
 TTGCTTTAGA GCCATTGACC GTAACAGCAT TCCAACTTC ATTAGGTGAT AGCTTTAATT 300  
 35 TCAAGGCTGC AATCGCCATA ACAAGTTGTA AGTTGTTTGT GGACACTACT ACCAGGGTTA 360  
 TAATCAGTTG GCTAATGCCA TCGGCACCGG TTAATGGTCC 400

(2) INFORMATION FOR SEQ ID NO: 4009:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 45 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4009:

ACAAACATTG AAATTAGAGG TATATAAAAA ATGCTTCTGC AATAGATGCA ATAAACATGC 60  
 AATACAATAT GGAGGCGAAG TAAATGAAAA GTATTACGTT TGAAGAACAT TATGTCATTG 120  
 55 AAGATATTCA AAAAGAAACG ATGAATGCGA TATCAGCAGA TCCTAAAGGT GTACCGATGA 180

ATCATGATGA ACGTATCCAA TTTATGAATA ATCAAGACGT TCAAATTCAA GTCTTATCTT 300  
 ATGGAAATGG TTCTGCTTCA AATTTGGTTG GTCAGAAAGC CATTGAATTA TGTCCAAAAG 360  
 5 GCAAATGATC CATTGGGCAA ACTATATTGC ACCATATCCC 400

## (2) INFORMATION FOR SEQ ID NO: 4010:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4010:

ACTAGAGAAG GTATGTTACG TGACAATGAA TTACTAAATG GTATTTATTC ATCGAGTTAC 60  
 20 ATCTATAGTT TATTAAATC AGAATACGAC CAAAATGAC AAATTAGACT TACAAAAGAG 120  
 TGATGACATT TAAATGGCA GCGCTCTTTT ATTTAATTTT TGAAAATAAA AGGTTGTTGA 180  
 CAGTATTATT TTATAACAAT ATAATGATTT TGATAATTAT TATCAACTAG ATGATGTTTA 240  
 25 TGGGAGGATG CTTTAAACA GCCGTTTTAA GTGTAATGTA TTATTTTAGC GTGTAGGGAT 300  
 GCGAAAATAT ATTTATAGGA CACATCTTGG GGATAATnGA TTTCTATAAT GAGGTGTCAA 360  
 30 ATGGAAAAGT TACCACGCTA TTATTAGCCn CCACGTTATT 400

## (2) INFORMATION FOR SEQ ID NO: 4011:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 494 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4011:

TnTCAATTAG AAAATATCTT ACCGCTGnCT CTATTTATAC AATCCTCGTA TTGAATGGnT 60  
 CGCTTTCCTA GGGTGCCGTC TCAGCATCGG CTTGCACTGG CACTGCTCCC TCAGGAGTCT 120  
 45 CGCCATTAAT ACTACGTATT AACATGTAAT TTTACTTTGA AATACTTTAA AAAAATAAGA 180  
 CACTTTGCCC AACTTACACT ACCAATAAAA ACTTCTGTTA GAATTCCTCA AAATGATATT 240  
 50 TCGCGACATG TTAATGAAAT TGTGAAACG ATACCTGATA GCAAATTCGA TGAATTCAGA 300  
 CATCATCGTG GCGCAACATC CTATCATCCA AAGATGATGT TAAAAATCAT CTTATATGCA 360  
 TATACTCAAT CTGTATTTTC TGGTCGTAGA ATAGAGAAAT TACTTCATGA CAGTATTCGA 420

GAATCCnAAT ACTG

494

## (2) INFORMATION FOR SEQ ID NO: 4012:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4012:

TTTCACTTCG CCAAGCCATT TTTCTTTGTG TTTACTTTTT ATTTTGACGT TTTAGACATA 60  
 AAAAAAGAGA CCTCACGGTC CAACTTGCCT GGCAACGTTT TACTCTAGCG GAAGTAATTG 120  
 GCTACCATCG TCGCTAAAGA CCTTTCTTGA CTGTGTGACAA TCGCTTGCTT CTTTCCTCTC 180  
 CTTCGGCTCT CGCTTACTCA TTTAGCTCTA CTAAACTCGT TCGGCTCTTT TCTCGTTTCG 240  
 TCAGATTCAA ACGTTTTTTCAC TTCGCCAAGC CATTTTTCTT TGTGTTTACT TTTTATTTTG 300  
 ACGTTTTTAGG CATAAAAAAA AGAGACCTTG CGGTCCCAAT GCGGGCTCAT CGCATCCATT 360  
 TTTTGGCCTG GGCAACGTTT TnATnCCAGC GGAAnTnAAT 400

## (2) INFORMATION FOR SEQ ID NO: 4013:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4013:

CGAACTGCCG AACCCGAAGA GCGGATTTAC AGTCCGCCGC GTTTACCACT TCGCTACCCC 60  
 TCCAGCTTAT TCATATAATT TAATAATCAA AATGGTGGAG AATGACGGGT TCGAACCGCC 120  
 GACCCTCTGC TTGTAAGGCA GATGCTCTCC CAGCTGAGCT AATTCTCCAA AATAATGACT 180  
 CCTACGGGAC TCGAACCCGT GTTACCGCCG TGAAAGGGCG GTGTCTTAAC CGCTTGACCA 240  
 AGGAGCCATG GCTCCACAGG TAGGACTCGA ACCTACGACC GATCGGTTAA CAGCCGATAG 300  
 CTCTACCACT GAGCTACTGT GGATTAATAT TATGCCTGGC AACGTTCTTA CTCTnAGCGG 360  
 AACGTGAATT CGACTTACCA TCGACGnTAA GGAGCTTnAC 400

## (2) INFORMATION FOR SEQ ID NO: 4014:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4014:

	ATTAGGACCT CAAGACGATA TTAATAAATT TGAATACTTA AAAAAATCTT CTCAAAATAC	60
10	AGGTACTTCA TTATTGGTAT TCAACTTAAA GATCATGATG ATTTAATACA ACTCAAACAA	120
	CGTGTGAAAT CATTTCGATC CTTCCAATAT TTATATTAAT GAAAATAAGA TGTTATATTC	180
	ATTGTTAATT TAACACATAG TAAGAAAAAC AGTCATAAAT TGATTTCTAA TTGAAATCAT	240
15	CTTATGACTG CTTTACATT ATACTTTACA TTTCTCGTTT CGTCAGATTC AAACGTTTTC	300
	ACTTCGCCAA GCCATCTTTC TTTGTGTTTG CTTTATTTT GACGTTTTCG ACATAAAAAA	360
20	nGnGACCTGC GGTCTCAATG CGGCTTCATC GCATCCACTT	400

(2) INFORMATION FOR SEQ ID NO: 4015:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 377 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4015:

	GAATGAAAAG CTCTAAAAGT TGTATTTTAA AAATAGTTCT TTAAATTATA TACCCACCAC	60
	ATTTGGGGAG GAACCTAAAA AAAAGCACTT CCCAAAAATG GAAAGTGCAA GTAGTGAGCC	120
35	ATAGAGGATT CGAACCTCTG ACCCTCTGGA TTAAGAGTCA GATGCTCTAC CAACTGAGCT	180
	AATGGCTCTG AATGGCTGGG CTAGCTGGAT TCGAACCAAC GAGTGACGGA GAAAGGTCC	240
40	GTTGCCTTAC CGCTTGGCTA TAGCCCAATA TATAGATGGT GGAGGGGGGC AGATTCGAAC	300
	TGCCGAACCC GAGGAGGCGG ATTTACAGTC CGCCGCGTTT AGCCCACTTC GATACCCCTG	360
	CCAGnTTATT CATATGA	377

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(2) INFORMATION FOR SEQ ID NO: 4016:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4016:

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ATGACGCACC TGACATCCTC TCGGTTTCATA TTCAGGCATA TCCGGACCAC AACTTGGATA 120  
 GTCAGTTTGT TGATTTTCCC AGGTAATCAC ACCATTTTTC ACAAATACTT TCCAAGAACA 180  
 5 TGAGCCTGTA CAGTTAACAC CATGTGTTGT TTCTTACTTC TTTATCGTGG CTCCAACGTT 240  
 CTCTGTACAT TTTTTCCTCAT TCTCTACTTT TACTTTCTAG GATCGACCAA TTCCCATGTA 300  
 10 AATTTTCTG TTGGCTTAAA GAAATCAATC CAAATTTCCC ATATTTATAT CCTCCTACGG 360  
 GTGAAAAATA CGGTGTGTAG AnGTCGTGGT TTTTnAAATA 400

## (2) INFORMATION FOR SEQ ID NO: 4017:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear  
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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4017:

25 CTTTGAGCGC CTCCGTTACC TTTTAGGAGG CGACCGTCCC AGTCAAAGTG CCCGnCTGAC 60  
 ACTGnCTCCC ACCACGATAA GGGCGTGGGT TAGAAAGCCA ACACAGCTAG GGTAGTATCC 120  
 CACCAGCGnC TCCACGTAAG CTAGCGCTCA CGTTTCAAAG GCTCCTACCT ATCCTGTACA 180  
 30 AGCTGTGCCG AATTTCATA TCAGGCTACA GTAAAGCTCC ACGGGGTCTT TCCGTCCTGT 240  
 CGCGGTAAC CTGCATCTTC ACAGGTACTA TGATTTCACC GAGTCTCTCG TTGAGACAST 300  
 GCCCAATCG TTACGTCTTT CGTTGCGGGT CGGAAGTTAC CCGACAAGGA ATTCGTTAC 360  
 35 CTTAGGACCT TATAGTTACG GCCGnCTTTA ATTGGGGTTT 400

## (2) INFORMATION FOR SEQ ID NO: 4018:

40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear  
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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4018:

50 TGTGATTTA AGAGGCATGC TACGAGGAAT GATTGGTCAT CCGAAAAAAG ATCGAGCGGC 60  
 ATATGAGGCA CGCAAGCGA TTCCAACAT TAATGAAAC AGTCCGCCAA TATTAATTGT 120  
 ACATGGAGGG AAAGACCAGC AAGTTGGTAT TCATCATGCG TATTATTTAG CGGACCAACT 180  
 55 AGAGTTAAAA GGTGCCACGC ATGnAAACAT TTTATCAAAT GGCAGAAGGA CATGTGCCAA 240

CGCATAGCTT AGTTATGGAA ACGTGGTGTG CGCATGGGGA ACTATTCAAG CTTTGGAGGA 360  
 TGTGGTACTT ACATGCGTTG GAATTAGGGG TCCGTTACT 400

(2) INFORMATION FOR SEQ ID NO: 4019:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4019:

GGAGGTTTGG CACCTCGATG TCGGCTCATC GCATCCTGGG GCTGTAGTCG GTCCCAAGGG 60  
 TTGGGCTGTT CGCCCATTAAG AGCGGTACCA AGCTGGGTTT AGAACGTCGT GAGACAGTTC 120  
 GGTCCCTATC CGTCGTGGGC GTAGGAAATT TGAGAGGAGC TGTCTTAGT ACGAGAGGAC 180  
 CGGGATGGAC ATACCTCTGG TGTACCAGTT GTCGTGCCAA CGGCATTAGC TGGGTAGCTA 240  
 TGTGTGGACG GGATAAGTGC TTGAAACATC TTAAGCATGA AGCCCCCTC CAAGATGGAG 300  
 ATTTCCCAAC TTCGGTTTnT AAGATCCCTC CAAAGnTGAT GGAGGTTTAA TAGGTTTCGA 360  
 GGTGGGAAGC AnGGTGGACA GTTGGGAGCT GGACGAnTAC 400

(2) INFORMATION FOR SEQ ID NO: 4020:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4020:

GAAGATGTTT GTCATTCTTC AAATAAACCA GAGCTAGTTG CAATTGCTGA ACCAGCATCT 60  
 AATAGACCGA AAAAGAGAAG TAGACGTGCG GCACCGGCAG ATCCTAATGC AACTCCAGCA 120  
 GATCCAGCGG CTGCAGCGGT AGGAAACGGT GGTGCACCAG TTGCAATTAC AGCGCCATAT 180  
 ACGCCAACAA CTGATCCTAA TGCCAATAAT GCAGGACAAA ATGCACCTAA CCGAnTnTTG 240  
 TCATTTTGAT GACAATGGTA TTAGACCAAG TACCAACCGT TCTGTGCCAA CAGTTAAACG 300  
 TTTGTTAATA ACTTGCCGGG CTTCACTA ATCAATGGTG GGCAAAGTAn GGGTGTTTAG 360  
 TCATGCAATG GGTAAGAACG AGCATGTTTG GATTTTCAGG 400

(2) INFORMATION FOR SEQ ID NO: 4021:

- (A) LENGTH: 396 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4021:

10 CTAAGTCATG AATGGGAAGT GGCTCGCGTT GAAGAAGGAC TGACTACTGC TGCCACACAG 60  
 CTTGCTAAAC AATTATCAGA ATTAGATTTA GCGTCACATC CTTTGTGAT GTCAGAGCAG 120  
 TTTGCAAGTn TAAAAGATCG TCCATTTTCAT CCATTAGCTA AAGAAAAAAG AGGATTAAAG 180  
 15 GAAGCGGATT ATCAAGTGTA TCAAGCTGAA TTAAATCAAT CATTTCCTTT AATGGTTGCA 240  
 GCAGTTAAAA AGACACATAT GATTCATGGC GATACTGCAA ATATCGATGA ATTAGAAAAT 300  
 TTGACAGTAC CTATAAAAGA ACAAGCGACA GACATGTTAA AATGATCCAA GGTATCANT 360  
 20 AGATGACTAT GTACCATTCC GGTACnTCCT GGCCAT 396

## (2) INFORMATION FOR SEQ ID NO: 4022:

- 25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 376 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4022:

GATTGGTCTG nAAGAAGAAT TAATGAAAAA GCTACGTGAA AAATTAGAAG CGGCATTGTA 60  
 35 TACGATTTAC GAATTGTCTC AAAACCGAAA AATAGATATG AGACTTGCAG CATATATCAT 120  
 AGGTATTAAA CGTACAGCAG AAGCAGCTAG ATATCGTGGT TGGGCATAAT TAATTATCAT 180  
 ATGTGATTTA ACGAGCTTGG GACAGAAAAC AAAGCCTTAA GCTCGTTAAT TTTATTTTAG 240  
 40 CAGTAGTTGA CTGTAAAACA ATGCCCGTGT AAACGCTCTT TTCAAAAATA GTCGGGGCCC 300  
 CAACACAGAG GCTGGTGGGA AAGTCAGCCT ACAATAGnGT GCAAGTTGGC nGGGGCCCCA 360  
 45 ACACAGAGGC TGGCGG 376

## (2) INFORMATION FOR SEQ ID NO: 4023:

- 50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 381 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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CAAATGGTGG AGCCATAGGA GGATTGGAAC CTCTGACCCT CTGATTAAAA GTCAGATGCT 60  
 CTACCAACTG AGCTAATGGC TCTTCCATGG nGcNggCCAG AGGACTTGAA CCCCCAACCT 120  
 5 ACTGATTACA AGTCAGTTGC TCTACCAATT GAGCTAGGCC GGCAATATGT AAGAATAAAT 180  
 GGTGGAGAGT GACGGGTTTCG AACCGCCGAC CCTCTGCTTG TAAGGCAGAT GCTCTCCCAG 240  
 10 CTGAGCTAAT TCTCCGATTT AAAACTGCCT GGCAACGTTT TACTCTAGCG GAAnTAATTC 300  
 GGACTACCAT CGACGCTAAA GGAGCTTAAC TTCTGTGTTT CGGCATGGGA ACAGGTGTGA 360  
 CTCCTTGCTA TATCACCAGA C 381

15 (2) INFORMATION FOR SEQ ID NO: 4024:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4024:

25 GCCCCTTATG ATTTGGGCTA CACACGTGCT ACAATGGACA ATACAAAGGG CAGCGAAACC 60  
 GCGAGTCGAA GCAAATCCCA TAAAGTTGTT CTCAGTTCGG ATTGTAGTCT GCAACTCGAC 120  
 30 TACATGAAGC TGAATCGCT AGTAATCGTA GATCAGCATG CTACGGTGGA ATACGTTCCC 180  
 GGGTCTTGTA CACACCGCCC GTCACACCAC GAGAGTTTGT AACACCCGAA GCCGGTGGGA 240  
 GTAACCTTTT AAGGAGCTAG CCGTCGAAGG TGGGGACAAA TGGATTGGGG TGAAGTCGTG 300  
 35 AACAAAGGTAG CCGTGATCGG AAGGTGCGGC TGGGATCACC TCCTTTGCTG AAGGATGATG 360  
 ATTTCCGnAA CATcTTCTT CCAGAAGATG CCGGTAATAA 400

(2) INFORMATION FOR SEQ ID NO: 4025:

- 40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 352 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4025:

50 CTTAGAAGTG AGAATGCCCG TGTGAGTAGC GAAAGACGGG TGAGAATCCC GTCCACCGAT 60  
 TGCTAAGGTT TCCAGAGGAA GGCTCGTCCG CTCTGGGTTA GTCGGGTCCT AAGCTGAGGC 120  
 CGACAnGTAn GCGATGGAT AACAGGTTGA TATTCCTGTA CCACCTATAA TCGTTTTAAT 180

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GCTGAGTATT AGGCAAATCC GGTACTCGTT AAGGCTGAGC TGTGATGGGG AGAAGACATT 300  
 GTGTCTTCGA GTCGTTGATT TCACACTGCC GAGAAAAGCC TCTAGATAGA AA 352

5 (2) INFORMATION FOR SEQ ID NO: 4026:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 370 base pairs  
 (B) TYPE: nucleic acid  
 10 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4026:

15 TGGGGCTCTT CCCGTTTCGC TCGCCGCTAC TAAGGGAATC GAATTTTCTT TCTCTTCCTC 60  
 CGGGTACTAA GATGTTTCAG TTCTCCGGGT GTGCCTTCTG ATATGCTATG TATTCACATA 120  
 20 TCGATAACAT GACATAACTC ATGCTGGGTT TCCCCATTCTG GAAATCTCTG GATCAAAGCT 180  
 TACTTACAGC TCCCCAAAGC ATATCGTCGT TAGTAACGTC CTTTCATCGGC TTCTAGTGCC 240  
 AAGGCATCAC CGTGCGCCCT TAATAACTTA ATCTATGTTT CCACCATTTT TATAAGTCAA 300  
 25 AnGTTAACAT GAAGTTAGGT TCTTTTATAA AAGGATTAAA nGGTTATTA ATCTTGtGnG 360  
 TGTTCTTTTCG 370

(2) INFORMATION FOR SEQ ID NO: 4027:

- 30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4027:

40 TCATGTTTCG CTGTTTAA TGCTGTTAAT GCGTTATCGA CACGATGTTT TTCATCTGAA 60  
 ATTTGTTGTG CAGTTGCATC GCCATTGTCA ATAACACGTT GAGCTGCAGT TATTTAGTT 120  
 TCTGCTCCG CTCTTCGCA TTATAGTTAT CAATACTTTG TTGCGTCATA CCAGCAGTTG 180  
 45 ATGTTACTTG GTTCACAGAA CTTTGTAAGT TATTTTtAGA CGTTACTAAT TGGCTATTAT 240  
 CTTCTTTATT TTGAAGTAAT GCTTTACTTG GATCAATCTT AGTTTGTGCG CACGAACTTT 300  
 AGTTAGTGCG TGCAGAACT TGTGTGGTG TTGCACGCTC ATtnATGAAG CACTGTTGGT 360  
 50 GCCTCCGTTT.TCGCATAntG GATTGTTGTT GCGCATGAGG 400

(2) INFORMATION FOR SEQ ID NO: 4028:

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(A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4028:

10 CTCATCGCAT CCATTTTTTG CCTGGCAACG TTCTACTCTA GCGGAACGTA AGTTGGCTAC 60  
 CATCGTCGCT AAAGACCTTT CTTGACTTGT GACAATCGCT TGCTTCTTTC CTCTCCTTCG 120  
 GCTCTCGCTT ACTCATTTAG CTCTACTAAA CTCGTTGCGC TCTTTTCTCG TTTCGTCAGA 180  
 15 TTCAAACGTT TTCACTTCGC CAAGCCATTT TTCTTTGTGT TTACTTTTAA TTTTGACGTT 240  
 TTAGACATAA AAAAAAGAGA CCTTGCGGTC TCAATGCGGC TCATCGCATC CATTTTTTGC 300  
 CTGGGCAACG TTCTACTCTA GCGGGAACGn AAGTTGGGCT TACCATCGAC GCTAAGAACC 360  
 20 TTTCTTGGAC TTGGTGGACA AACGGnGTGG CTGCTTTTCC 400

## (2) INFORMATION FOR SEQ ID NO: 4029:

25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4029:

AGGACTTGAA CCCCCAACCT ACTGATTACA AGTCAGTTGC TCTACCAATT GAGCTAGGCC 60  
 35 GGCAATATGT AAGAATAAAT GGTGGAGAAT GACGGGTTTCG AACCGCCGAC CCTCTGCTTG 120  
 TAAGGCAGAT GCTCTCCAG CTGAGCTAAT TCTCCGATTT AAAACTGCCT GGCAACGTTT 180  
 TACTCTAGCG GAAnTAATTC GGACTACCAT CGACGCTAAG GAGCTTAACT TCTGTGTTTCG 240  
 40 GCATGGGAAC AGGTGTGACC TCCTTGCTAT AGTCACCAGA CATATGAATG TAATTGATA 300  
 CATTCAAAAC TAGATAGTnA AGTGAAAAGT GATTTTGGnT TCGCAAAACC ATTTGATTTT 360  
 GATTGAAGTC CTTGATCGA TTGAGTGATT CGTGCAGCTn 400

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## (2) INFORMATION FOR SEQ ID NO: 4030:

50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 390 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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5 GATGATAAAT CATGTTTTTC ATACCAAGTC GCTGCCGGCA AAACAATGTC AGAATATAAC 60  
 GGTGTTGCCG TCATTCTGAA GTCTAAAGAG ACCACTAAAT CTAACCTACC TGTGTTTTCT 120  
 10 TCACGCCACG TAATTTCTTC TGGCTTTTCA TCTTCATTG GTGTAGCTAA TAACCCTGAT 180  
 TTTGTGCCAA GTAAATGCTT CATAAAGTAT TCTTGACCTT TTGCAGAACT TGAAATTAAG 240  
 TTTGAACGCC ATATAAATAA TGATTTTGGA TGATTCTTTT CAAATCAGGA TCTTCTATTG 300  
 15 CAAATTGTGG TTTGTnTTGG ATTTCACnTC ATCAATTGCA CGTTGCAAAA TCGCTTCATG 360  
 TGAATCTATA CCCTGCATCT TGTAGCnTCC 390

15 (2) INFORMATION FOR SEQ ID NO: 4031:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 20 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4031:

25 TGGTTCGAAT,CCAGCTAGCC CAGTTATTGG CGGCATAGCA AGTGGTAAGG CAGAGGTCTG 60  
 CAAAACCTTT ATCACCGGTT CAAATCCGGT TGCCGCCTCC AGGTTTATGC GGGAGTAGTT 120  
 30 CAACTTTTAG AACACGTTCC TTCCCGGAAn GAGGTATAGG TGCAAATCCT ATCTTCCGCT 180  
 CCATAATTTA ATAATAATGC GGGAGTATTT CAATCTTAG AATACATTCC TTCCTGGAAT 240  
 GAGGTATAGG TGTAATCCT ATCTTCCGCT CCATAATTTA ATATTTGCGG GGAGTAGTTC 300  
 35 CAACTTTTAG AACACGTTCC TTCCCGGGAA GGAGGTATAn GTGTATCCTA TCTTCCGnC 360  
 CATAATGCCT TCCAAAGGGG AATTTTTTTGG TTTnACCATT 400

40 (2) INFORMATION FOR SEQ ID NO: 4032:

40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 45 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4032:

50 GTATCGATGA GTTCTTTCGG TGCCTCTTCG ACAGCCATTT TGAATTCGAC AAAATGCATC 60  
 ACATCGGGAT GACCATTAAAT TGCATTAAAC GTGTCTTGTA AATCTTTTGA TGATTCAACG 120  
 55 TCATGAATTT CAACATTTTT ACCACCAAAT ACAGCTGGTA AAGCTTTATA ATCCCACATG 180

TTATTAATCA CCAATAATAC CGGGTTAATA TGCTGTCTAA TCATAGTTGG AAATAGCTTG 300  
 AACAGTTAGT TGGCCATGAG CCATCACCCA TTTAATAATA AGTTACGACG GATCTTTGGT 360  
 5 CTGCCAATTG GGGGAnCnCA ATGTTGCAGG GnaATGCTAT 400

## (2) INFORMATION FOR SEQ ID NO: 4033:

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4033:

CACGACGTC TGAACCCAGC TCGCGTACCG CTTTAATGGG CGAACAGCCC AACCCTTgGG 60  
 20 ACCGACTACA GCCCCCAGGA TCGATGAGC CGACATCGAG GTGCCAAAct CCCCCTCGAT 120  
 GTGAActCTT GGGGGAGATA AGCCTGTTAT CCCCggGGTA GCTTTTATCC GTTGAGCGAT 180  
 GGCCCTTCCA TGCGGAACCA CCGATCACT AAGTCCGTCT TTCGACCCTG CTCGACTTGT 240  
 25 AGGTCTCGCA GTCAAGCTCC CTTATGCCTT TACACTCTAT GAATGATTCC AACCATTCTG 300  
 AGGGAActTTT GAAGCGCTCC GTACCTTTTA AGAnGGCGAC CGGCCcAGTC AAActGGCCC 360  
 30 CTGACACTGT CTTCCAACAC GATAAGTGGT GCGGTTAGA 400

## (2) INFORMATION FOR SEQ ID NO: 4034:

## (i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4034:

AATTCATGT GTACGGTTGA AATGCGCAGA GATATGGAGG AACACCAGTG nCGAAGCGAC 60  
 45 TTTCTGGTCT GTAActGACG CTGATGTGCG AAACGTGGGG ATCAAACAGG ATTAGATACC 120  
 CTGGTAGTCC ACGCCGTAAA CGATGAGTGC TAAGTGTTAG GGGGTTTCCG CCCCTTAGTG 180  
 CTGCAGCTAA CGCATTAGC ACTCCGCCTG GGGAGTACGA CCGCAAGTTG GAAActCAAA 240  
 50 GGAATTGACG GGGACCCGCA CAAGCGTGGn AGCATGTGGT TTAnTTCGAA CAACGCAGAG 300  
 AACCTTACCA AATCTTGACA TCCTTTGACA ACTCTAGAGA TAAAGCCTCC CCTTCGGGGA 360  
 CAAATGACAG TGGTGCanGT TGTCTCACT CGTGTCGTGA 400

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4035:

10 TTCGCTTTGC CCGTCTGTCA CATTACTGTA AAATTCTATA AATAGAATTT TTGATGACGG 60  
 GTCCCTTCCT AGGGTGCCGT CTCAGCCACC CCAACCGGCA CATTGTTGTA AGCTGACTAT 120  
 15 ATGTCAC TTC TGTGTTGGGG CCCCTGTCTT CGACTGGCAC TGCTCCCTCA GGAGTCTCGC 180  
 CATTAACTACT ACGTATTAAC ATGTAATTTT ACTTTGAAAT ACATTAAAGC CCAAATTAAT 240  
 CAAAAGCTTT CTGAACCAGA AACGAAAAAA ATCTATAGTC ATAGAAAAAT TTATGTAGAG 300  
 20 CCTGTTTTTG GATTTATGAA GGCTATTTGG GGTTCAC TCG AATGTCAGTT CGAGGAATAA 360  
 TAAAGTAAAC GAGAGCCAGG TTGTAATTA TGGCACTAAT 400

## (2) INFORMATION FOR SEQ ID NO: 4036:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4036:

35 TAAATGTTGA AAAAGCACGA TTAGATAGAA TTTTGAATAA CAATGAAATT CGTCAAATGA 60  
 TCACAGCATT TGGTACAGGA ATCGGTGGCG ACTTTGATCT AGCGAAAGCA AGATATCACA 120  
 AAATCGTCAT TATGACTGAT GCCGATGTGG ATGGAGCGCA TATTAGAACA TTGTTATTAA 180  
 40 CATTCTTCTA TCGATTATG AGACCGTTAA TTGAAGCAGG CTATGTGTAT ATTGCACAGC 240  
 CACCGTTGTA TAAACTGACA CAAGGTAAAC AAAAGTATTA TGTATACAAT GATAGGGGAC 300  
 TTGATAAACT TAAATCTGAA TTGAATCCAA CACCAAATG GCTATTGCAC GTACAAAGGC 360  
 45 TTGGAGAATG AATGCACTCC ATTTGGGAAC ACATGACCTG 400

## (2) INFORMATION FOR SEQ ID NO: 4037:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4037:

TCGTCGCTAA AGACCTTTCT TGACTTGTGA CAATCGCTTG CTTCTTTCCT CTCCTTCGGC 60  
 5 TCTCGCTTAC TCATTTAGCT CTACTAAACT CGTTGCGGTC TTTCTCGTT TCGTCAGATT 120  
 CAAACGTTTT CACTTCGCCA AGCCATTTTT CTTTGTGTTT ACTTTTTATT TTGACGTTTT 180  
 AGACATAAAA AAAAGAGACC TTGCGGTCTC AATGCGGCTC ATCGCATCCA TTTTTCGCTT 240  
 10 GGCAACGTTT TACTCTAGCG GAANTAAATT GGGCTACCAT CGACGCTAAG AACCTTCTTT 300  
 GACTTGTGAC AATCGCTTGC TTCTTTCCTC TTCTTCGGCT CTCGCTTACn CATTTAGCTC 360  
 15 TACnAAACTC GTTTCGCTCT T 381

## (2) INFORMATION FOR SEQ ID NO: 4038:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 360 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4038:

CTGTTTGTCA TACTTCATAA ATCCTTTAAA TTCACCCATC GATCTCCCC CTTTCCTTAA 60  
 TACACAACGG CTGGTTTATG TTTAGCATCG ATTGTTTTAC TGTCAATCGTA AAATGCAGCT 120  
 30 AACATCGCTT CATCTTCATT GTCATGTAAT GATTTGTGCA AATGAATTTT TTGCATCATT 180  
 AATTGATAAT CTTTAGGAAT AACTTTAAGC ACGACATCTT CAATGCGATC AAAATGTTTT 240  
 35 AACACATGAA TCGCTCTCGT ACTATTCGTG TGTGACACAT GTnCTTCCAG CATTTGCTTA 300  
 ATGAATGCTT TnCTTCTTG GTGTTTAATC TTTGTAAACG AAAGCGTATC TAGTGATAnG 360

## (2) INFORMATION FOR SEQ ID NO: 4039:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4039:

AGTGCGAACC CATAACCTCT TGATCCGTAG TCAAACGCTC TATCCAATTG AGCTACGGGC 60  
 50 GCATATGTTT TTATTGAAAA TGGTGCCGAG GACCGGAATC GAACCGGTAG TGAnTGCACT 120  
 CACCGCAGAT TTAAAGTCCT GTGCGTCTGC CAGTTCCGCC ACCCCGGCAC TATAAAAATG 180

GAACCTCTGC ACCCTCTGGA TTA AAAAGTC AGATGCTCTA 400

(2) INFORMATION FOR SEQ ID NO: 4040:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4040:

CTTTCTTGAC TTGTGACAAT CGCTTGCTTC TTTCTCTCC TTCGGCTCTC GCTTACTCAT 60  
TTAGCTCTAC TAAACTCGTT GCGCTCTTTT CTCGTTTCGT CAGATTCAAA CGTTTTCACT 120  
TCGCCAAGCC ATTTTCTTT GTGTTTACTT TTTATTTTGA CGTTT TAGAC ATAAAAAAG 180  
AGACCTCAG GTCTCAACTT GCCTGGCAAC GTTCTACTCT AGCGGAACGT AAGTTGGCTA 240  
CCATCGTCGC TAAAGACCTT TCTTGACTTG TGACAATCGC TTGCTTCTTT CCTCTCCTTC 300  
GGCTCTCGCn TACTCATTTA GCTCnACTAA ACTCGTTGCG CTCTTGTCTT CGTTTCGGGC 360  
AGATTCAAAC GntTGTCA 378

(2) INFORMATION FOR SEQ ID NO: 4041:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4041:

GTACCTTAAC AATATCTCGA AATGGACGAA CTAAATTATG AACCGCATGA AAGGATACTT 60  
GCGAATCATT TGAGCATGCT TGAATCATAA TATCACCATC GCTGTAATCG TCTATTAACT 120  
GATCATTCGG AAAATGCGGT AAATCTTTAA AGGCATCGGG AATTTTACTA GATAACCCAA 180  
TTTTCTTCAT CAAAGACTTA CTAATCCCAA AGGTAATCGT TAACTTGCTT GCACCTAATC 240  
CTATCGATTG ACCGGTATCT ACTGGTGGGC ATTAAAGGAT TGTTACTCGG GCTTGGCCAA 300  
CTGTATCACC ATCCATCATA CGATTGAGCC ATAACGGTCC ACTTTTTTAA ACATTGGCTT 360  
TATTGGCACC CnAACCTTTG GACTTCnAAT CTAACGGCCA 400

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4042:

GACTTGCAAA CGTTGTGATG ACGGTCAAGA AACTGGTAA CACACCAGAC GGACGTAAAG 60  
 CTGGCGAACC ATTTGCTCCA GGTGCAAACC CAATGCATGG CCGTGACCAA AAAGGTGCAT 120  
 TATCTTCATT AAGTTCTGTA GCTAAGATCC CTTACGATTG CTGTAAAGAT GGTATTTCAA 180  
 ATACATTCAG TATCGTACCA AAATCATTAG GTAAAGAACC AGAAGATCAA AACCGTAACT 240  
 TAACTAGTAT GTTAGATGGT TACGCAATGC AATGTGGTCA CCACTTAAAT ATTAACGTAT 300  
 TTAACCGTGA AACATTAATA GATGCAATGG AACATCCAGA AGGAATATCC ACAGTTAACA 360  
 ATCCGTGTAT CTGGTTACGC TGTTAACTTC ATTAAATTAA 400

## (2) INFORMATION FOR SEQ ID NO: 4043:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4043:

CTATTTTATC TAAAGTTAAA CCTGACCCAC CTAGAATTGA CGCAAACCTCT GTGACATATA 60  
 AAGCAGGTCT TACAAACCAA GAAATTAAAG TTAATAACGT ATTAAATAAC TCGTCAGTAA 120  
 AATTATTTAA AGCAGATAAT ACACCATTAA ATGTCACAAA TATTACTCAT GGTAGCGGTT 180  
 TTAGTTCGGT TGTGACAGTA AGTGACGCGT TACCAAATGG CGGAATTAAA GCAAAATCTT 240  
 CAATTTCAAT GAACAATGTG ACGTATACGA CGCAAGACGA ACATGGTCAA GTTGTTACAG 300  
 TAACAAGAAA TGAATCTGTT GATTCAAATG ACAGTGCACA GTGAACAGTG GACACCACAA 360  
 TTGACAAGCC AACTACTGAA GGCGCnGTGn TTATTAAAAG 400

## (2) INFORMATION FOR SEQ ID NO: 4044:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4044:

5 AAAATGGCTT GATTTGAAAA ACGACCAGCA TCGCTACTG GnATAATAGC GAGGCTACCA 60  
 TGTGTGTTTCA TCGTAGnCGC ATGTTAGTTA ATCCAGGGAT ACAAGCATCA TGATCAATAT 120  
 TAAAGCCATA TTCAAACAAT TGACCATAAG GTTCAATGTA AGCAGCGCCG GTGCACTTGC 180  
 10 ATTCCAGCTG AATTAGAGCG ACGTGCAGCA TAAGCCAAGT CTTCTTTTGT AATATAGCCT 240  
 TCTTTTGTG ATGTGTTTAC GGTCCATTGG GTGGATAATA CAAAGCGATT CGAAATTTTG 300  
 ATGCCATTAG GTAAGTGGAT TGATTGTAAA AGTGGTTTGT ATCGGTACAT ACTATGATTC 360  
 15 CnTTTCCATT GCAAT 375

## (2) INFORMATION FOR SEQ ID NO: 4045:

## (i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4045:

25 GTTCCAATGA AGATAGCTAG AAATGATATC CAAAACACAT GATGCATCAC TGGTGATGCT 60  
 30 CGACTAATTG TATTCCATGA TGCATTAATA ATAATGACCA ATACACATAA AATAAGCAGC 120  
 CATTATCGT TTATTTTAAA AATATAATGC AGCAAAAATC CCAAATGAT TAATTGCACA 180  
 ACTGCTCGTA ATGTCGCAAC AATTAAATCT TTAATAATAT GTAAACCTTC TTTATATGAA 240  
 35 ATGATAATCG GAATGACTAA AAGCAATGCC GTCAATCCAA GTGCCGTATT ACTCATGTnG 300  
 ATTCAACTCC TCTGTATTAG AAATTTGACC ATCAACAATT GTTATACGCT TTTTGNAAGT 360  
 GGTCGCATAC TTTGGGGCAT CGCTGTGGGG TAGGGGnGn 400

## (2) INFORMATION FOR SEQ ID NO: 4046:

## (i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 375 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4046:

50 CGAGTCTGAG TCGCTGTCTG AATCTGAATC GCTGTCTGAG TCCGAATCGC TATCTGAATC 60  
 TGAGTCGCTG TCTGAGTCTG AATCGCTATC TGAATCTGAG TCGCTATCTG AGTCTGAGTC 120

TGAGTCTGAG TCGCTATCTG AGTCTGAGTC GCTGTCTGAA TCTGGAGTCG CTGTCTGAAT 240  
 CTGGAATCGC TGTCTGGAGT CTGAATCGCT ATCTGAGTCT GGAATCGCTA TCTGAGTCTG 300  
 AATCACTGGT CTGGAGTCCG AGTCACTGTC TGAATCTGAC TGCACnACn GGATTCTGAG 360  
 TCGCTAACnG GAATC 375

(2) INFORMATION FOR SEQ ID NO: 4047:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4047:

ATGGGTAAAA AGGCATTAGA GTCAATCATT GATAACGCTG ATGAAACAAC TCAAGAGCGT 60  
 TTACGTTTCTAG GATATGAAGA TGCTGTAGAT TATAACCGTT ATGTCGGTAA TATTTATACT 120  
 GGATCATTAT ATTAAAGCCT AATATCATT CTTGAAAATC GAGATTTACA AGCTGGTGAA 180  
 ACAATCGGTT TATTCAGTTA TGGCTCAGGT TCAGTTGGTG AATTTTATAG TCGGACATTA 240  
 GTTGAAGGCT ACAAAGATCA TTTAGATCAA GCTGCACATA AAGCATTATT AAATAACCGT 300  
 ACTGAnGTAT CTGTTGGATG GCATATGGAA ACATTCTTCC AAACGTTTTG GATGACGGTG 360  
 GAATTTGACG GnGGACCAAG ATGcnTGTTT CAGGAGGTCC 400

(2) INFORMATION FOR SEQ ID NO: 4048:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4048:

CAAACCATCT GACATAATAT ACACTTGGAT GTTAGATAAG GGTTTGCCAA TTGGAATCGT 60  
 CTCAGGTATC AATCACCACA ATGATGTGAC CAATACGATG TGATGACTGT TGACTCAGAT 120  
 GGTCCATAGG CATTGAAATA CGTGCCACAA TGCTTCTCAA TATATTTAAC AAAGGATGCC 180  
 GTACTAGTTG CCCCgcCTGT AATCAACTTT TCAATATAAA AGTCTTCCAT AACACTACAC 240  
 ATCTGTAACG GAATCGACGC AACCGTCACA CGATGCTTAT TAATGAGTTG TTGTAAGTGT 300  
 TCTGGATTAA CACGnTCCTC TCTATCTGGA nTCACAAGCG TATGACCATT AACAAACAAC 360

## (2) INFORMATION FOR SEQ ID NO: 4049:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4049:

TCTGCATGTT CTCGAGATCC ACCAAATGTT AAATGGGTAT GTGCATCTAC TAATGCTGGG 60  
 GACACTACCT TCCACTAGC ATCAATCGTC TCAGTCGCAT CGTAGTCATC TGTATGTGTT 120  
 CCAGCATATA CAATTTTGGC CATCTTTAAT GACAACTGTA CCATTTTTC AACAATTTGA 180  
 ATTCATCTAA TTCCTTACCC TTCAAAGGTT TATCTGTTGA TCTCGGTAAA ATTAATTGCT 240  
 GCTATATGAT TAAATATTA AAA TCATTCATTA CTATCACCTG CTTATCAATC ATGGAATAGA 300  
 ATACCTTTTC ATTAGCGTTT GAATAGCGAG TCATAGCCAG CATCAACATG TCGGGCAACA 360  
 CCCATACCGG GGTTCATCGTC CAATACACGT TCCAACCTnC 400

## (2) INFORMATION FOR SEQ ID NO: 4050:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4050:

ATCACCCATG TTCTGACTCC CAAGTTAAAT TAATTGGCAT TCGGAGTTTG TCTGAATTCG 60  
 GTAACCCGAG AGGGGCCCCCT CGTCCAAACA GTGCTCTACC TCCAATAATC ATCACTTGAG 120  
 GCTAGCCCTA AAGCTATTTT GGAGAGAACC AGCTATTTCC AGGTTCGATT GGAATTTCTC 180  
 CGCTACCCTC AGTTCATCCG CTCACCTTTT AACGTAAGTC GGTTCCGTCC TCCATTCACT 240  
 GTTACCTGAA CTTCAACCTG ACCAAGGGTA GATCACCTGG TTTCGGGTCT ACGACAAATA 300  
 CTAAACGCCT ATTCAGCTCG ATTTCGTACGG CTCCACATTT ACTGCTAAnC TTGCATCAAT 360  
 CGTACTCGCG GTCAATCTAC AAAAGnACGC ATCACCAnTA 400

## (2) INFORMATION FOR SEQ ID NO: 4051:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4051:

5 AGTGAAAATG ACTTTATCGG GCTGTTTCAGC GATATGGATT TGAGTTCAAC GCGACTAGGT 60  
 AACAATGTCA AAGAACGTAC TGCTTTAATC TCTAAAGTCA TGGTTAATCT TGACGACTTA 120  
 10 CCATTCGTTT ACAGTGACAT GGAAATTGAT ATGTTAGGTG ATGCATATGA ATTCTTAATC 180  
 GGGCGCTTTG CGGCGACAGC GGGTAAAAAA GCAGGCGAGT TCTATACACC ACAACAAGTA 240  
 TCTAAGATAC TGGCGAAGTT GTCACAGACG GTAAAGATnA ATTACGTCAC GTGTAACGAC 300  
 15 CCAACATGTG GgntCCGGTT CATGTGTGGTA ACGTGTGGT AAAGAACGCA AGTGTATCGT 360  
 TAATTCGGAC nAAGAACGTA ACAATACTAC nTACGACTTA 400

## (2) INFORMATION FOR SEQ ID NO: 4052:

20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 390 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 25 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4052:

30 TCCTACAACC CCAACAAGCA AGCTTGTGGT GTTGGGCTCT TCCCGTTTCG CTCGCCGCTA 60  
 CTAAGGGAAT CGAATTTTCT TTCTCTTCCT CCGGGTACTA AGATGTTTCA GTTCTCCGGG 120  
 TGTGCCTTCT GATATGCTAT GTATTCACAT ATCGATAACA TGACATAACT CATGCTGGGT 180  
 35 TTCCCCATTC GGAAATCTCT GGATCAAAGC TTACTTACAG CTCCCCAAAG CATATCGTCG 240  
 TTAGTAACGT CCTTCATCGG CTTCTAGTGC CAAGGCATCC ACCGTGCGGC CCTTAATAAC 300  
 TTAATChATG TTTTCCACCA TTTTTTATAA GTnCAAAGGC TTCACATACG GCTTCGGTTT 360  
 40 TTCATTAATT TTAAATGGCh CAATTTAACA 390

## (2) INFORMATION FOR SEQ ID NO: 4053:

45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 50 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4053:

55 AACATACCGA TGTATATAAT CTATACACAA AGGATAATTA CTTATGCAAA GGCGGAGGAA 60

GTCGATTGCG AATGATTTAA GAGGGAACAT GGATGCGAGT GAATTCCGTA ATTACATTTT 180  
 AGGCTTGATT TTCTATCGCT TCTTATCTGA AAAAGCCGAA CAAGAATATG CAGATGCCTT 240  
 5 GTCAGGTGAA GACATCACGT ATCAAGAAGC ATGGGCAGAT GAAGAATATC GTGAAGACTT 300  
 AAAAGCAGAA TTAATTGATC AAAGTCGGTT ACTTCATTGA GCCACAAGAT TTATTCAGTG 360  
 10 CGATGATCGT GAAATTGANA CGCAnGATTT CCGATATAGA 400

## (2) INFORMATION FOR SEQ ID NO: 4054:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4054:

GTAAGACCAT CGTACTTGAG TCTTCAAGTG TTCTTGATAA AACGGAACGA GAGACTTGGT 60  
 ATTTTTCGAA CAAATCTTTC ATTAACACAC CGACCATAAT AATTACAATC GAAGCAACAC 120  
 25 CTGCAGCGAA TACAAGCGCA ATACAACAAA TAACAGTAAT ACATATTAAA CTTCTACAG 180  
 AATGGATGCC TTTAGAAATA GTAGTTAATA AGACTTCTAA ACATCCTGCT TTTTCTACAA 240  
 30 TACCTGCAAA TGCATATCCG CAAAATATCG TTACTAATAT TTGGGnCATATA CTCATCATAC 300  
 CACCTGTTC TAACAAGCTT TCACACTGGA TGAATATGAG nTGATGTATC ATTGATCGTT 360  
 AAACCCTAAT GTGCTTTGAA CCATCGTCAT TTGAATGTGA 400

## (2) INFORMATION FOR SEQ ID NO: 4055:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4055:

CGTCTACAAG TTCAAAATTC AAGTCTTCCA TAATTGGTTT AACAATCACT TCTACTTGTT 60  
 CTGTAATTTT ACTCATAACAG GCCTCCCTTT TTGGCAAATA GAAAAGAGCG GGAATCTCCC 120  
 50 ACTCTTCTGC CTGAGTTCAC TAATTTTAA GCAACTTAAT TATAGCATAA GTTTATGCTT 180  
 GAAACAAATG ACTTCACTAT TAATCAGAGA TTCTTGTAAG AGTTTGTTCC TTTATTTAC 240  
 CATTACATTT GAATAGACTC GTAAGACATT GAAAAGAAAT ACGGGCATAA TTTTGTGTCC 300

TCATTTTACA TATCAAATAT CGGAAGTTGA GCTTTATCTG

400

(2) INFORMATION FOR SEQ ID NO: 4056:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 481 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4056:

15	ATTTTGGTTT ACTTCATGTT GAGTTTTAGA CATTTTAACC ATCTCCAATA TAAAAATAAA	60
	TTAAATTAAA TTCTCAGGGA CTTCATGAC GCCACCTGTA TTGCGCTAG TTAGTAGGGC	120
	AGTATAACGA GCTAGATAAC CTGTTTTTAC TTTCGCTTTA AATGGTGTTA AAGATTCTCG	180
20	GCGACGCGCT AGAACATCTT CAGGCTGGTT TACGTTTAAT GTACGATTTC TTAAATCAAT	240
	AGTAATCTCA TCACCATCTT CAATTAAgGc AATTGGTCCA CCAGATGCAG CTTCAGGGGA	300
	AATATGaCCA ACTGcAATAC CTCTTGTTGGc ACCGGtAAAA ACGCCCATCA GTKaATTaAT	360
25	GCaACATCTT TACCTAAGCC GCGaCCAACA ATAGAGGAAG TAGGTGCTAA CATTTTCAGG	420
	nCATACCTGG GTCCACCTTT TAGGTGCCTT TCAnTATCTn ATGGACAACG ACGTGGGCCT	480
30	G	481

(2) INFORMATION FOR SEQ ID NO: 4057:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 379 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4057:

	TTTTTGCTG GCAACGTTCT ACTCTAGCGG AACGTAAGTT GGCTACCATC GTCGCTAAAG	60
45	ACCTTTCTTG ACTTGAGACA ATCGCTTGCT TCTTTCCTCT CCTTCGGCTC TCGCTTACTC	120
	ATTTAGCTCT ACTAACTCG TTGCGCTCTT TTCTCGTTTC GTCAGATTCA AACGTTTTCA	180
	CTTCGCCAAG CCATTTTTCT TTGTGTTTAC TTTTATTTT GGACGTTTTC GACATAAAAA	240
50	AAAGAGACCT TCGGGTCTCA ATGCGGCTCA TCGCATCCAT TTTTGCCTG GCAACGTTCT	300
	ACTCTAGCGG AAGTAAATTG GGCTACCAnc GACGCTAAGA ACCTTTCTTG GACTGTGACA	360
55	ATCGGCTGCh TCTGTnCCT	379

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4058:

CTGCATCACT GCCATAAAAA CTACCGTCAG CAGCGATAGn CGGCCAATCA TACCAGGAAC 60  
 AAGACCGGGC TTGTCAGCGA TACTAACAGC GATATATCCA GCTAGTATTG GAACCATAAA 120  
 TTAAAGGCT AAACACCAA TGTTTTCAAT GGATTTCCTA AATGAATCAT CTGGGATGAC 180  
 TAATCCTTTT GATGTCGTTT CACCGCCTAG AGTCAGCGCG ATGGCGATAA GGAGTCCACC 240  
 AACTACGATA AAAGGAACCA TAAACGATAC ACCGTTTATT AAATGTTGAT ACACCATTG 300  
 AATACCATTT TAGACTnACC GCGATCTTTC GAATGATAAT TTGTTTCAGA TGGTTAAATA 360  
 GGCGCATTTG ATTTAATGAT ACGTGGATTT GGACCCTCGG 400

## (2) INFORMATION FOR SEQ ID NO: 4059:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4059:

TTAAAAAACT GCCTGGCAAC GTTCTACTCT AGCGGAACTA AGTnGAnCTA CCATCGACGC 60  
 TAAGGAGCTT AACTTCTGTG TTCGGCATGG GAACAGGTGT GACCTCCTTG CTATAGTCAC 120  
 CAGACATATG AATGTAATTT ATACATTCAA AACTAGATAG TAAGTAAAAG TGATTTTGCT 180  
 TCGCAAAACA TTTATTTTGG ATTAAGTCTT CGATCGATTA GTATTGCTCA GCTCCACATG 240  
 TCACCATGCT TCCACCTCGG AACCTATTAA CCTCATCATC TTTGGAGGGA TCATTATAAC 300  
 CGAAATTGGG GAAATCTCAT CTTGAGGGGG GCTTnCATGC TTAGATGCTT TCCAGCACTT 360  
 ATCCCGT 367

## (2) INFORMATION FOR SEQ ID NO: 4060:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4060:

5 TTCCGnACTC ACATAGCGAC TCAGGATTCA GACAGCGCAT TCAGATTTCAG ACACCGCATT 60  
 CAGATTTCAGC ATAGCGATTTC AGCATTCCGC ACAGTGA CTC AGnATTCCGA CAGTGACTCG 120  
 GATTTCAGATA GCGATTTCAGA TTCCGACAGT GACTCAGATT CCGACAGTGA CTCAGACTCA 180  
 10 GACAGTGATT CGGATTTCAGC GAGTGATTTCG GATTTCAGATA GTGATTCCGA CTCCGACAGT 240  
 GACTCGGATT CAGATAGCGA CTCAGACTCG GATAGCGACT CGGATTTCAGA TAGCGATTTCG 300  
 GACTCAGATA GCGATTTCAGA ATCAGACAGC GATTTCAGATT CAGACAGCGA CTCAGACAGT 360  
 15 GACTCAGATT CAGA 374

## (2) INFORMATION FOR SEQ ID NO: 4061:

## (i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 432 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4061:

AAAATCATAA TATTTGGCAA TTTTTC AAC TTGACTCTGG TCCTTCTGCA TAACTGCCGT 60  
 30 AAATAATTCA CCTTCATCAC ACGCTGTACC TACCAATAAT CCCTCAGCAT ATTCATCTAA 120  
 CAATGAACGT GGAATTCGAG GTGTACGGTA GAAATACTTC ACCAATGATG CACTTACAAT 180  
 TTTAAATAGA TTTTAAAGAC CTTGTTGGTT TTGTACAATT AATGTGACAT GACTAGGTCT 240  
 35 TGCACGTTTA TATGCATCTT CATTACTGAG TTTTtKGTtG ATTCGTTAT GATTTAATAC 300  
 GCCTAAWTCy TTCATTTGTT GAACCATTTT TATGAAAATG TAAGCTGTTG CTTCTGTATC 360  
 ATAAATGGCA CGGTGATGTT GCGTTAATTC TACGCCATAT TTTTtagCCA AGAAATTCAA 420  
 40 ACCATGTTTA CC 432

## (2) INFORMATION FOR SEQ ID NO: 4062:

## (i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 386 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4062:

55 TATCTTCGTT CTCAATAGAA TGATTTA AAC CTTCGATTTC TTTATCTAAA TGACTACCAA 60



TTTTTCTTC AACTAAGTCA CGATATAATG TTTTGAATT TTCGTTCAAT TTCGATTTCGT 180  
 GATTTTGAAT ACTTTTCTTC CACACAAATG TATACCTATT GGCATTAGCT TCTACTTTTG 240  
 5 TACCATCAAT AAGATTTTGC TTAAACATT GACTATGAAA CTGGGATAAA TAAAGAnTCA 300  
 ATTAACGCAT CAGTATTAGG GAnTCACTCT AATACGATTA ATAGTTTTTA TAAGAAGGTG 360  
 nTTGGATTTG GAGCTAACCA CATCCA 386

(2) INFORMATION FOR SEQ ID NO: 4063:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 386 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4063:

TAGGAGAGCG TTCTAAGGGC GTAGCATGAT CGTAAGGACA TGTGGAGCGC TTAGGAGAAT 60  
 GCCGGTGTGA GTAGCGAAAG ACGGGTGAGA ATCCCGTCCA CCGATTGACT AAGGTTTCCA 120  
 25 GAGGAAGGCT CGTCCGCTCT GGGTTAGTCG GGTCTTAAGC TGAGGCCGAC ACGTAGGGCG 180  
 ATGGATAACA GGTTGATATT CCTGTACCAC CTATGAATCG TTTTAATCGA TGGGGGGACG 240  
 CATAGGTATA GCGGAGGTGA CGATTGGGAT TGCACGTCTT AAGCAGTAAG GCTGAGTATT 300  
 30 AGGCAAATCC GGTACTCGTT nAAGGCTTGA GCTGTGGATG GGGAGAAGAC ATnGAGTCTT 360  
 CGAGTTCGTT GgnTTTCACA ATGGCC 386

(2) INFORMATION FOR SEQ ID NO: 4064:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 386 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4064:

TAAGGCAGAT GCTCTCCCAG CTGAGCTAAT TCTCCGATTT AAAACTGCCT GGCAACGTT 60  
 TACTCTAGCG GAACGTAAGT TGGAGCTACC ATCGACGCTA AGGAGCTTAA CTTCTGTGTT 120  
 50 CGGCATGGGA ACAGGTGTGA CCTCCTTGCT ATAGTCACCA GACATATGAA TGTAATTAT 180  
 ACATTCAAAA CTAGATAGTA AGTAAAAGTG ATTTTGCTTC GCAAACATTT ATTTTGATTA 240  
 AGTCTTCGAT CGAnTAGTAT TCGTCAGCTC CACATGTCAC CATGCTTCCA CCTCGAACCT 300

AGGGGGGGCT TCATGCCTTT AGAATG

386

(2) INFORMATION FOR SEQ ID NO: 4065:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4065:

15 AATTCTTTTCG CTACTTGAAT GACAACACTT TGTTTTACGC CTGAAATGGC TTCTTGCCAA 60  
 GCAGGTGTAT ATTTTGATTC TGCATCGTCG TATCCTTTTG ATTCTAATTT ATGATCAAAA 120  
 CGACGCACGC CATATTGACT TGCCATTAAAG TCAAAAATTG TAGCAATACG GACTTTGTCA 180  
 20 CCATTGCTA AAGTGAATTG TCGAGTTGGA ATTGGACGAT TGAATATCCC ATCTCCATCA 240  
 CTATCAAAGT ATGGGAATTG AATTGTTTCT AATTCGTATC CACCTTCTGT CATTGATAAT 300  
 GTAGGGTTAA TTTTAGAACC ATCTTCTGTT TCTAGTTTTA AGTTCCACTT CTTACCTTCT 360  
 25 TCCCAACGTG GACCCATGGT GCCATTAnGn ACTACTAAAC 400

(2) INFORMATION FOR SEQ ID NO: 4066:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4066:

ATTTTGAAAT TGAGAAAACA ACTTATTGAA AAACATAATC TTTACGGTAA CATGGGTTCA 60  
 40 GGAACAATCG TTATTAAAAT GAAAAACGGT GGGAAATATA CGTTTGAATT ACACAAAAAA 120  
 CTGCAGAGCA TCGTATGGCA GACGTCATAG ATGGCACTAA TATTGATAAC ATTGAAGTGA 180  
 45 ATATAAAATA ATCATGACAT TCTCTAAATA GAAGCTGTCA TCGGAAAAAC AAGAAGTTAA 240  
 GTGACAACGG TTTACATGTT GCTTAGCTTC TTTTATTATG CGTAATGATG TAAAAAGACG 300  
 NATATTCATT TGTTTGTAAG AGTGGCATTG TATGTCTTAA AGTGACGnAA CTTCCAATGT 360  
 50 GCCCAGTGTT TGATTCACAT CAAATCCATT TTTATTTAAC 400

(2) INFORMATION FOR SEQ ID NO: 4067:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4067:

CCTCATTCCA	GGAAGGAATG	TATTCTAAGA	GTTGAAATAC	TCCCGCATT	TTATTAAATT	60
ATGGAGCGGA	AGATAGGATT	TGCACCTATA	CCTCGTTCCG	GGAAGGAACG	TGTTCTAAAA	120
GTTGAACTAC	TCCCGCATAA	ACCTGGAGGC	GGCAACCGGA	TTTGAACCGG	TGATAAAGGT	180
TTTGACAGACC	TCTGCCTTAC	CACTTGGCTA	TGCCGCCAAT	AACTGGGCTA	GCTGGATTCTG	240
AACCAACGAG	TGACGGAGTC	AAAGTCCGTT	GCCTTACCGC	TTGGCTATAG	CCCATTAAATA	300
ATAAGGGCGG	CTGAAGGGGA	TGAACCCCTC	GAATGTCGGA	ACCACAATCC	GATGTGTAA	360
CCACTTCACC	ACAGCCGCCA	TGGCAGGGGC	AGTAGGAATC			400

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(2) INFORMATION FOR SEQ ID NO: 4068:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4068:

TATCTAATAG	TTTTACTTTA	AGTCCAGCAT	TCACAAAAAG	TGCTGCCAGT	TGAGCGCCCA	60
TTGTGCCTGC	GCCAAGAACG	GTTACTTTAT	TAATTGTCAT	AGTGATTCCT	CCAATTTAGT	120
TGAGGATAAG	ATAACCATTA	AGATAATTGG	AATAACGTTG	CTATTTTATA	AAATTAATTA	180
AGTATCTTTG	ACAGTCATCT	TAGCCTCTTA	TTTAAGGAAA	AAGCTTTATG	CTTAAAATAA	240
GTCTTTTTTTA	GTGAAATTAA	TGCATCTCAT	ATAATTATTT	GCTATTTATA	CGAAAGCAGA	300
ATCTCCAGTC	AAAGCGCGTC	CANTACTAAG	GCATTAATTT	CATGTGTACC	TCGTACGTGT	360
AAATCGnTTC	TGCATCAGnG	AGGAAACGTG	CAATATCATA			400

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(2) INFORMATION FOR SEQ ID NO: 4069:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 356 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4069:

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AAAAAGAAGA ATTGAAACGC CATATAAAGT AACGTTAAAT AATAACGAAA AAAGGGCACT 120  
 ATTCAAACAA TTAGCGTATG TTGAAGGGTT TGAAAAATAT CTTCATAAAA ACTTCGTTGG 180  
 5 TGCAAAGCGT TTTTCAATTC nCGGGGTAGA CGCACTTGTA CCGATGTTAC AACGTACTAT 240  
 TACGATTGCT GCGAAAGAAG GTATTAAAAA TATACAAATA GGCATGGCTC ACCGTGGGAC 300  
 10 GTTTAAACGT TTTTAACGCA TGTnCTTAGA AAAAACCGTA CGAAATGATG ATTTCh 356

## (2) INFORMATION FOR SEQ ID NO: 4070:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4070:

AAACGTTTAG GGAAATTAT CACACAGATA CAACAATACA CAGATATTGA TTACCCGATA 60  
 GCGATTGTCT TTCAAGCATC GTGTTTTAAC GAGTTTGTG TTAAGGGGCG TTTAAGTAAT 120  
 25 ATTATTTCAA AATTGCAACA CTATTCAATT GAGGCGAAAC CAGGTATATG TATTATAGGG 180  
 GAAGTTGTG ATTATACTGA AAACACTCCT AAATCATATG ATCCTATGAA GCAATTTTAT 240  
 30 GTAGTAAGTG GTTCTAAACA TGACGCCCTT ATGCTCTGTG AACATTATAT GACGAAGGTT 300  
 ATGGCTGTTG CTAAACCCCA ATGATACATC GAATGGGCAC CATTATCCAn TCGTCGCAAT 360  
 AATGGATTAC CCAAGGATGC CATTTAnTTA AGCCnGCCAn 400

## (2) INFORMATION FOR SEQ ID NO: 4071:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 361 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4071:

CCTCTGGAAA CCTAGTCAA TCGGTGGACG GGATTCTCAC CCGTCTTTTG CTA CTCTCACAC 60  
 CGGCATTCTC ACTTCTAAGC GCTCCACATG TCCTTACGAT CATGCTTCAA CGCCCTTAGA 120  
 50 ACGCTCTCCT ACCATTGTCC AAAGGnATn CCACAGCTTC GGTAATATGT TTAGCCCCGG 180  
 TACATTTTCG GCGCATGTGC ACTCGACTAG TGAGCTATTA CGCACTCTTT AAATGGATGG 240  
 CTGCTTCTAA GCCAACATCC TAGTTGTCTG GGnAACGCCA CATCCTTTTC CACTTAACAT 300

T

361

## (2) INFORMATION FOR SEQ ID NO: 4072:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4072:

15 ATGGTGACAA AAACATCGCA TTATTACTAG GTGTCGGCAC AGGCGTTTGT GGTGCTGCTG 60  
 CTATTGCCGC AGTCGCTCCA ATATTCAAAT CACGTGAAAA GGATACAGCT ATTAGTATCG 120  
 GTATCATCGC ATTGATTGGT ACGATATTTT CACTTATATA TACAGCTATC TACGCTATCT 180  
 20 TTTCAATGAC GACAAATGTT TATGGCGCTT GGTCTGGTGT TAGTCTTCAT GAAATTGnCA 240  
 CACGTTGTCT TAGCTGGTGG CTTTGGTGGT AGTGATGCAC TTAAAATTGC ACTTCTTGGT 300  
 AAAC TTGGTA GGAGTATTCT TACTGGATTG CCATTAAACCA TCGTACTTAA TTTTAAATAT 360  
 25 GCGGTTnCCG TTnCATCAGG AnTCATCTAG GCAAGGGGTC 400

## (2) INFORMATION FOR SEQ ID NO: 4073:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4073:

GCGACGATCA TTTTAGAATC CGCTTGGGCG ATTAATTCTT TAGAAGTGGA TGAGGCAAAA 60  
 40 TGTTCAATTAT CAGGAACTAA AGCAGGTGCT GATATGAAAG ATGGTCTACG TATTCATGGT 120  
 GAAGACATGG GTACACTTTA TACCAAACAC GTTGAATTGG AAAACAAAGG CGTCGACTTT 180  
 TATGAAGGTA ATGAAGTGGA TGAAGCTGAA GAAGAAGCAA AAGCTTGGAT TGATGCAGTT 240  
 45 GTAAATGATA CTGAACCACT TGTGAACCGG AACAAGCAAT GGTAGTTACC AnAATTCTTG 300  
 AAGCGATTTA TCCGTCTGCC AAATCCAGGC CAAAGCCATT TACTTTGGAA TAACATCnTA 360  
 50 CCGGTAAGGG GGCnCATCCT GGACCAAATT TAAAAGTTGG 400

## (2) INFORMATION FOR SEQ ID NO: 4074:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4074:

	TCTTCCTAAT ACCTTTCCAC GATCTTCAGC TGGCGCCTCT GCACTCGCAA ACGCACTTGA	60
10	TGCATCAACA ACACCACCAA ATAGTCCCTG CAATAACCTC ACAAGTACAA ACTGTAATGG	120
	TGTCGTACAC AATGCCATTA AAAATAAGCA TACCGCCAAA CCAAGTAACG CTCTTAACAC	180
	CATCCATTTT CGGCTGATCT TATCACCTAG CTTCCTCCAT ATCGGCGGAG TTATGCATCG	240
15	TCGTTACAGC TGGAGCAGCA ATCGCTATAC CACTCCACan CTGTATTTCT ACGGACTGAT	300
	AGGATTTTGT AGTGATGnCC ATGATGAAAT GGGCAATAAT GGGCACAAGT ACTGTTCACT	360
	CCAGCCAATC GTTATGAAAC TGGACTGGGG CCATnAAATG	400

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(2) INFORMATION FOR SEQ ID NO: 4075:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 380 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4075:

	GGTTCAGAAC GTCGTATGnA GTTCGnTCCC TATCCGTCGT GGGCGTAGGA AATTGAGAG	60
	GAGCTGTCCT TAGTACGAGA GGACCGGGAT GGACATACCT CTGGTGTACC AGTTGTCGTG	120
35	CCAACGCATA GCTGGGTAGC TATGTGTGGA CGGGATAAGT GCTGAAACTC TAAGCATGAA	180
	GCCCCCTCA AGATGAGATT TCCCACTTC GGTATAAGA TCCCTCAAAG ATGATGAGGT	240
	TAATAGGTTT CGAGGTGGAA GCATGGTGAC ATnTGGAGCT GACGAATACT AATCGATCGA	300
40	AGACTTAATC AAAATAAATG TTTTGCGACA AATCCACTTT TACTTACTAT CTAGTTTGAA	360
	TGATAAATTA CATCCATATG	380

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(2) INFORMATION FOR SEQ ID NO: 4076:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 380 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4076:

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TTTGCCTAAT ACTCAGCCTT ACTGCTTAGA CGTGCAATCC AATCGCACGC TTCGCCTATC 120  
 CTTACTGCGTC CCCCCATCGA TTAAAACGAT TATAGGTGGT ACAGGAATAT CAACCTGTTA 180  
 5 TCCATCGCCT ACGCCTGTCT GCCTCAGCTT AGGACCCGAC TAACCCAGAG CGGACGAGCC 240  
 TTCCTCTGGA AACCTTAGTC AATCGGTGGA CGGGATTCTC AnCCGTCTTT CGCTACTCAC 300  
 10 AnCGGCATTTC TCACTTCTAA GCGGTCCACA TGTCTTACGA TCATGCTTnA AGGCCTTAGG 360  
 AAGGTTCTTA CCATGGTCAA 380

## (2) INFORMATION FOR SEQ ID NO: 4077:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 370 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4077:

GCAGGTCTGA CTCTAGAGGA TnCCCACGCG CGCAAGATT AAATCGAAGA AACCAGCAAC 60  
 25 AGATTCTCTCA AAATAGCGCG GCGAACAACG AAACATCAAA TAGTGCACCT GCAGCTGGTA 120  
 ATGGTGTAGC ATCAACGCCA CCAAGTGCAC CAAGTGGCGA TACTGCACCA AATAATAATG 180  
 30 TTACGCAAAA TACCGCACCA AATAGTAATA ATGCGCCTGT ATCGACTACA CCACAAAGTA 240  
 CAAGGCGGGA AAAAAAGATGG TCAAAGTTTT GTAGATATAA CAACAACACA AGTCAGCACA 300  
 GCTAACGAGA ACACACAAAA CATTACAGAT AAAGATGTTA AATCAATGGA AGCGGCATTA 360  
 35 ACGGGCTCTT 370

## (2) INFORMATION FOR SEQ ID NO: 4078:

40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 351 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4078:

AAACATTTTA TCAAATGGCA GAAGGACATG TGCCAAGACC ACCAGCGATG GTTGAAACAT 60  
 50 TGAATTATAT TAAAGAGTTT ATGAACCAAG TTGAGTCGCA TAGCTAGTAT GAAACGTGGT 120  
 GTGCGCATGG GAACTATCAA GCTTTGAAGA TGTGGTACTA CATGCGTTGG AATTAGGGAT 180  
 CGGTACTTTA TATGAAGACG TGCTGCTTCC ATTAAATGAG TGATGCGATT TTGGCATGAA 240

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TAAGAGGGGC CAACCATGT TAGAATAAC AACGGTTGGC TCTTTAantG T

351

(2) INFORMATION FOR SEQ ID NO: 4079:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4079:

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TTGAAGTAAC TAAATTAATA TTATGTTGTT CAATTAAAAG CTTCATACAA ACCTAATCTA 60

TTTGCACTCC ACCGCTAACA CCGAACACTT GTCCGGTTGT ATAACITGAT TCTTCTGACG 120

CTAATAGCAC ATAAGTTCCA CATAACTCAA CAGGTGACC TGCACGACCT AAAGGTGTTT 180

20

TTTGACCAAA TGTTGGGATT TTACTTTGAG GTTGTCCACC AGAAATTTGT AATGGTGACC 240

AGAATGGACC AGGCGCTACA CAGTTCACCT TAATTCCTTT TGGTCCTAAT TCTTCTGAAA 300

AACTTTTAGT TAATGAAATA ATTGCTGCCT TTTGAAGGGG CATAATCCAT GAAGAATaNG 360

25

GCCAGGGaNT AAAACCCTGG AChAAAGAAG CCGTGGAAT 400

(2) INFORMATION FOR SEQ ID NO: 4080:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4080:

TCGTTGGACA CAATCTGAAA AATAAATAGA TATAAATTCG CGAGATATAT TCGTATTTAT 60

40

AGTAAAATTA AATAAAGAGA TTATATAACA CGAGGAGTAG TAAGTATGAA ATTTGAGAAA 120

TATATAGATC ACACTTTATT GAAGCCTGAG TCAACACGTA CGCAAATCGA TCAAATCATC 180

45

GATGAAGCGA AACATTACAA TTTTAAATCT GTATGTGTGA ATCCAACACA TGTTAAATAT 240

GCAGCAGAGC GACTAGCTGA TTCAGAGGTG CTCGTTTGTA CGGTAATAGG ATTCCCATTA 300

GGTGCCTCGA CAACTGGCAA CGAAAGCATT TGAAACAGAA GATGCAATTC AAAATGGTGC 360

50

AGATGAATTG GACATGGTCA TCCACATCGG CGCATTAATA 400

(2) INFORMATION FOR SEQ ID NO: 4081:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 base pairs

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(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4081:

	CGACTAGTGA GCTATTACGC ACTCTTTAAA TGATGGCTGC TTCTAAGCCA ACATCCTAGT	60
10	TGTCTGGGCA ACGCACATCC TTTTCCACTT AACATATATT TTGGGACCTT AGCTGGTGGT	120
	CTGGGCTGTT TCCCTnChCG AACACGGACC TTATCACCCA TGTTCGACT CCCAAGTTAA	180
	ATTAATTGGC ATTCGGAGTT TGTCTGAATT CGGTAACCCG AGAGGGACCC CTCGTACCAA	240
15	ACAGTGCTCT ACCTCCAATA ATCATCACTT GGAGGCTAGC CCTAAAGCTA TTTACGGAGA	300
	GAACCAGCTA TCTCCAGGTT CGATTGGAAT TTCTCCGChA CCCTCAGTTC ATCCGCTCA	359

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(2) INFORMATION FOR SEQ ID NO: 4082:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 379 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4082:

30	TTTGACATTT AGTGTAAGCG TnTTACAAAT AAAGCGTGT GTTTTTGAAT TAAATGCATT	60
	TCACATTAGT ATTCATATTA TTTTtaggag GAATTtATAT GACATTTGAA AAAGAAACGG	120
	TCTTAAAAAC ATTATTTTCCT GAAGATGTAC TTAGTATTGC TAAAGGTTTA ACAGACGGTG	180
35	AAGTCGAATT TTTACAACAA GTAGATTCAT TGGCTAGAAA GTAAGTACCG TGGAAAATAT	240
	TAATCAACAT TGGATAGACG CTACTGTACC CGAGGACTAT TTTAAAGATC TGGGGAGAAT	300
	TAAATTATTT TAACAATCCA TTACTTTACA AGGGATCGTC CAAACGCCAA AnGGCCTAGT	360
40	CCAACTATTT nCAGTTTTT	379

(2) INFORMATION FOR SEQ ID NO: 4083:

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(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4083:

	TTGAAACAGC CAGAGGTGTT TTATACCCAG GTGTTTCAGA TATGTATGAT GCGAAACAAT	60
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TTGGAACATA TGGTCCTAAC AAAGATGTTG TAGGCATATC TACTCGTCTT ATTAGAGTGA 180  
 CATATGATAA TAGACAAACA GAAGATTTAA CTATTTTATC TAAAGTTAAA CCTGACCCAC 240  
 5 CTAGAATTGA CGCAAACCTCT GTGACATATA AAGCAGGTCT TACAAACCAA GAAATTAAAG 300  
 TTAATAACGT ATTAATTAAC TCGTCCGTGA AATTATTTAA GCCGATAATA CACCATTAAA 360  
 TGTnCAAT ATTACCCnGG GTAGCGGGTT TTAGTTCGG 400

## (2) INFORMATION FOR SEQ ID NO: 4084:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4084:

AGCATATCGT CGTTAGTAAC GTCCTTCATC GGCTTCTAGT GCCnAGGCAT CCACCGTGCG 60  
 CCCTTAATAA CTTAATCTAT GTTCCATCC TACAGGAAAC GCGTTAGTAA TCTTGTGAGT 120  
 25 GTTCTTTTGA ACATAGCGAT TATTTCTTAT GAATTCAAGC TTATTTAAAA CTCTTTATTC 180  
 ACTCGGTTTT GCTTGGTAAA ATCTATATTT TACTTACTTA TCTAGTTTTT AATGTACAAT 240  
 TTCTTTTTAG TCAAGCGCTC GCATAAGCAA TATCACTTTA ACCAAAAAAT ATTTGAATGT 300  
 30 TAAATAAACA TTCAAAACG AATACAATAT GTCACATTAT TCCGCCATCT nCTGAAGAAG 360  
 ATGTnCCGA ATATnATCCT TAGAAAGGAG GTGGATCCCA 400

## (2) INFORMATION FOR SEQ ID NO: 4085:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4085:

TTACTTATCT AGTTTTCAAT GTACAAATAA TGGTGGAGAC TAGCGGGATC GAACCGCTGA 60  
 CCTCCTGCGT GCAAAGCAGG CGCTCTCCCA GCTGAGCTAA GCCCCCAAAT AGGTATTAAA 120  
 TTAATGGTGG GCCTAAGTGG ACTCGAACCA CCGACCTCAC GCTTATCAGG CGTGCGCTCT 180  
 50 GAACCAGCTG GAGCTATAGG CCCATTAATT TGAATGAAC AAACATTCAA AACTGGAATA 240  
 CAATATGTCA CGTTATTCCG CATCTTCTGG AAGAAGATGT TTCCGAATAn ATCCTTAnGA 300

AAGCATTGTGTT TCCCACCTTC GACGGCTGAG CTCCTAAAAG

400

(2) INFORMATION FOR SEQ ID NO: 4086:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 361 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4086:

GTCATTGGAA ACTGGAGnAC TTGAGTGCAG AAGAGGAAAG TGGAAATCCA TGTGTAGCGG	60
TGAAATGCGC AGAGATATGG AGGAACACCA GTGGCGAAGC GACTTTCTGG TCTGTAAGTG	120
ACGCTGATGT GCGAAACGTG GGGATCAAAC AGGATTAGAT ACCCTGGTAG TCCACGCCGT	180
AAACGATGAG TGCTAAGTGT TAGGGGGTTT CCGCCCCCTTA GTGCTGCAGC TAACGCATTA	240
AGCACTCCGC CTGGGGAGTA CGACCGCAAG TTGnAAACTC CAAAGGAATT GACGGGCGCA	300
CAAGCGTGGG AGCATGTGGT TTAATTCGAA CCAACGnATA GAACCTTACC AAATCTTGGA	360
C	361

(2) INFORMATION FOR SEQ ID NO: 4087:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4087:

GACCTTGCAG GACTCGAACC TGCACCGAA CGTTATGAG CCGTTAGCTC TAACCAACTG	60
AGCTAAAGGT CCTAAATATA ATTTTACAAC TAATAAATAG TGGCGGTGGA GGGGATCGAA	120
CCCCCGACCT CACGGGTATG AACCGTACGC TCTAGCCAGC TGAGCTACAC CGCCTTATAT	180
AGTTTGTAATA TAATATGGTG GAGACTAGCG GGATCGAACC GCTGACCTCC TCGGTGCAAA	240
GCAGnCGCTC TCCCAGCTGA GCTAAAGCCC CCATAAATAA TTACAGTATA TCGGGAAGAC	300
AGGATTTCGAA CCTGCGACCC CTTTCCCAAA CCAAGTGCTT TTACCAAGTT GGTACTTCCh	360
GTATAATTTA ACGGGCCCGA TAGGAGTTTCG GAACCCCTTAA	400

(2) INFORMATION FOR SEQ ID NO: 4088:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4088:

	AGCTATTATT TTTGACAGAT TCCATATCGT TCAACATTTA AATAGAGAAC TTAATAAGTA	60
10	TCGTGTACAA GTTATGAATG AATACCGTAA TAAAAAAGGA CCTGATTATA CAATTTTAA	120
	GAATAACTGG AAAGTCCTAT TGATGGATAC TAGTAAAACC ATATTTAGTA AATACAGATG	180
	GAATAAATCT TTTAAGGCTT ATAAACGCTC ATCTGACATT GTAGGAATTC ATGCTTTCAA	240
15	AAGACGATAT ACTACGACAC TCCTACGAAC TTGTCCCAAG GGATTACGGA AAAGGCCCTA	300
	AGGGTTATGT TAATTGGCCC TAAATTTATT AAATGCGTTT GAAATTCAGT TAGTTAAAAA	360
	GTCTGTGAGT GAnGGGTGTA TGGGAAAGTG GTTAAATAT	400

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(2) INFORMATION FOR SEQ ID NO: 4089:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 374 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4089:

	ATCGTTTTAG ATAAGACGGG TACATTACAA ATGGTCGTCC AGTCGTGACA GATTATCATG	60
	GTGACAATCA AACGCTACAA CTACTTGCTA CTGCTGAAAA AGATTCTGAA CACCCATTGG	120
35	CAGAAGCCAT TGTCAATTAT GCAAAAGAAA AGCAATTAAT ATTAAGTGA ACAACAACAT	180
	TTAAAGCAGT ACCTGGGCCA TGGTATTGAA GCAACGATTG GATCATCACC ATATATTGGT	240
	TGGTAACCGT GAAATTAATG GCTGACAATG GATATTAGCT TGCCTAAGCA TATTTnnGGA	300
40	TGGATTTAAC ACATTATGAA CGAGATGGTA AAAGTCTAG CTCATTGCTG TTGAATTATT	360
	nCATAACGGT ATCA	374

45

(2) INFORMATION FOR SEQ ID NO: 4090:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 367 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4090:

55

TTAATAACGT ATTAAATAAC TCGTCAGTAA AATTATTTAA AGCAGATAAT ACACCATTAA 120  
 ATGTCACAAA TATTACTCAT GGTAGCTGTT TTTGTTCCGT TGTGACAGTA AGTGACGCGT 180  
 5 TACCAAATGG CGGAGTTAAA GCAAAATCTT CAATTTCAT GAACAATGTG ACGTATACGA 240  
 CGCAAGACGA ACATGGTCAA GTTGTTACAG TAACAAGAAA TGAATCTGTT GATTCAAATG 300  
 ACAGTGCACC AGTAACAGTG ACACCACANT TACAAGCAAC TACTGAAGGC GCTGTATTTA 360  
 10 TTAAGTT 367

## (2) INFORMATION FOR SEQ ID NO: 4091:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4091:

TAATATTATA TTGCTAGTAG TTGACTGAAT GAAATGCGC TTGCAACAAG CTTTTTTCAA 60  
 25 CTCTAGTCAG GGGCCCCAAC ACAGAGAATT TCGAAAAGAA ATTCTACAGG CAATGCGAGT 120  
 TGGGGTGTGG GCCCAACAC AGAGAATTTT GAAAAGAAAT TCTACAGGCA ATGCGAGTTG 180  
 GGGTGTGGGC CCAACACAG AGAATTTTCA AAAGAAATTC TACAGGGCAA TGCGAGTTGG 240  
 30 GGTGTGGGCC CCAACATGAG AGAAATTGGA TTCCCAATTT CTGACAGACA ATGCAAGTTG 300  
 GCGGGGGCCC CAACACAGAA GCTGGACGAA AATCCTTGAA CGAATGAATG TGGCAATTGG 360  
 35 CGGGGGCCCC ACACAGAAGn TGACGAAAAT nCTnGAACCA 400

## (2) INFORMATION FOR SEQ ID NO: 4092:

40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4092:

GCATTTCTCA TAACACAAGG AATTTCAACA AGTCCGGCTA CTGGATCACA AACTAAACCT 60  
 AATAAATTAC TTATCGCTAA TGCCATAGCG TGCCCGGATG CTTCTGGTGA TCCTCCGAAT 120  
 50 ATAGCTACTG CTGCAGCTGC GGCCATTGCA GATGCTGAAC CAACITCAGC TTGGCAGCCA 180  
 CCTGTTGCAC CAGCTACACT TGCATTGTTT GCTACGACAC GCCCAAACAA TGCTGAAGTG 240

55

CCGGGAATGG TAnCCGAGGG AAnCAGCTGT GGGCGTTGCA CAAATAATAC CCCATCGCAG 360  
 CATTTGACCT TCATTGTTT GCAATGGGAA CCTTTGACTG 400

(2) INFORMATION FOR SEQ ID NO: 4093:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4093:

TGACTTACGT ACTGTTCAAC CAATCGATGT TGACACAATT GTAGCTTCAG TTGAAAAAAC 60  
 TGGTCGTGCA GTTGTAGTTC AAGAAGCACA ACGTCAAGCT GGTGTTGGTG CAGCAGTTGT 120  
 AGCTGAATTA AGTGAACGTG CAATCCTTTC ATTAGAAGCA CCTATTGGAA GAGTTGCAGC 180  
 AGCAGATACA ATTTATCCAT TCACTCAAGC TGAAAATGTT TGGTTACCAA ACAAAAATGA 240  
 CATCATCGAA AAAGCAAAAG AAACTTTAGA ATTTTAATAC ATTTTAAAAG TTAACGAATT 300  
 AGCGTATTTT AGTCTCATTG ATTAAnATGA AATGnGnTAA TTTACGGAAT CCTA 354

(2) INFORMATION FOR SEQ ID NO: 4094:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4094:

CGTTAACATG AAGTTACGTT CTTTTATAAA AAGATTTAAA CGCGTTATTA ATCTTGTGAG 60  
 TGTTCTTTTCG AACACTAGCG ATTATTTCTT ATGAATTCAA GCTTATTTAA AACTCTTTAT 120  
 TCACTCGGTT TTGCTTGGTA AAATCTATAT nTTACTTACT TATCnAGTTT TCAATGTACA 180  
 AATAATGGTG GAGACTAGCG GGATCGAACC GCTGACCTCC TCGGTGCAAA GCAGGCGCTC 240  
 TCCCAGCTGA GCTAAGCCCC CAAATAGGnA TTAAATTAAT GGTGGGCCTA AGTGGACTCG 300  
 AACCACCGAC CTCACGCTTA TCAGGCGTGC GCTCTAACCA GCTGAGCTAT A 351

(2) INFORMATION FOR SEQ ID NO: 4095:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4095:

5 ATTGTTGCGA CTGGCACACC CGAAGATATT GCTCAGACAA AGTCATCATA TACAGGAAAG 60  
 TATTTAAAAG AAGTACTTGA ACGAGATAAA CAAAATACTG AAGATAAATA AGATTAAAAG 120  
 AAGTGAAGGA TGTATAATT TATCCTTCGC TTCTTTTAT TAATTTAGTA ATGAATAGTA 180  
 10 GAAAGAAAAG ATGCGTAAAA AGAATTATGT TAAGATAGGG TCAATCTAGA GTAGTTAAAC 240  
 ATAAATCGAA CTnGGAGTGG GACAGAAATG ATAAAGAATC ACTAATGATT TATTATGTAG 300  
 TGGTTCTTTG TCATTAGCCA CAGCTATTTG TGTACTTAAA AnTAGGTATG CCAGTGTGCA 360  
 15 CTCCTTGAGA GGAAATACTn ATTT 384

## (2) INFORMATION FOR SEQ ID NO: 4096:

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 387 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4096:

CTGCATCTTC ACAGGTACTA TGATTTCACC GAGTCTCTCG TTGAGACAGT GCCCAAATCG 60  
 30 TTACGCCTTT CGTGCGGGTC GGAACCTACC CGACAAGGAA TTTCGCTACC TTAGGACCGT 120  
 TATAGTTACG GCCGCCGTTT ACTGGGGCTT CGATTCTAG CTTCGCAGAA AGAGCCGACT 180  
 CCTCTTGAAC CTTCCAGCAC CGGGCAGGCG TCACCCTGAT GACATCACCT TACGGTTTAG 240  
 35 CAGAGACCTG TGTTTTTGAT AACAGTCGC TTGGGCCTAT TCACTGCGGC TCTTCTGGGC 300  
 GTTAACCCTn AAAGAGCACC CTTTCTCCCG AAATnACGG GGTCATTTTG GCCGAGTTCC 360  
 TTAACGAGnA TTCGCTCGGT GCAACTT 387

## (2) INFORMATION FOR SEQ ID NO: 4097:

## (i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4097:

50 CCACTCACAT TCACACATCG ATTCACACAC CGCACTCAGC ACTCAGnATA CCGCATTCAG 60

TCAGATAGCG ACTCAGATTC GGATAGCGAC TCAGACTCAG ATAGCGATTTC AGATTCAGAT 180  
 AGCGATTTCGG ACTCAGACAG TGATTTCAGAT TCAGACTCAG ATAGCGACTC AGATTCTGAC 240  
 5 AGCGATTTCAG ACTCAGACAG CGACTCAGAC TCAGACAGTG ATTCAGATTC AGACAGCGAC 300  
 TCAGATTTCAG ATnGCGACTC AGACTCAGAT AGCGACTCAG ATTCAGATAG CGATTTCGGAC 360  
 TCAGACAACG ACTCAGATTC AGATAGCGAT TCAGATTTCAG 400

(2) INFORMATION FOR SEQ ID NO: 4098:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 15 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4098:

TCGTACCTGA ACTACTTTGT ATTAAAATAG TTACAACGAT ACCTGCAATA ACACCTAATA 60  
 CTGGATTTCGA TGTAATTTG TTTAAAATAT CTCGTAGCCT GTCTCCTGCT GATGCTTGAA 120  
 25 GCCCGTCTCC CATGATTTTT AAGCCGTAAA GGAAAATACC TAAACCACCT AAAAAGGAGA 180  
 AAATGACTTC TGTAACCGAC ATTTCCATTA TTTCACCTCA AATAAGCTTT ATATTTAGAT 240  
 TATCGCTTAT AATTGTAAAT TTAATGTTAA GATTAGGTAA AATTATTTAA CAATATATGT 300  
 30 TATTTGTATA TGACTTGTA AATATCGTCA CTTATTATGT AAATTTTCAG TGGTGGAAT 360  
 GGCCAGTTTG CCAAGCACTG GTTTGACCA ATGGnGGCA 400

(2) INFORMATION FOR SEQ ID NO: 4099:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 base pairs  
 (B) TYPE: nucleic acid  
 40 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4099:

ATCCTTTTCC ACTTAACATA TATTTTGGGA CCTTACCTGG TGGTCTGGGC TGTTTCCGGA 60  
 CCGAACACGG nACCTTATCA CCCATGTTCT GACTCCCAAG TTAAATTAAT TGGCATTTCGG 120  
 AGTTTGTCTG AATTCGGTAA CCCGAGAGGG CCCCTCGTCC AAACAGGGCT CTACCTCCAA 180  
 50 TAATCATCAC TTGAGGCTAG CCCTAAAGCT ATTTCCGAGA GAACCAGCTA TCTCCAGGTT 240  
 CGATTGGAAT TTCTCCGCTA CCCTCAGTTC ATCCGCTCAC TTTCAACGTA ATCGGTTCCG 300



## (2) INFORMATION FOR SEQ ID NO: 4100:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4100:

TAGAACTTGT TGCCAAACAG CATGCTTAAT TTCAATATCT TCTTTGACTG CTTCGATATA 60  
 TAAATCAGCA TCATCATTTA CCAAGTCATC ATCAAAATTA CCATATGTTA AATGACTCGC 120  
 TAGATTTAAG TCGAATAGTA GCGGCCGTTT CTTATCTGTA ATTTTATCGT AAGATTTTTT 180  
 CGCAATGAGA TTTGGATCGT TTTTGTCCAC TACAATATCT AATAGTTTTA CTTTAAGTCC 240  
 AGCATTCAACA AAAAGTGCTG CCAGTTGGAG CGCCCATGTG GCCTGCGCCA AGAACGGnTA 300  
 CTTTATTAAT TGGTCATAGT GANTCCnCCC ATTTAGTTGA GGGATAAGAT AACCATT 357

## (2) INFORMATION FOR SEQ ID NO: 4101:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 346 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4101:

TAACTCAGGC TGGGGACATA AATCAATATT CTATGCTCTA CGAATTATAT TGGCAGTAGT 60  
 TGACTGGnCG AAAATGCGCT TGTAACAAGC TTTTTTCAAT TCTAGTCAGG GGCCCCAACA 120  
 CAGAGAATTT CGAAAAGAAA TTCTACAGGC AATGCGAGTT GGGGTGAGGG CCCCACACA 180  
 GAAGCTGACG AAAAGTCAGC TTACAATAAT GTGCAAGTTG GGGATGGGCC CCAACAAAGA 240  
 GAAATTGGAT TCCCAATTTT TACAGACAAT GCAAGTnGGG GTGGGACGAC GnGATAAATT 300  
 TTGCGAAAAT ATCATTCTCTG TCCCACTCCC ATCAAAAGAA TGACAT 346

## (2) INFORMATION FOR SEQ ID NO: 4102:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

AATGATGAAA ATCAATTAGA CAAAGCAGGT AAATTAAGTG ATGTCGCGTC ATTTAAGGAA 60  
 GCGATTCACA ATCGAGAATC ACAAAGTACA ACTGGTATCG GCGAAGGTAT TGCCATTCCA 120  
 5 CATGCCAAAG TGGCCGCAGT TAAGTCACCA GCTATTGCGT TTGGTAAATC TAAAGCAGGC 180  
 GTAGATTATC AAAGTTTGGG ATATGCAACC AGCACACTTA TTCTTTATGA TTGCAGCGCC 240  
 AGAAGGTGGC CCCAAACACA TTCTAGATGC TTTACTAAAG TTGnCTGGTA TTTTAATGGG 300  
 10 ATGAAAATGT ACGTGAGGAA ATnTTACAT GGCTTCATCA nCTGAAGAAG TACTAGCGAT 360  
 CAT 363

(2) INFORMATION FOR SEQ ID NO: 4103:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4103:

25 GAGTGCAGCG GATAACATTA AACCGACGAC AnCTTTTTTA TGTTcAGGTT TAGCTGTGTG 60  
 ATAAATTGCA AGTGCggCAC CACATAAGCC GAACATCATC GTAATAAAAC GGCCTGACAT 120  
 AAAGCGTGAC ACACCTGAAT AATACTTCGT CACATCTGga TCACCAAGTT GAGCAAAGAA 180  
 30 GATGTTCTGC GTACCTTGAA CTAAGTGCCC TTTGACTTCT AAAGTACCAC CAAGTGCCGT 240  
 CTGCCAAAAC GGTAAGTAAA AAATATGGTG TAAACCGAGT GGACCTAACA ATCTTAAGAT 300  
 GAAGCCATAA rCAAAAGTAC CsGTTGGcAC CTGTTtTCGT TACAAATCCA CCAACATGek 360  
 35 AaTGCCGgTT TGTATGGTTG GcCCAAnTGA nAACATCATA 400

(2) INFORMATION FOR SEQ ID NO: 4104:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 358 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4104:

50 AATTGAGAAT TTGTCGCTAT TTGTAAATTG TATCCTGGCT TAAGTTGGCC AAAGTGTCTT 60  
 ATTTTTTTAA AGTATTTAAA AGTAAAATTA CATGTTAATA CGTATATTAA TTGGCGAGAC 120  
 TCCTGAGGGA GCAGTGCCAG TCGAAGCAGG GGCCCCAACA CAGAAGCTGA CATATAGTCA 180

CAAAAATTCT ATTTATAGAA TTTTACAGTA ATGTGCCAGA TGGGCATAGC GACCCATTCA 300  
 ATACGAnTAT nTGAnTAAAT AGAGAACAGC AGTAAGATAT TTTCTAATTG AAAATTAT 358

(2) INFORMATION FOR SEQ ID NO: 4105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4105:

GACGCGTTAC CAAATGGCGG AATTAAAGCA AAATCTTCAA TTTCAATGAA CAATGTGACG 60  
 TATACGACGC AAGACGAACA TGGTCAAGTT GTTACAGTAA CAAGAAATGA ATCTGTTGAT 120  
 TCAAATGACA GTGCAACAGT AACAGTGACA CCACAATTAC AAGCAACTAC TGAAGGCGCT 180  
 GTATTTATTA AAGGTGGCGA CGGTTTGTGAT TTCGGACACG TGGAAAGATT TATTCAAAC 240  
 CCGCCACATG GGGCAACGGT TGCATGGCAT GATAGTCCAG ATACATGGAA GGAnTACAGT 300  
 CGGTAACACT TCATAAACT GCGSTTTGTn ACCATTACCT AATnGTCAAG GGTACGGCGT 360  
 TAATGTTTGA AGGTTCCCGT TCCAAGGTTT TTTCCCGTTT 400

(2) INFORMATION FOR SEQ ID NO: 4106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4106:

GAAGTTAAGC TCCTTAGCGT CGATGGTAGT CGAACTTACG TnCCGCTAGA GTAGAACGTn 60  
 TGCCAGGCAG TTTTTTAATC AAATTTTGGT TAAAAAATAA AATGGACAAG ATAAAAAAG 120  
 TTATTGACTT AAATGTTAAT AAAATGTATA ATTAATTCTT GTCGGTAAGA AAAATGAACA 180  
 TTGAAAACTG AATGACAATA TGTCAACGTT AATTCCAAAA AACGTAAC TAAGTTACAA 240  
 ACATTATTTA GTATTTATGA GCTAATCAAA CATCATAATT TTTCATGGGA GAGTTTGGAT 300  
 CCTGGGCTCA GGATGGAACG CTGGGCGGCG TGCCCTAATA CATGGCAAGT CnGAGCGAAC 360  
 GGGACGAGAA GGCTTTGCTT CTCCTGGATG TTAACCGGCh 400

(2) INFORMATION FOR SEQ ID NO: 4107:

- (A) LENGTH: 343 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4107:

10 GATTGTGCCA CGCTTTTAAC CGAAATACAA CATCATCATT GACAATTTGT TGATTTGAAA 60  
 AATCTTTCTC TTCAATAAAT ACATACGTTT GCATCGTATG TGCTTTCATG TAACTCAATA 120  
 TTGGTTTTAA ATGCATTTCA GGAATTAAAT AATGTTTACT AGAACCTGCT GTCGCTACAA 180  
 15 GTCCTATTAC CTGTGCACGA AACGCATTGA CTGGAAGTAG ATCAAACACA TTTnnCAAAG 240  
 CACCAGGGAT GGAAAGCTTG AAAAATTGGA AAACCAATAA AATCACATC AGCCTGCATT 300  
 AACGACGTCG TTAATTTATA TACATCTCCT GTAGTATCTA Gnt 343

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## (2) INFORMATION FOR SEQ ID NO: 4108:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4108:

30

ATACAAAACA CCAGGTCGTG AAGATAAACA ATCACAAGCG GCTACTGCTT CAGCAACTGA 60  
 ATTACCATAT GCAGTATTAG AAGCTATGGG TGGCAAAGCA AACATTAAAC ATTTAGACGC 120  
 35 TTGTATCACA CGTCTACGGT TGAAGTTAAC GACAAATCTA AAGTTGATGT TCCTGGTTTG 180  
 AdAGATTTAG GCGCATCTGG TGTATTAGAA GTCGGCAATA ATATGCAAGC AATTTTTGGT 240  
 CCTAAATCTG ACCAAATCAA ACATGAAATG CAACAGATTA TGanTGGTCA AGTAGTAGAA 300  
 40 AATCCTACTA CTATGGAAGA CGATnAAGAC GAACTGTTG TGGGTTGGCA G 351

40

## (2) INFORMATION FOR SEQ ID NO: 4109:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4109:

CCTTTTTCAA AATCATTGGA TGCATCGATA AATAGTACGT TGTCGTCTTG TTGGCGACAT 60

55

CCAATCACGG CTTCTAAGTA GTTCTTTTCT TCTATTAAAT AGCGACGnAT CACACCTTCT 180  
 GCGGCACCAC GGAATAATAC ACCATGTGGG AGTACGACTG CnATGGTACC TTCATCGTCT 240  
 5 AAGGTAATGT ACCCTGTGGT TGAATAAAGG CAAAATCTGC TTTGGGATTT TGGCGCAACT 300  
 TTGCCCGTAA CCACTGAATC GTTCATCATT TTCAAATTTT TGAATCnGCT GGTCCATTCG 360  
 CACTGTA 367

(2) INFORMATION FOR SEQ ID NO: 4110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4110:

GTCGTCCGAT TGAAGGATGG AGTACTGTCTG CATTTGCGAA AGACTGGCAA GGACCACCAC 60  
 GTTTGCAAAA CGGAACAAGT TGGTTCTATT TTGCAACAGA CCAATGGAAA TATGAAGAGT 120  
 25 CAAATGTAGA TCGTTTAAAA TCTCCATTAG CTAAACAGA GGAGTTAAAG CATCAACATC 180  
 CAGCTGATTA TAATGTTTTA GCAGCTAGAC TTGGTTGGTT ACCATCATAT CCACAATTTA 240  
 ATAAAAATAG TTTGTTGTTT GCAGAAGAAG CTAAAGATGA AGGTATAGAT TCAAATGAAG 300  
 30 CGATTTTGCC ACGTGCAATT GATGAAGTGA ATCAAACCA AACACCATTT GCCATANGAA 360  
 AATCCTGATT TGGAAAAGGA TCCTnCCAAA ATCCAnnATT 400

(2) INFORMATION FOR SEQ ID NO: 4111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4111:

TCAGATGAAG CTAAAGTAA AGGTATTACA TGTGCAAGTG CAGGTAATCA TGCTCAAGGT 60  
 GTTGCCTATA CAGCTAAAAA ACTTAATTTA AACGCTGTTA TCTTTATGCC AGTCACTACA 120  
 CCTTTACAAA AGGTAAATCA AGTAAAGTTC TTTGGAAATA GTAACGTTGA AGTTGTACTC 180  
 50 ACTGGTGATA CATTTGATCA CTGTTTAGCT GAAGCTTTAA CTTATACAAG TGAACATCAA 240  
 ATGAACTTTA TAGATCCATT CAATAATGTT CATACAATTT CTGGACAAGG TACGCTTGCT 300

AATTGGTGGT GCGGTTTTAA TTTCCAGTAT TAGTACTAAC

400

## (2) INFORMATION FOR SEQ ID NO: 4112:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 362 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4112:

GCCCTTAATA ACTTAATCTA TGTTCACC ACCATTTTATAA GTCAAACGCT CACATACGGC 60  
 TTCGTTTTCA TTATTTTAAA TGCTCATTTA CATAAGTAAA CTCTGCTTTA AAATAATTTA 120  
 ACTCATTGTC TGCTAAACGT TTTCTTTTAT AAAAAGATTT AAACGCGTTA TTAATCTTGT 180  
 GAGTGTTCCT TCGAACACTA GCGATTATTT CTTATGAATT CAAGCTTATT TAAACTCTTT 240  
 TATTCACCTCG GntTTGCTTG GGAAAATCTA TATTTTACnT ACTTATCTAG TnTTCAATGT 300  
 ACAATAATG GTGGGCCCAA GTGGACTCGA ACCACCGACC TCACGCTTAT CAGGGCGTGC 360  
 GG 362

## (2) INFORMATION FOR SEQ ID NO: 4113:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 363 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4113:

CAGGTGGTTT TCGGAAAAGT GAAGTATGGC GTCAAATGAT GTCAGATATA TTTGACACAG 60  
 AGTTAGTGGT TCCTGAAAGT TATGAAAGTT CATGCTTAGG TGCCTGCGTG CTCGGACTTA 120  
 AAGCTGTAGG TGACATTGAA GATTTTTCAA TCGTTTCATC GATGGTCGGT GCCACAAACA 180  
 ATCATACGCC GATTGAAGAA AATGTCCTG TTTACCAAGA GATCGTATCC ATTTTATCA 240  
 ATTTAAGTCG TTCTTTAACA GAGAATTATG ACAAATTGCA GATTTCAACG CCACATATCG 300  
 CTGAAATAAA ACnCCATAAA TACGnCACTC AAGCATCTTA GATAAAGTTG TnGGCCATGC 360  
 TAC 363

## (2) INFORMATION FOR SEQ ID NO: 4114:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 394 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4114:

	GGTCTGGGCT TGGTTCCGGT TCTGGGTCTG GACTTGGTTC TGGATCTGGC GTTGGTTCTG	60
10	GTTCTGGGTC TGGACTTGGT TCTGGGTCAA CCGGCGGCC TGGAGTTGGG TCTTTCGGAT	120
	TTACTGCTGA ATCACCATCA GCACTTCCAC CACCATAACG TACAACATTC TCATTATTCC	180
	AACCGAAAAT ACTGTAGTCT CTATTTGTGA CAGGATCAAC ATTTTCTTGA ATAACCTGAG	240
15	TTTTTAAGTT CTTACCTGTA TTGTCGTAAT GCCCTTCTAC TAATACTACA TATGTTTTAG	300
	TAATATCACC AAATTAATAC TAGCTACATT GGATGcncAT AATAGATCTA TTTTAAATGG	360
	nCTGTACTCC TTAAGGTAGA GCATTGGACT GCAn	394

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(2) INFORMATION FOR SEQ ID NO: 4115:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4115:

	GGCGATTATA TTAAAAAGCC AATTACAGAA TGTAGTGGTA ATGAAATATG CCAAGAATGG	60
	CTGTATCACT TAGGTGTATC AACTGACAAA ATTGAAGACT TAGCAAAACA TGCATCTAAT	120
35	ACGATTCCTG TTTATATGCC ATATATCACA TCTTATTTCA TGACGCGTGC TATCGGCGAC	180
	AGACCTTTAG TCGTCCCGCA TCAATCTCAG AACTTAGCAT TTATTGGTAA CTTTGCCAGA	240
	AACAGAGCGA GACTGTAT TTACAACAGA ATATTCGGTT CGTACTGCCA GGAAGCTGT	300
40	TTATCAATTA CTAAATATAG ATCGTGGTAT TCCAGAAGTC ATCAATAAGT CCATTGGATC	360
	TTnCGCGTnC TTAATGGGAT GGCCATATAC GAACTGGATG	400

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(2) INFORMATION FOR SEQ ID NO: 4116:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4116:

55

TTAAAGGGCG AAATAGAAGT GCCGGGCGAT AAGTCAATGA CACACCGTGC AATCATGTTG 120  
 GCGTCGCTAG CTGAAGGTGT ATCTACTATA TATAAGCCAC TACTTGGCGA ATGTCGTCGT 180  
 5 ACGATGGACA TTTTCCGACT GTTAGGTGTA GAAATCAAAG AAGATGATGA AAAATTAGTT 240  
 GTGACTTCCC CAGGATATCA ATCCTTTAAC ACGCCACATC AAGTATTGTA TACAGGnAAA 300  
 TTCnGGGTAC GACAACACGA TTATAGGTTG TTAAGTGGGT TAGGTATTGA AAGTGGTTTG 360  
 10 GTCnGGGCGA ATGTTTTCCA ATTGGGTAAA AGGCCCATGG 400

## (2) INFORMATION FOR SEQ ID NO: 4117:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 389 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4117:

AATAAAAAGG AACAAAACGA TGGCTATTGA TATGGACACA AATCATAAAT AGCTGCTTTG 60  
 25 TTCCTTTTTT AATTTATATA TTTAnAATAC ACATATTCAA GAGCCTCGAG ATATAAGTCA 120  
 ATGTACTAGG CCACACAATT TAATATTGAC AGTAATTACC CGAACGAAAA TCGCCCCCGG 180  
 30 GGCCCCAACA TGGGGAATTT CGAAAAGAAA TTCTACAGAC AATGCAAGTT GCGGGGGCCC 240  
 CAACATAGAA GCTGGCCAAT AGTTAGCTTT CAATAATGTG CCAGTTGGGG TAAGGGCCCC 300  
 AACACAGAAG CTGGCCAATA GTCAGCTTTC AATAATGTGC CAAGTTGGGG TAAGGGCCCC 360  
 35 CCACCACAGG GAATTCGAA AGAAATnCT 389

## (2) INFORMATION FOR SEQ ID NO: 4118:

40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 371 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4118:

AGGTAGGACT CGAACCTACG ACCGATCGGT TAACAGCCGA TAGCTCTACC ACTGAGCTAC 60  
 50 TGTGGATTAA TATTATGCCT GGCAACGTTT TACTCTAGCG GAAnTAAGTT GACTACCATC 120  
 GACGCTAAGG AGCTTAACTT CTGTGTTCCG CATGGGAACA GGTGTGACCT CCTTGCTATA 180  
 GTCACCAGAC ATATGAATGT AATTTATACA TTCAAACTA GATAGTAAGT AAAAGTGATT 240

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ACATGTCACC ATGCTTCCCA CCTCGAACCT ATTAAACCTC AnCATCTTTG AAGGGGATCT 360  
TATnAACCGA A 371

5 (2) INFORMATION FOR SEQ ID NO: 4119:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 341 base pairs  
(B) TYPE: nucleic acid  
10 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4119:

GCACTATTAG CCCAGTTAGA GAAAGATTGA CCTAATCTAT CCAACCAATC AGCCGACCAT 60  
TGAAACAGTG GTGCTAATTG CCGTGAATAC ATTGACTAAT CCGTCACCAA AACCACCTGC 120  
20 AGCACTTAAT AGCTTGTTAA ATACCGAAAC ACCCGTTGTA TTCATCATAT TAAAGAATCT 180  
TGAAGCTACA CTGCTATTTT CAGCCCATtn AAGCACGCTT TGAGACGCTT CTTCCATTCC 240  
TCTTGAAATA CCACTAAAAA ACGGnTGTA GCTCTGCATT GCAGTTTTAA CAGTATTTAA 300  
25 ACCATTTGCA AGAGTTGTGA AGnTAGCGGA TTGATTTTGC T 341

(2) INFORMATION FOR SEQ ID NO: 4120:

- (i) SEQUENCE CHARACTERISTICS:  
30 (A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4120:

GGTTGAGAAA AGCCAACACA GCTAGGGTAG TATCCCACCA GCGCCTCCAC GTAAGCTAGC 60  
40 GCTCACGTTT CAAAGGCTCC TACCTATCCT GTACAAGCTG TGCCGAATTT CAATATCAGG 120  
CTACAGTAAA GCTCCACGGG GTCTTTCCGT CCTGTCGCGG GTAACCTGCA TCTTCACAGG 180  
TACTATGATT TCACCGACTC TCTCGTTGAG ACAGTGCCCA AATCGTTACG CCTTTCGTGC 240  
45 GGGTCGGAAC TTACCCGACA AGGAATTTG CTACCTTAGG ACCGTTATAG TTACGGCCGC 300  
CGTTTACTGG GGCTTCGATT CGTAGCTTCG CAGAnAAACG CACTTCCTGT TAAACCTTTC 360  
50 CAGCACCGGn CAGGCGTTCA CCCTnATTAC ATCAACTTTA 400

(2) INFORMATION FOR SEQ ID NO: 4121:

- (i) SEQUENCE CHARACTERISTICS:  
55 (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4121:

AATAAATCTT GCTTTATTCT TTTTACCACT AATATCTAAA TGAGTTGGAT ATTAACTTT 60  
CGCATTAAATT TCAATATTAA ATTGCGTTAC CGCGACAAGC GCAAACACAA CATAcataAT 120  
AAGATTGGCT AAAAAGATAT AGTTAAAGCT AAATTCTGCG ACAAAGCCGC CCATTGCAGC 180  
ACCGACAGCC ACACCAATAT TTTGCGCTAA GTATATCGCA TTAAACGTTT GTCTTCCGCC 240  
ATTGCGCCAC ACTGCTCCAG CCATAGCGTA TATCGCAGGA ATAATCATT CCGCCACCAA 300  
CCCTAACATT ACCAGGCCAT ACCAGCATA CCGGGCCAC CCGnGGAAGG AAATTAAGTA 360  
GCGGTGGTAC TACCAAnGAC CAGTGGAAGG TnCCAATTAA 400

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(2) INFORMATION FOR SEQ ID NO: 4122:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 362 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4122:

GATAACTAAT AAAGTTTAGT TAAGTATTTT AATAACAAGT AGTATGTCAT TCTAGTAGCT 60  
AGAACAGATA TACTACTTGT TTGTTTTTGT GGAAATTTGA GTATATTCAA AAGGATAAGn 120  
ACGAGAATTT CGTTATTAAA CTACGAATTC TCGATTTTTT TATATTTTAA GATAGGTTTA 180  
TTTCTGAAAA CTTAATAGAA AGGGGTTTGA CAAAGCTAAA GTGAAGTTTG ACGgTATAAA 240  
CGCAAATTAA ATATACTTTT ATAGAAAATT AACTCAGGCT GGGACATAAA TCAATATTCT 300  
ATGCTCTACG GAGGTATATT GGCAGTAGTT GACTGAACGA AAnGCGCTTG TnACCAGCTT 360  
TT 362

45

(2) INFORMATION FOR SEQ ID NO: 4123:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 352 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4123:

55

CGCGAGGTGG TTTACAAGGA TTGTTGACAT TTCAAGACTT ACCAGTAACA AGTTATACAA 120  
 TCTGGGGTGG TGTCTCAGAT ATTGATTAA TGTATGAAGA ACGTGTGAT TTAAGAGGCA 180  
 5 TGCTACGAAG AATGATTGGT CATCCGAAAA AAGATCGAGC GGGCATATGA GGCACGCCAA 240  
 GCGATTCCAA ACATTAATGA NAACAGTCCG CCAATATTAA TTGTACATnG GAGGGGAAAAG 300  
 10 ACCCAGCAAG TTGGGTATTn CATCATGCGT ATTATTTTAA GCGGACCAAC TA 352

## (2) INFORMATION FOR SEQ ID NO: 4124:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4124:

AACCAGGTGA TCTACCCTTG GTCAGGTTGA AGTTCAGGTA AACTGAATG GAGGACCGAA 60  
 CCGACTTACG TTGAAAAGTG GAGCGGATGA ACTGAGGTA GCGGAGGAAA TTCCAATCGA 120  
 25 ACCTGGAGAT AGCTGGTTCT CTCCGAAATA GCTTTAGGGC TAGCCTCAAG TGGATGATTA 180  
 TTGGGAGGTA GAGCACTGTT TGGACGAGGG GCCCCTCTTC GGGTTTACCA ATTTAGACA 240  
 AACTCCGAA TGCCAATTAA TTTGAACTn GGAGTTCAGA ACATGGGTGA TAAGGTCCnT 300  
 30 GTTTCGnAAn GGGAAACAGC CCAGACCACC AGTTAAGGTC CCCAAATGTA TGTTTAAGTG 360  
 GAAAAGGGTT TTGGCGTTGC CCCGACAACT AGGATGTTGG 400

## (2) INFORMATION FOR SEQ ID NO: 4125:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4125:

GGCTTATTAA TCAAAAAATT TATAAGAAT ATGTAGAAAA CTTTTATTTA CATCGAGGCT 60  
 ACACGCTACA ACAGAAAATT AAAATTTTAA TTAGCTTATA CATTGTAATA GGTTTTTCAA 120  
 50 TTTATATGGT GGATGTTCTT GCAGTCCGTG TAGGATTAAT CATAATGGTT ATCATACTAA 180  
 CCGCTGTACT CTTTACATTT GTAAAAACAT TACCCAAATC AAATCATAAA ATAGAGGAGT 240  
 GATTGCCCAT GTTTATGGCA GAAAATAGAT TACAATTACA AAAAGGCAGT GCGGAAGAAA 300

TTGTCATAA AACATTAAAT ACCGGGATAC AGCCGAGTAA

400

(2) INFORMATION FOR SEQ ID NO: 4126:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4126:

15	AATCTATATT TTACTTACTT ATCTAGTTTT CAATGTACAA TTTCTTTTTA GTCAAGCGCT	60
	CGCATAAGCA ATATCACTTT AACCAAAAAA TATTTGAATG TTAAATAAAC ATTCAAACCT	120
	GAATACAATA TGTACATTA TTCCGCATCT TCTGAAGAAG ATGTTCCGAA TATATCCTTA	180
20	GAAAGGAGGT GATCCAGCCG CACCTTCCGA TACGGCTACC TTGTTACGAC TTCACCCCAA	240
	TCAATTTGTCC CACCTTCGAC GGCTAGCTCC TAAAAGGGTT ACTCCACCGG CTTCGGGTGT	300
	TACAACTCT CGTGGGTGTG GACGGGGCGG TGTGGTACAA nGACCCGGG AACGThATTC	360
25	AnCGGTAGCA TGGCTGGATC TAACGATTTA CTAnGCGGAT	400

(2) INFORMATION FOR SEQ ID NO: 4127:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4127:

35	CGAAATTTGT AGTAAAGAT GTGCAACCAG CGAAACCAAC TGTGACTGAA ACAGCGGCAG	60
40	GAGCGATTAC AATTGCACCT GGAGCAAACC AAACAGTGAA TACACATGCC GGTAACGTAA	120
	CGACATACGC TGATAAATTA GTTATTAAAC GTAATGGTAA CGTTGTGACG ACATTTACAC	180
	GTCGCAATAA TACGAGTCCA TGGGTGAAAG AAGCATCTGC AGCAACTGTA GCAGGTATTG	240
45	CTGGAACTAA TAATGGTATT ACTGTTGCAG CAGGTACTTT CAACCCTGCT GGATACAATT	300
	CCAAGTTGGT TGCAACGCCA AGGAAGCGGA GAGACCAGTG AAGTGATTGA GCCACCGTAA	360
50	TGGTTGGnTT CCCCAGTTTG TCGGCAnCCA CAACCGGAAC	400

(2) INFORMATION FOR SEQ ID NO: 4128:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4128:

	GATTAGTGAA AAGTTGGTTG TACTATTACC GTTAAAATTT GGAGATTATC TGTCGTCTTC	60
10	AAGTATGCGT TCATTAAATTG ATATTGGCGC ACCGTATAAC CATGTCAAAG TACCATTTCG	120
	AATGCAGTCA TTAGGCGCAT TAAGGCTAAC GCCTACGCGT TACATGAAAA ACGGAGAACA	180
	AGCAGAACAA TTATTACGTC AGCTTATAGA AAAAGATGAA GCACTAGCTA AGTATGTCAT	240
15	GGGTTGTGAT GAAACAGCTT GGTGGTCATA TATGGGTCCA GATAATGATA TTTTCCAAGA	300
	TCCATTAnGG CCATCTAACT GTTCCAGCTA AGGAAAGTAT CCCCGAAGTG GCTAAGCCCA	360
	AAAATGATTA CGCCAACCAG CTAGTGGTCC ATnGGCCAGC	400

20

(2) INFORMATION FOR SEQ ID NO: 4129:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 374 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4129:

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	AGAGGTCGGT TGCCTTACCG CTTGGCTATA GCCCAATATA TAGATGGnGG AGGGGGGCAG	60
	ATTGGAActG CCGAACCCGA AGAGCGGATT TACAGTCCGC CGCGTTTACC ACTTCGCTAC	120
35	CCCTCCAGCT TATTCATATA ATTTAATAAT CAAAATGGTG GAGAATGACG GGTTCGAACC	180
	GCCGACCCTC TGCTTGTAAG GCAGATGCTC TCCCAGCTGG AGCTAATTCT CCAAAATAAT	240
	GACTCCTGAC GGGACTCGAA CCCGTGTTAC CGCCGTGAAA GGGCGTGTTT TTGAACCGCT	300
40	TGGACCAAGG GAGCCATGGC TCCAACAGGT GAGGGACTCG AACCTnACGG ACCGATTCCG	360
	TThAACAGCC GGAT	374

45

(2) INFORMATION FOR SEQ ID NO: 4130:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 431 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4130:

55

ATTAAATTC AGTTGTTGCA ATTCCTTCAT CTGTAGGTAC ATCATCGTTA AGGCCAACAA 120  
 GTGCTTCAGA AACATTTTCGT GAATGATAAC CGATACGTTT AAGAACrCsA ATCATATCGA 180  
 5 TATATAGTAA TCCGCCTTTT GTTGTACATT CACCACGATT AAGGCGTTTA ATATGACCTT 240  
 TCGGTAGTTT ATGTTCAATA TTAAATGATT CTCTACTACG TTCTACAATT TCATCTTTTT 300  
 10 TCGTTTTGTC ATAAACATCT AACATGTCGA TGGCTTTATC AAATGACTCA GCAACATGGT 360  
 TCGAATAAAT TATCCATACC GCGTTGTGCA TCTnCTGGTA ATGCGAATAT CTTTCATCATG 420  
 TTGGCGGTTT T 431

## (2) INFORMATION FOR SEQ ID NO: 4131:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4131:

TTTAGTTGAA GCGCGTGTG TCGCATTGTC TGTTTGTGTC GGTGCTTCTA CTTTAGTTGA 60  
 GGGCGGTGTT GTCGCGTTTG GTTTTGATTG CGGTGCTTCT ATTTTAGTTG AGGGCGGTGT 120  
 25 TGATGTGGTG CTTCCACTTT AGGnAAATGA GTGTTGTCGC GTTTGCTGCT TGCCTGTGCG 180  
 30 TTGTGATTAC ACCTGTTGTT AAAAGGCCTA GTGCTAAACT TGTTTTAGCA ATCGTTGTTA 240  
 TTTTCATAGT TGTATGCTCC ATTCGTAATT ATTAGATTTG TTCGATACAT TCATTGAATC 300  
 ATACAGCTTT ATTATAGAGG CGTATTGCTC CATTACATT AAACCTGTnT AACCAGATTG 360  
 35 GAAGCAGCGT TGAATnAAAT GAAGAAAGCC AGAAGTTCGT 400

## (2) INFORMATION FOR SEQ ID NO: 4132:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4132:

CCATTCAGTG TATGCTTTTG GCCACCACCT TGACGTTGTT GTTGCTGTTG TTGATTTTGA 60  
 50 TTAGCTTGTT GTTGATTTTG ATTATTTTGT GCTTGATTGT TCGCTTGATT AGCGTTGTTT 120  
 TGATCATTAT CAGATTCATC TTTAGTCGCT TTGCTTGAT CCTCTTTTGA TTTATCACTG 180

TCAGCATTAT TTTTATTTGT ATTGCGGATT TTATTTTCTT TTGTACCATT ATTATGATTG 300  
 TTTAATGCCA TGCCTCCAAA TATCGCTAAA TGCACCGATA AATnAGTACA GCTGCAATGA 360  
 5 ATGTAACAA TACTTTGGGC CAGnCACCGT TTTTACGGTn 400

## (2) INFORMATION FOR SEQ ID NO: 4133:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 417 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4133:

TTGAATACTT TTCTTCACA CAAATGTATA TCTATTGGCA TTAGCTTCTA CTTTTGTACC 60  
 20 ATCAATAAAA ATTGAATTAT TATCAATAAG ATTTTGCTTT AAACATTGAC TATGGAAGTG 120  
 AATAAATAAA GATTCAATTA ACGCATCAGT ATTAGGATTC ACTCTAAAC GATTAATAGT 180  
 TTTATAAGAA GGTGTTTGAT TTTGAGCTAA CCACATCATT CGAATACTGT CATGAAGTAA 240  
 25 TTTCTCTATT CTTGACCAG AAAATACAGA TTGAGTATAT GCATATAAGA TGATTTTAA 300  
 CATCATTTTT GGGATGATAG GATGTTGCGC CACGATGATG TCTGAATTCA TCGAATTCGC 360  
 TAnCGGGTAC CGTCCACCA ATTCCATTAA CATATCGCGG AATATCATTT TGAGGAA 417

## (2) INFORMATION FOR SEQ ID NO: 4134:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 354 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4134:

GGTTTAATAT GGACCTTTGC CGTnTTTATG TTCAATATTA AATGGATTCT CTAACGTT 60  
 CTACAATTTT ATCTTTTTTC GTTTTGTCAT AAACATCTAA CATGTCGATG GCTTTATCAA 120  
 45 ATGACTCAGC AACATGGTTG nAATAATTTA TCCATACCGC GTTGTGCATC TTCTGTAATG 180  
 CGnAATATCT TCATCATGTT GGTCGTTTTA ATTGAGCGAC ATACTCTTCT GTTAGCTCTG 240  
 CTACTTTTAA AATAGAGCGA TTGACATCAA ACATAACTGC TAAACGCTCA ACGTCTGCCT 300  
 50 TCGTAATGGC TTTTGTAGAA ATTCTAACTA AATAATTTTC AATGCTATCA TTGT 354

## (2) INFORMATION FOR SEQ ID NO: 4135:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4135:

10 CTGGGATCGC CACCTTTAAG TCTAACCAACC TTGTTATATC GACGCGCTGC TTCCACGATA 60  
 CAGTCATTTA TTTTCTTCTG CTGAATATGT TTTGCATACG GCTTTTTTACC AACATCGATA 120  
 ATTTCAAGTAG TCAAATTCGC ATATTGTAAA ATTAACGGAT TCACTAATCG ATCATATAGA 180  
 15 ATGACATCCG CTTACGTAT TAAACGCTCA GCCTTTTTCG TCAAATAATT CGGATTACCT 240  
 GGACCCGCAC CTATCAAGTA AACCTTGCCA TATTCCTCTA CAGACATATA TATACGGTCC 300  
 20 CGTCTGTAAC TTCTACCTCA TAAACATCTA CACAACCTTC ATCAGGTCTG GACAATACCT 360  
 GATTAAACA ATTTTGTATC GTGGGGGGGC AAATACATAT 400

## (2) INFORMATION FOR SEQ ID NO: 4136:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4136:

35 ACCACTGAAT CGTTCATCAT TTTCAAATTT TGAATCTGCT GTCCATTTTCG CACTGTATGG 60  
 TGGGTTTCGCA ATAACCGCAT CAAATGTATT GCCTAAAAAG GCTGGATTTT CCAATGTGTC 120  
 ATCATTACGG ATCTCGAAGT TCTCATAACG CACATCATGT AATAACATAT TCATGCGTGC 180  
 40 TAAGTTGTAT GTAGTATTGn TACGTTCTTG TCCGAAATAA CGATACACTT GCGTTTCTTT 240  
 ACCAACACGT AACAACAATG GAACCGGAnC CACATGTTGG GTCGTACACG TGGACGTAAT 300  
 TTATChTTAC CGTGCTGTGA CAATCTTCGC CAGTATCTTA GATACTTG 348

## (2) INFORMATION FOR SEQ ID NO: 4137:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4137:



TGGACAATAC AAAGGGCAGC GAAACCGCGA GTCAAAGCAA ATCCCATAAA GTTGTTCTCA 120  
 GTTCGGATTG TAGTCTGCAA CTCGACTACA TGnAAGCTGG nAATCGCTAG TAATCGTAGA 180  
 5 TCAGCATGCT ACGGTGAAAT ACGTTCCCGG GTCTTGTA CAACCGCCCGT CACACCACGA 240  
 GAGTTTGTAA CACCCGAAGC CGGTGGAGTA ACCTTTTAAG GAGCTAGCCG TCGAAAGTGG 300  
 GGACAAATGA TTGGGGTGAA TCGTAACAAG GTAAGCCGTG ATCGGnAAGG TCGGGCTGGG 360  
 10 AT 362

## (2) INFORMATION FOR SEQ ID NO: 4138:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 384 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4138:

ACATATCGAT AACATGACAT AACTCATGCT GGGTTTCCCC ATTCGGAAAT CTCTGGATCA 60  
 25 AAGCTTACTT ACAGCTCCCC AAAGCATATC GTCGTTAGTA ACGTCCTTCA TCGGCTTCTA 120  
 GTGCCAAGGC ATCCACCGTG CGCCCTTAAT AACTTAATCT ATGTTTCCAC CATTTTTATA 180  
 30 AGTCAAACGC TCACATACGG CTTCGTTTTT ATTATTTTAA ATGCTCATT ACATAAGTAA 240  
 ACTCTGCTTT AAAATAATTT AACTGCATTG TCTGCTAAAC GTTTTCTTTT ATAAAAAGAT 300  
 TTAAACGCGT TATTAATCTT GTGAGTGTTT TTTCGAACAC CAGCGATTAn TTCnTGAGGA 360  
 35 ATTCAAGCCT AntTAAACC CTTA 384

## (2) INFORMATION FOR SEQ ID NO: 4139:

40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4139:

CTCATTATGG GACGTGCACA AGATGGTTTT CTTGATCAAG ACAAATATGA CATTATTTTC 60  
 50 AAAACAGCTG AAAATTTAGA CGTACCGATT TATCTACATC CCGCGCCAGT TAACAGTGAC 120  
 ATTTATCAAT CATACTATAA AGGAAATTAT CCTGAAGTAA CTGCGGCAAC ATTTGCTTGT 180  
 TTTGGTTATG GTTGGCACAT TGATGTCGGC ATTCATACAA TACATCTnGT nTnATCTGGT 240

55

TCCTTAGAAC GAATGGATGA AGCTTATCCG TGAACATTG AACCACCCCG GAAGCAATAC 360  
 TTAAAAATAA ATTTAATATC ACACCGGGTG GCATGGTACC 400

(2) INFORMATION FOR SEQ ID NO: 4140:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4140:

CAACCACATT CGCTCGGCTC ACCTTAGAAT TCTCATCTTG AACTACCTGT GTCGGTTTGC 60  
 GGTACGGrCA CCTATTTTCT ATCTAGAGGC TTTTCTCGGc AGTGTGAAAT CAACGactCG 120  
 AAGACTCAAT GTCTTCTCCC CATCACAGCT CAGCCTTAAC GAGTACCGGA TTTGCCTAAT 180  
 ACTCAGCCTT ACTGCTTAGA CGTGCAATCC AATCGCACGC TTCGCCTATC CTA CTGCGTC 240  
 CCCCCATCGA TTAAACGAT TATAGGTGGT ACAGGAATAT CAACCTGTTA TCCATCGCCT 300  
 AAGCCTGTG GGTCTAGCTT AAGGACCCGA CTAACCCAG AACC GGAAGA GCCTTCCTCT 360  
 GGAAACCTT AGTCAATCCG TTGGACCGGG ATCTCAACCG 400

(2) INFORMATION FOR SEQ ID NO: 4141:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4141:

CATATCGATA ACATGACATA ACTCATGCTG GGTTTCCCCA TTCGGAAATC TCTGGATCAA 60  
 AGCTTACTTA CAGCTCCCCA AAGCATATCG TCGTTAGTAA CGTCCTTCAT CGGCTTCTAG 120  
 TGCCAAGGCA TCCACCGTGC GCCCTTAATA ACTTAATCTA TGTTTCCACC ATTTTATAA 180  
 GTCAAACGCT CACATACGGC TTCGTTTTCA TTATTTTAAA TGCTCATTTA CATAAGTAAA 240  
 CTCTGCTTTA AAATAATTTA ACTCATTGTC TGCTAAACGT TTTCTTTTAT AAAAAGATT 300  
 AAACGCGTTA TTAATCTTGT GAGTGTCTT TCGAACATAG GCGGAGTATT TCTTAAGGAA 360  
 TnCAAGCnTA TTTAAACTC TTAATCACnT GGTTTTGCnT 400

(2) INFORMATION FOR SEQ ID NO: 4142:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4142:

10 GTTGCCTCT TTTCTCGTTT CGTCAGATTC AAACGTTTTC ACTTCGCCAA GCCATTTTTC 60  
 TTTGTGTTTA CTTTTATTTT TGACGTTTTA GACATAAAAA AAGAGACCTC ACGGTCTCAA 120  
 CTTGCCTGGC AACGTTCTAC TCTAGCGGAA CGTAAGTTGG CTACCATCGT CGCTAAAGAC 180  
 15 CTTTCTTGAC TTGTGACAAT CGCTTGCTTC TTTCCTCTCC TTCGGCTCTC GCTTACTCAT 240  
 TTAGCTCTAC TAAACTCGTT GCGCTCTTTT CTCGGTTCGT CAGATTCAAA CGTTTCACTC 300  
 GCCAAGCCAT TTTCCTTGGG TTACTTTTAA TTTGACGTTT AAGGCATAAA AAAAAGAGAC 360  
 20 TTGCGGGCTC AAATGCGGnT CATCGCATCC ATTTTTGnCh 400

## (2) INFORMATION FOR SEQ ID NO: 4143:

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## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 369 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4143:

TTTAAAATTG ACATTATTAC TGACCAACA AGTGCACATG ATCCGCTAAA TGGATATGTG 60  
 35 CCACAAGGAA GCGAAAGTAT TGCCTGAAAA AGATCCGAAA AAATATGTTG AACTGTCACA 120  
 AGCTTCAATG GCAAAGCATG TTGAATTAAT GCTTGGAATT CAAAAACGT GCGCTGTAG 180  
 40 CATTTGATTA TGGTAACAAT ATTCGTCAAG TAGCCTTCAA TAACGGAnGn ATAAATGCTT 240  
 TTGGACTTCC CAGGTTTTGT ACCAGCTTAC ATTAGACCAT ThATTCTGTG TAGGTTAAAG 300  
 GGCCATTCCG CTTTGCTGCG TTGGAGTGGT GGATCCAAAA GATATCGAGC GTGCCGGATG 360  
 45 GAGGAAATG 369

## (2) INFORMATION FOR SEQ ID NO: 4144:

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## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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GGAAAGATAA ATAGCTTCAT CAATGTCATG CGTCACTAAA ATAATAGTTG ATTGCGTTTT 60  
 ATGTTTTAGT TGCCTAGTT GATCCTGAAG TTTATAACGT GTAAATGCAT CTAATGCACC 120  
 5 TAATGGCTCA TCCATCAATA TAACGTTAGG CTTATGCACA TCGCTCGAC ATAGTGCCAC 180  
 ACGTTGTTTC ATACCCCGG ACAGTTGCTC GGGAAAATGC TTTCCCTGT CTTCTAAATC 240  
 AACTAATTTA AGCTGTGCT TAATCTCTTC ATCACTAATT TTCTGTTGTA ATCCAATCCT 300  
 10 AATGTTGTCA TTAATCGTTT TCCAGGCAGC AAATTATGGT GTTGAAATAG CATAACAAN 360  
 CCGGAGnGGC 370

15 (2) INFORMATION FOR SEQ ID NO: 4145:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 370 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4145:

25 CGAGGTAGCA AAGAACAAAT TCGAAATAT GTACCTAAAT TACAGTCACA TGAAGTGGT 60  
 ACATGCTTTG CTTTAACTGA ACCAGAACAC GGTTCGGACG TTGnGGAGG TCTTGAAACA 120  
 30 GTCGCTGAAC GCCAAGGCGA TACTTGGGTT ATCAATGGTG AAAAGAAATG GATTGGTGGT 180  
 GCACATGTAT CTGATGTCAT TCCAGTATTC GCAGTAAATA AAGAACTGG GCAAACCCCA 240  
 TTGCTTTGTA GTCAGACCAG AACAAGATGG GCGTCGATAT TGAAGTCATT GGATAATAAA 300  
 35 ATCGCACTTC GGCATTGTTT CTAACGCCCT AATTTnAATT AAnTAATGTT CAAAGTAGGA 360  
 TTGAAGCGGG 370

(2) INFORMATION FOR SEQ ID NO: 4146:

40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 380 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4146:

50 TGGGGTGTTC TTACCAATAA AGCGTTGCAA GGTGGCGGTA GTTTAATCGA TTATGGTTGC 60  
 CACTTGTTAG CTACTAGGTA AAGATATGGT GCCGCATGAA GTCTAGGAAA AACATATAAT 120  
 CAATTGAGCA AACAAACGAA TCAAATTAAT GATTGGGGAA CATTGTATCA TACTAAATTT 180

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GAATGTTTCGT GGTCTGCAAA TATCAAAGAA GATAAGGTTT ACGTTnTTTT ATCAGGAGGA 300  
 GGATGGCGGT ATCCAATTTA TTTCCATTTG GAAATATATG GnGCCCCGTT TTGGGAACnC 360  
 5 ATTTTTTGA AAGCCAAGCT 380

(2) INFORMATION FOR SEQ ID NO: 4147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4147:

TACTTATCTA GTTTTCAATG TACAATTTCT TTTTAGTCAA GCGCTCGCAT AAGCAATATC 60  
 20 ACTTTAACCA AAAAATATTT GAATGTTAAA TAAACATTCA AAAGTGAATA CAATATGTCA 120  
 CATTATTCGG CATCTTCTGA AGAAGATGTT CCGAATATAT CCTTAGAAAG GAGGTGATCC 180  
 AGCCGCACCT TCCGATACGG CTACCTTGTT ACGACTTCAC CCCAATCATT TGTCCACCT 240  
 25 TCGACGGCTA GCTCCTAAAA GGTTACTCCA CCGAnTTCGG GTGTTACAAA CTCTCGTGGT 300  
 GTGACGGGCG GTGTGTACAA GACCCGGGAC GTATTCACCT GGCAGCTTgn CTGGGTTTAC 360  
 nT 362

(2) INFORMATION FOR SEQ ID NO: 4148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4148:

CACCATACAT GCGAAATGGA CAGCAGATTC AAAATTTGAA AATGATGAAC GATTCAGTGG 60  
 TTACGGCAAG CTTGCGCCAA AATCCAAAGC AGACTTTGCC TTTATTCAAC ACATGGTACA 120  
 45 TTACCTAGAC GATGAAGGTA CCATGGCAGT CGTACTCCCA CATGGTGTAT TATTCGTGG 180  
 TGCCGCAGAA GGTGTGATTC GTCGCTATTT AATAGAAGAA AAGAACTACT TAGAAGCCGT 240  
 50 GATTGGGTTA CAGCCAATAT TTTCTATGGG nCAAGTATTC CAACATGTAT TTAGTATTAA 300  
 AAATGTCGCC ACAAGACGCC ACGTACTATT ATCGATGCAT CCAATGATTT GAAAAGGAAA 360  
 AATCAAACCA TTAAGCGTGC CAAGCGACGA TATnGnCTA 400

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4149:

10 CAGCTATTGA TATCGATTAC CATACTGCTG TGGATAGCGA CAGGTTTCACG TTGGAGGATA 60  
 CACTGAGTCC TCTGAGGAAT CAAATCCAAT TGACTTTGAA GAATCTACAC ATGAAAATTC 120  
 15 AAAACATCAC GCTGATGTTG TTGAATATGA AGAAGATACA AACCCAGGTG GTGGTCAGGT 180  
 TACTACTGAG TCTAACTTAG TTGAATTTGA CGAAGAGTCT ACAAAAGGTA TTGTAAGTGG 240  
 CGCnTGAGCG ATCATACAAC AGTTGAAGAT ACGAAGAATA TACACTGAAG TAATCTGATT 300  
 20 GAATAGTGGA TGAATACCTG AAGAGCATGn TCAGCACAAG ACCAGTCGAG GAATnACTAA 360  
 AACCATCATC ATATTcnCAT CTGGTTAGGA CTGAAATGGC 400

## (2) INFORMATION FOR SEQ ID NO: 4150:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4150:

35 AAGGACGACA TTAGACGAAT CATCTGGAAA GATAATCAAA GAAGGTAATA ATCCTGTAGT 60  
 CGAAAATGTT GTCTCTCTTG AGTGGATCCT GAGTACGACG GAGCACGTGA AATTCCGTCG 120  
 GAATCTGGGA GGACCATCTC CTAAGGCTAA ATACTCTCTA GTGACCGATA GTGAACCAGT 180  
 40 ACCGTGCAGG AGAAGGTGAA AAGCACCCTG GAAGGAGTTG AAATAGAACC TGAAACCGTG 240  
 TGCTTACAAG TAGTCAGAGC CCGTTAATGG GTGATGGCGT GCCTTTTGTA GAATGAACCG 300  
 GCGAGTTACG ATTTGATGCA AGTTAAGCAT AAATGTGGAG CCGTAGCAGA ACnnGTTnTG 360  
 45 AATAGGCGTT A 371

## (2) INFORMATION FOR SEQ ID NO: 4151:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4151:

5 TCAGCTTTTT TGATATGTAT TTTATAATGT ACAGCTCGTT GACnnTAATT TTCCTTATAT 60  
 TAAGTGCCAT CAATACAAAA CCTAGCTCTC GTTTAACTTT ATTTATTCCT CGAACTGACA 120  
 TTCGAGTGAA CCCAAAATAG CCTTCATAAA TCCAAAAGCA GGCTCTACAT CAATTTTTCT 180  
 10 TTGACTATAG ATGTTTTTCG TTTCTGGTTC AGAAAGCTTT TGATTAATTT GGACTTTAAA 240  
 GTATTCCCAA TTATAATTCT TCATGGATTT TCTTATTGGG ATTTGGAATT TGGTTTCATG 300  
 CATTGATGTC TCAAAGAACA TGATGGAACA GTCCAnCACA TTCCAGATAG TTTGGAAGTC 360  
 15 TCGTTT 366

## (2) INFORMATION FOR SEQ ID NO: 4152:

## (i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4152:

25 TTTGCCTGGC AACGTTCTAC TCTAGCGGAA CGTAAGTTGG CTACCATCGT CGCTAAAGAC 60  
 CTTTCTTGAC TTGTGACAAT CGCTTGCTTC TTTCTCTCC TTCGGCTCTC GCTTACTCAT 120  
 30 TTAGCTCTAC TAAACTCGTT GCGCTCTTTT CTCGTTTCGT CAGATTCAAA CGTTTTCACT 180  
 TCGCCAAGCC ATTTTTCTTT GTGTTTACTT TTTATTTTGA CGTTTtagAC ATAAAAA 240  
 35 GAGACCTTGC GGTCTCAATG CGGCTCATCG CATCCATTTT TTGCCTGGCA ACGTTCTACT 300  
 CTAGCGGGAC GTAAGTGGCT ACCATCGACG CTAAGAACCT TTCCTGGACT TGGTGGACAA 360  
 TCGCnTGCCT CCTCCTCCT CCTCGGGCTC TCGGCTTACG 400

## (2) INFORMATION FOR SEQ ID NO: 4153:

## (i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4153:

50 TGATATTCCT GTACCACCTA TAATCGTTTT AATCGATGGG GGGACGCATA GGNATAGGCG 60  
 ACGTGCGATT GGATTGCACG TCTAAGCAGT AAGGCTGAGT ATTAGGCAAA TCCGGTACTC 120

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CCGAGAAAAG CCTCTAGATA GAAAATAGGT GCCCGTACCG CAAACCGACA CAGGTAGTTC 240  
 AAGATGAGAT TCTAAGGTGG AGCGAGCGAA CTCTCGTTTA AGGACTCGGG CAAATGGACC 300  
 5 CCGTTACTTC GGGGAGAnGG GTGCTCTTTA nGGGTTTACG CCCAGAAGAG CCGCATTGAA 360  
 TAAGGCCCAA GCGnTGTTTT ATCCAAAACA CGGTCTCTGC 400

## (2) INFORMATION FOR SEQ ID NO: 4154:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4154:

TTTTAGCAAT CATTTTAACA GTCAGTCATA TTAAAGGCTG GCTAACGATT GTTATCTnGT 60  
 nCAGATTGTGT AAGTTAAGAT TTCTTGTAAT GTGTATGCAG CACCATATGC TTCAAGTGCC 120  
 CATACCTCCA TCTCACCAA AC GTTGTCCA CCGAATTGCG CTTTACCGCC AAGTGGTTGT 180  
 25 TGTGTAACAA GTGAATATGG TCCTGTTGAA CGCGCATGTA ATTTATCATC AACCATGTGC 240  
 GCAAGTTTCA ACATGTACAT TACACCTACT GAAATACGGT TATCGAATGG TTCACCTGTA 300  
 CGTCCATCAT AAAGTACAGT TTTACCATCA CGAGCCATAC CAGCTTCTTC AATTGTTGGA 360  
 30 CCATACATCG TCATCGTTTG CACCGTCAAA TACTGGTGGA 400

## (2) INFORMATION FOR SEQ ID NO: 4155:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 361 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 35 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4155:

GATCCGAAGT TACCAACAGG AGAGAAAGAG GAAGTTCAG GTAAACCAGG AATTAAGAAT 60  
 45 CCAGAAACAG GAGATGTAGT TAGACCACCG GTCGATAGCG TAACAAAATA TGGACCTGTA 120  
 AAAGGAGACT CGATTGTAGA AAAAGAAGAA ATTCCATTCT AGAAAGAACG TAAATTTAAT 180  
 50 CCTGATTTAG CACCAGGGAC AGAAAAAGTA ACAAGAGAAG GACAAAAGG TGAGAAGACA 240  
 ATAACGACGC CAACACTAAA AAATCCATTA ACTGGAGAAA TTATTAGTAA AGGTGAATCG 300  
 AAAGAAGAAA TCACANAAGT CCAGTTAATG AATTAACAGA TTCGGTGGCG AGAAATACCG 360



## (2) INFORMATION FOR SEQ ID NO: 4156:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4156:

CAAAGTGACA GGTGGTGCAT GGTGTGCGTC AGCTCGTGTC GTGAGATGTT GGGTTAAGTC 60  
 CCGCAACGAG CGCAACCCCTT AAGCTTAGTT GCCATCATT AAGTTGGGCAC TCTAAGTTGA 120  
 CTGCCGGTGA CAAACCGGG GAAAGGTGGG GATGACGTCA AATCATCATG CCCCTTATGA 180  
 TTTGGGCTAC ACACGTGCTA CAATGGACAA TACAAAGGGC AGCGAAACCG CGAGTGCAAG 240  
 CAAATCCCAT AAAGTTGTTC TCAGTTCGGA TTGTAGTCTG CAACTCGACT ACATGAAGCT 300  
 GGAATCGCT AGTAATCGTT AGATCCAGCA TGGCTAACGG TGGATACGT TTCCCGGGGT 360  
 CCTTGTTACA CACCGCCCGT 380

## (2) INFORMATION FOR SEQ ID NO: 4157:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4157:

TGGAGAAGGA CCCAAAAATG TTGCCGTTTC AAGGTTATGT TTTACAACAT TTCGAACCTA 60  
 TGGATGATGG ATTCTGCCAA GTTAAATATA CTGAAGATGT ATTGGAGCAA TTCGGTATTC 120  
 AGCCAAATGA AGCATCTCAG TTTGTTAATA CAATTGCTGA CATCAAAGGC TTGAAAATAT 180  
 GGGTATTTGC AGTCGATGGA AGGTAATGAA ATCAGATGTC GATTACGTTT TAAAGGGCAA 240  
 TTGGATTATT AATGATATTG CGCAGATTTT GGTGGCGGTG GTCATCCGAA TCGCTCAGGA 300  
 GTTTCAGTGG ACCAGCTGGG GTGGATTTGA GCCACTTGCT ACCAGCTTTA CGGCACCAAA 360  
 ACTTnACTTA TAGGAAGGGG CCCATTCCAT CCAGGTGGGC 400

## (2) INFORMATION FOR SEQ ID NO: 4158:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4158:

5 AAATCTCTGG GATCAAATCT TACTTACAGC TCCCCAAAGn CATATCGTCG TTAGTAACGT 60  
 CCTTCATCGG CTTCTAGTGC CAAGGCATCC ACCGTGCGCC CTTAATAACT TAATCTATGT 120  
 TTCCACCATT TTTATAAGTC AAACGTTAAC ATGAAGTTAC GTTCTTTTAT AAAAAGATTT 180  
 10 AAACGCGTTA TTAATCTTGT GAGTGTTCCT TCGAACACTA GCGATTATTT CTTATGAATT 240  
 CAAGCTTATT TAAAACTCTT TATTCACCTG GTTTTGCTTG GTAAAATCTA TATTTTACTT 300  
 ACTTATCTAG TTTTCAATGT ACAAATAATG GTGGAGACTA GCGGGATCGn n 351

## (2) INFORMATION FOR SEQ ID NO: 4159:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 420 base pairs  
 (B) TYPE: nucleic acid  
 20 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4159:

25 AGTTAAAGGA ACTTTTAAAG TGGTTGGCCG CCGTnATTGC CTTCTnACC TTTTGTCTCT 60  
 TCTCTTGTtTA CTTTTTCTGT CCCTGGTGCT AAATCmGGAT TAAATTTACG TTCTTTCTTG 120  
 30 AATGGAATyT CTTCTTTTTC TACAATCGAG TCTCCTTTTA CAGGTCCATA TTTTGTTACG 180  
 CTATCGACCG GTGGTCTAAC TACGTCTCCT GTTTCTGGAT TCTTAATTCC TGGTTTACCT 240  
 GGAACCTTCyT CTTTCTCTCC TGTTGGTAAC TTCGGATCAA ATTCTCTCTG ATGACCTGGT 300  
 35 GTTATCGTTT CTGGTCCGTA TTCTGTTAAT TCATTAATCG GATCTTTTGT GATTTCTTCT 360  
 TTTGGTTCAC CnTTnACGAA TAATnACTCC AGTAAAGGAT TTTTAAAGTG TTGGTGTCTG 420

## (2) INFORMATION FOR SEQ ID NO: 4160:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 359 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 45 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4160:

50 ACGATAATGG TGACGGGTTA CAAAGCCAAC ACAGCTAGGG TAGTATCCCA CCAGCGTCCT 60  
 CCACGTAATC TAGCGCTCAC GTTTCAAAGG CTCCTACCTA TCCTGTACAA GCTGTGCCGA 120

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TGCATCTTCA CAGGTACTAT GATTTACCCG AGTCTCTCGT TGAGACAGTG CCCAAnTCGT 240  
 TACGCCTTTC GTGCGGGTCC GAACTTACCC GACAAGGAnT TTCGCTACCT TAGGACCGTT 300  
 5 ATAGTTACGG CCGCCGTTTA CTGGGGCTTC GATTCGTAGC TTCGCAGAAAn TAACCACTC 359

## (2) INFORMATION FOR SEQ ID NO: 4161:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4161:

ATTGACTAAG GTTTCAGAG GAAGGCTCGT CCGCTCTGGG TTAGTCGGGT CCTAAGCTGA 60  
 20 GGCCCGNAAC GGTAGGGCGA TGGATAACAG GTTGATATTC CTGTACCACC TATAATCGTT 120  
 TTAATCGATG GGGGGACGCA TAGGGATAGG CGAACGTGTC GATTGGATTG CACGTCTAAG 180  
 CAGTAAGGCT GAGTATTAGG CAAATCCGGT ACTCGTTAAG GCTGGAGCTG TGATGGGGAG 240  
 25 AAGACATTGT GTCTTCGAGT CGTTGATTTT ACGTCCGA GAAAAGCCTC TAGATAGAAA 300  
 ATAGGTGCCC GTGACCGCAA ACCGACACAG GTAGTnCAAG ATGAGAAAnTC T 351

## (2) INFORMATION FOR SEQ ID NO: 4162:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4162:

AnCGTCCTGC TTTGCACGCC AGAGGTCAGC GGTTCGATCC CGCTAGTCTC CACCATTTAT 60  
 TTTTACACG ATGAACATTG AAACTGAAT GACAATATGT CAACGTTAAT TCCAAAAAAC 120  
 GTAACATAA GTTACAAACA TTATTTAGTA TTTATGAGCT AATCAAACAT CATAATTTTT 180  
 45 ATGGAGAGTT TGATCCTGGC TCAGGATGAA CGCTGCCGGC GTGCCTAATA CATGCAAGTC 240  
 GAGCGAACGG ACGAGAAGCT TGCTTCTCTG ATGTTAGCGG CGGACGGGTG AGTAACACGT 300  
 GGATAACCTA CCTATAAGAC TGGGGATAAC TTCGGGGAAC CGGAGCCAAT ACCGGATAAT 360  
 50 AnTTTGAACC GCATnGGTCC AnAAGTGAAA GACCGGCTTG 400

## (2) INFORMATION FOR SEQ ID NO: 4163:

(A) LENGTH: 342 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4163:

10 ATTTTATATA TGAAATAATC TGGGACAACA TTCATAAATC TTATTGTCGT CCATTTTTTTT 60  
 AAAATAATAC CAATCTCATT TTAAATTCT AACTTGGTT TCGTATAATA CGCTCTTAA 120  
 TCTTTAAATT TAGGATTTAT TTCTGTTGGT ACTTGTTTTG TGGTTGGCGA TTGTGGTGTG 180  
 15 TCTGATTTAG TAGATTGCAT TGGTTGTGGC GTGTTTGTG ATGGAGGTGT TGTCACTTTA 240  
 GTTGnAAGGC GGTGTTGTCG CATTGCTGT TTGTTGCGGT GCTTCTACTT TnATTGCAGG 300  
 CGGTGTTGTC GCGTTTGGTT TTGnATGCCG TGCTTCTATT TT 342  
 20

(2) INFORMATION FOR SEQ ID NO: 4164:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4164:

30 TCACGACACG AGCTGACGAC AACCATGCAC CACCTGTCAC TTTGTCCCCC GAGGAAGGGC 60  
 TCTATCTCTA GAGTTGTCAA AGGATGTCAA GATTTGGTAA GGTTCCTTCG GTTGCTTCGA 120  
 35 ATTAAACCAC ATGCTCCACC GCTTGTGCGG TTCCCCGTCA ATTCCTTTGA GTTTCAACCT 180  
 TGCGGTCGTA CTCCCCAGGC GGAGTGCTTA ATGCGTTAnT GCCAGCACTA AAGGGGCGGA 240  
 AACCCCTAA ACACTTAGCA CTCCATCGTT TACGGCGTGG AACTACCAGG GTATCTAATC 300  
 40 CTGTTTGATC CCCACGCTTT CGCACATCAG GTCATTAACA GACCAGAAAT CGCTTGCCCA 360  
 nGGGGGTnGC nCCAAAACCTT TGGGGATTTA ACGGTAAAAA 400

(2) INFORMATION FOR SEQ ID NO: 4165:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4165:

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GCATTAATTT CATGTGTACC TTCGTACGTG TAAATCGCTT CTGCATCAGA GAAGAAACGT 120  
 5 GCAATATCAT AATCGTCAGC TAGTATGCCA TTACCACCTG TAATACCGCG GCCCATAGCT 180  
 ACTGTCTCAC GCAAACGTAA GGCATTCATC ATCTTCGCCG TTGAAGTTGC AACCTCGTCA 240  
 TATTCACCAT GTGCTTGCAT ATTAGCTAAT TGAGCACATG TTGCCATTGC TTGAGCTAAA 300  
 10 TTAnCTTGCA TCATTGCTAG CTTTCCTGTA TTAACGGATA TTAATAATnG GTTGCCGAAT 360  
 GCTTACGCTC AGGGACnTAA CnAAGTGGCA CGTAAGCGGC 400

## (2) INFORMATION FOR SEQ ID NO: 4166:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear  
 20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4166:

AAAGTTCTTT GGAAATAGTA ACGTTGAAGT TGTACTCACT GGTGATACAT TTGATCACTG 60  
 25 TTTAGCTGAA GCTTTAACTT ATACAAGTGA ACATCAAATG AACTTTATAG ATCCATTCAA 120  
 TAATGTTTCAT ACAATTTCTG GACAAGGTAC GCTTGCTAAA GAAATGCTAG AACAAGCAAA 180  
 30 GTCTGACAAT GTTAACTTTG ATTATCTATT TGCCGCAATT GGTGGTGGCG GTTTAATTTT 240  
 AGGTATTAGT ACTTACTTTA AAACCTATTC ACCTACCACG GAAAATTATA GGTGTTGGAA 300  
 CCTTCAGGTG GCAAGTAGTA TGGTATGGAA TCnGGTGGTG GGTAAATAAT CcGGTnGTC 360  
 35 CACATTGGCC CTAATAACCG ATAAAATTTG GGGGGCCGGG 400

## (2) INFORMATION FOR SEQ ID NO: 4167:

40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 358 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4167:

CTTATAATCC ACACCCTGAG CAAACGCTnC TTATGACAGA GTATTAAAAT AAGCCGATAA 60  
 50 AGATACACAC CTTTACCGAC TATTTAAAAT AACTTCACC AATTCATTTT AATTTAATGG 120  
 ATTGAAGTAA CTAAATTAAT ATTATGTTGT TCAATTAAAA GCTTCATACA AACCTAATCT 180  
 ATTTGCACTC CACCGTAAC ACCGAACACT TGTCCGGTTG TATAACTTGA TTCTTCTGGA 240

GTGTTTTGTA CCAAATGnTT GGGGATTTTA CTTnGTGGGT TGTCCACCAG AAATTTGT

358

(2) INFORMATION FOR SEQ ID NO: 4168:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4168:

15	TTTCTTGACC ATATGGACGT AAAGAGATGT TAGCATCACA ACGTAAAGAT CCCTCTTCCA	60
	TCTTAACGTC TGATACACCA GTGTATTGAA TAATTGAACG CAATTTTTTCT AAATATGCAT	120
	ATGCTTCTTT AGGTGAACGA ATATCTGGTT CAGATACGAT TTCAATTAGC GGTGTACCTT	180
20	GACGGTTCAA GTCAACTAAT GAATACTCAC CTTTATGTGT TGACTIONACCA GCATCTTCTT	240
	CCATGTGGAA GACGAGTAAT ACCGATTCGT TTTGTTTCAC CGTOGACTTC GATATCGATA	300
	TATCCATTTT CACCAATTGG TTGATCAAAT TGAGAAhTTG AGAGCTTnTG GnTTAGCTGG	360
25	ATAGAAATAG TTCTTACGGT CAACTTAGAT CCGTTGCGAT	400

(2) INFORMATION FOR SEQ ID NO: 4169:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4169:

	ACCATGTTTG AATGAATCCA TTGGAATCAT TATTGAAGTA AATTAAGGAA TCTATAATGT	60
40	TCGTTAAATA AACTGATCC CGTTGTGCTT CACACCCGAT AGATAGGGAT TTACAGATAA	120
	ATTCAGGTCT CTTCCACGTC ATATTGGAC CCATCGAAAA TTCGGGTTCT CAAATCATCG	180
	AACATAACAA AAGAAGCTAA GCAACATGTA GGCCGTTGTC ACTTAACITC TTGTTTTTCC	240
45	GATGACAGCT TCTATTTAGA GAATGTCATG ATTATTTTAT ATTCACTTCA ATGTTATCAA	300
	TATTAGTGCC ATCTATGACA TCTGCCATGC GATTTTCTTG TAATTTTTTG TGCAATCAAC	360
50	GTGTACnTCC ACGGTTTTCA TTTAAhAACA ATTTACCGGA	400

(2) INFORMATION FOR SEQ ID NO: 4170:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 395 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4170:

TACCGAATCG AAGCCCCAGT AAACGGCGGC CGTAACTATA ACGGTCCTAA GG TAGCGAAA	60
10 TTCCTTGTCG GGTAAGTTCC GACCCGCACG AAAGGCGTAA CGATTTGGGC ACTGTCTCAA	120
CGAGAGACTC GGTGAAATCA TAGTACCTGT GAAGATGCAG GTTACCCGCG ACAGGACGGA	180
AAGACCCCGT GGAGCTTTAC TG TAGCCTGA TATTGAAATT CGGCACAGCT TGTTACAGGA	240
15 TAGGTAAGGA GCCTTTGGAA ACGTGAGCGC TAnTTTACGT GGnAGGCGCT GGGTGGGGAT	300
ACTTACCCTA AGCTGTGTTG GCTTTCTAAC CCGCACCAnt TATCGTGGTG GGGAGACCAT	360
GGTCAAGCGG GGCATTTTGA ATGGGGGGCG GTTCG	395

20

(2) INFORMATION FOR SEQ ID NO: 4171:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 371 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4171:

TACATTATAG CTTTAATCGT TTGAAGTATA GTTTGAAACC AGTAGTCACA GCTGTTCAAG	60
GTCGTGCCTT AGGCGGTGGC TGTGAGCTTG TACTTTACTC ACCTATTGTT GTCGTGCAA	120
35 GTGAAACATA TATCGGTCTT GTTGAAGCAG GTGTGGCTT ATTACCGAGT GCGGTGGCC	180
TTGCAGAAAT GGCTGATCGC ATATTACGCA CATCGCATAA GTTTGATGAC AAACAAGCTT	240
CCATGACAAA AGTACTGACG AATATCGCAT TCGGAAnGCT CTACAAATGC CTTTGAGGCA	300
40 CGTCGTATGG GTATTTACCG TGGATACAGA TACGATnATT TCCAATACAG CACAACGnGT	360
CGAAGTGGCG C	371

45

(2) INFORMATION FOR SEQ ID NO: 4172:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 361 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4172:

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GCTGAGCTAA GCCCCATAA TAATTACAGT ATATCGGGAA GACAGGATTC GAACCTGCGA 120  
 CCCCTTGGTC CCAAACCAAG TGCTCTACCA AGCTGAGCTA CTTCCCGTAT AATTAACGCG 180  
 5 CCCGATAGGA GTCGAACCCA TAACCTCTTG ATCCGTAGTC AAACGCTCTA TCCAATTGAG 240  
 CTACGGGCGC ATATGTTTTT ATTGAAAATn GTGCCGAGGA CCnGAATGAA CCGGTACGTG 300  
 ATCATTACCG CAGATTTTAA GTCCTGTGCG TCTGCCAGTT CCGCAnCCCG GACTATAAAA 360  
 10 T 361

## (2) INFORMATION FOR SEQ ID NO: 4173:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 380 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4173:

GTACAGATGC ATTGTTAAAC AATCAGTTGC AACAGCTGTT GAAACTGGTA GAGTATCTAA 60  
 25 TGGTGATTTA ATCATTATTA CTGCTGGTGT ACCAACTGGT GAAACTGGAA CTACTAATAT 120  
 GATGAAAATC CACCTAGTTG GTGACGAAAT TGCTAATGGT CAAGGTATTG GACGTGGATC 180  
 AGTTGTTGGT ACTACGTTAG TTGCTGAAAC TGTTAAAGAT TTAGAAGGTA AAGATTTATC 240  
 30 TGACAAAGTT ATCGTTACTA ACTCCATCGA TGAAACGTTT GTACCTTATG TAGAAAAAGC 300  
 TTTAGGCTTA ATTACAGAAG AAATGGTATT nCACACCCAG TGCCATGGTT GGTTAGGAAA 360  
 AGnAATCCCA CCGTTGTAnG 380

35

## (2) INFORMATION FOR SEQ ID NO: 4174:

40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4174:

CGATTGGATT GCACGTCTAA GCAGTAAGGC TGAGTATTAG GCAAATCCGG TACTCGTTAG 60  
 CTGAGCTGTG ATGGGGAGAA GACATTGAGT CTTGGAAGTC GTTGATTCA CACTGCCGAG 120  
 50 AAAAGCCTCT AGATAGAAAA TAGGTGCCCC TACCGCAAAC CGACACAGGT AGTCAAGATG 180  
 AGAATTCTAA GGTGGAGCGA GCGAACTCTC GTTTAAGGAA CTCGGGCAAA ATGGACCCCG 240

55



GCCCAAGCGC TGTTTATCCA AAACACAGTC TCTGCTAAC CGTAGGGGAT TGTATAGGGG 360  
 CTTACGCCTG CCCGGTGCCT GGAAGGTTTA AAAGGGTGGT 400

5 (2) INFORMATION FOR SEQ ID NO: 4175:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 348 base pairs  
 (B) TYPE: nucleic acid  
 10 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4175:

AGCCATGGCT CAGCGAGGTA GGAAGTGAAC CTACGACCGA TCGGTTAACA GCCGATAGCT 60  
 CTACCACTGA GCTACTGTGG ATTAATATTA TGCCTGGCAA CGTTCTACTC TAGCGGAACG 120  
 20 TAATTCGnAC TACCATCGAC GCTAAGGAGC TTAACCTCTG TGTTCGGCAT GGGAACAGGT 180  
 GTGACCTCCT TGCTATAGTC ACCAGACATA TGAnTGTAAT TTATACATTC AAAACTAGAT 240  
 AGTAAGTAA AGTGATTTTG CTTGCGAAAA CATTATTTT GGATTAAGTC TTCGATCGAT 300  
 25 TAGTATTCGT CAGCTCCACA TGTGCACCAT GCTTnCCACC TCGAACCT 348

(2) INFORMATION FOR SEQ ID NO: 4176:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 344 base pairs  
 30 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4176:

CATTTTTTTA AAATAATACC AATCTCATTT TTAAATTCTA AACTTGGTTT CGTATAATAC 60  
 GCTCTTAAAT CTTTAAATTT AGGATTATTT TCTGTGGTA CTGTTTTGT GGTGGCGAT 120  
 40 TGTGGTGTGT CTGATTAGT AGATTGCATT GGTGTGGCG TGTGTGTTGA TGGAGGTGTT 180  
 GTCACTTTAG TTGAAGGCGG TGTGTGCGCA TTTGCTGTTT GTTGGGTGC TTCTACTTTA 240  
 45 GTTGAGGGCG GTGTTGTCGC GTTGGTTTTT GATTGCGGTG CTTCTATTTT AGTTGAGGGC 300  
 GGTGTTGAnT GTGGTGCTTC CACTTAGGG nAAGATnAGT GGTG 344

(2) INFORMATION FOR SEQ ID NO: 4177:

- 50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 362 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

55

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4177:

5 CAGAACCTTG AATGAATCG CGATGGAATA TCTCTATCTG AATACAGATT TCTTTTGTG 60  
 CGCCAATGGC CTTGGAATTG TTAAATAAA TCTATTGCG CTTCTTTATC AATGTCATAA 120  
 CCTAATGCTT TTAACCTTCTC TGAGAAGCGT GTTTACCAGA TAATTTTCCT AATGGAAGTT 180  
 10 CAGTCGTGCT TACACCAACA AGTTGAGGTG TCATAATTTC ATATGTTTCA CGATGTTTTA 240  
 ATACGCCATC TTGGTGAATA CCGATTTCAT GACTAAATGC ATTTGGCCAA CAATTGCTTT 300  
 ATTTCTAGGC ACTCGAATAC CTGCATATCT TGAATTAA TCCGAGGTTT TAGTTCCTCG 360  
 15 AG 362

## (2) INFORMATION FOR SEQ ID NO: 4178:

## (i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4178:

25 GGAGCTAATA CCGGATAATA TTTTGAACCG CATGGTAAAG ATGGAAAGAC GGTCTTGCTG 60  
 TCACTTATAG ATGGATCCGC GCTGCATTAG CTAGTTGTA AGGTAACGGC TTACCAAGGC 120  
 30 AACGATGCAT AGCCGACCTG AGAGGGTGAT CGGCCACACT GGAAGTGA, CACGGTCCAG 180  
 ACTCCTACGG GAGGCAGCAG TAGGGAATCT TCCGCAATGG GCGAACTTn ACGGAGCAAC 240  
 35 GCCGCGTGAG TGATGAAGGT CTTCCGATCG TAAACTCTG TTATTAGGGG AGGACATATG 300  
 TGTAAGTAAC TGTGCACATT TTTGACGGTA CCTnATCAGG AAGCCACGGT TTAGTAGGGG 360  
 CCCAGAAGCC CCGGTTAATA CGTGGGTGGG nAAGGGTTTT 400

## (2) INFORMATION FOR SEQ ID NO: 4179:

## (i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 371 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4179:

50 GTTGTTTCAG CAGCGACACA GTGTATTCCA TTCTTAGAAA ATGATGACTC AAACCGTGCA 60

55

GTTGGTACAG GTATGGAACA CGTTGCAGCA CGTGATTCTG GTGCGGCTAT TACAGCTAAG 180  
 CACAGAGGTC GTGTTGAACA TGTGAATCT AATGAAATTC TTGTTCTGTCG TCTAGTTGGA 240  
 5 AGAGAACGGC GGTGAACAT GAAAGGTGGA TTAAGATCGC TATCCATTAG CTAAATTTAA 300  
 ACGTTCAAAC TCAGGTACAT GTTACAACCA ACGTCCAATC GTTGCCAGTT GGGAGATGTT 360  
 GTTGGnnnTA C 371

(2) INFORMATION FOR SEQ ID NO: 4180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4180:

AAAGGGAATC GAATTTTCTT TCTCTTCCTC CGGGTACTAA GATGTTTCAG TTCTCCGGGT 60  
 GTGCCTTCTG ATATGCTATG TATTCACATA TCGATAACAT GACATAACTC ATGCTGGGTT 120  
 25 TCCCCATTCTG GAAATCTCTG GATCAAAGCT TACTTACAAC TCCCCAAAGC ATATCGTCGT 180  
 TAGTAACGTC CTTTCATCGG TTCTAATGCC AANGCATCCA CCGTGCGCCC TTAATAACTT 240  
 30 AATCTATGTT TCCACCATT TTATAAGTCA AACGCTCACA TACGGCTTCG TTTTCATTAT 300  
 nThAAATGCT CATTTACATA AGTAAACTCT GCTTTAAAAT AATT 344

(2) INFORMATION FOR SEQ ID NO: 4181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 343 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4181:

CCGTGATCGG AAGGTGCGGC TGGATCACCT CCTTTCTAAG GATATATTCTG GAACATCTTC 60  
 TTCAGAAGAT CGGGAATAAC GTGACATATT GTATTTCAGTT TTGAATGTTT GTTCATTCAA 120  
 ATTAATGGGC CTATAGCTCA GCTGGTTAGA GCGCACGCCT GATAAGCGTG AGGTCCGTGG 180  
 50 TTTCAGTCCA CTTAGGCCCA CCATTAAATTT AATACCTATT TGGGGGCTTA GCTCAGCnGG 240  
 GAGAGCGCCT GCTTTGCACG CnGAGGTCAG CGGTTTCGATC CCGCTAGTCT CCACCATTAT 300  
 TTGTACATTG AAACTAGAT AAGTGAnGTA AAAATATAGA TTT 343

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4182:

CAGAGCCAAC TCGTATGTGA TTTGTCTGCG CCAATGTATG CATCATCAAA AGTTCTGGAC 60  
 TACTACACGC AAACGCTGGT ACATTATGAT GTTCCGTAAA CCAAATTCGC TTAAAGCCAA 120  
 GTCGATCTGC TAATTTTGCA AGTGCTACTG AATCTTGCAA TGCCTTTTGT GCATCCTTAC 180  
 CTTTCATCTAT TAAGGCATAG TCTAATACGC TTAATTTAAC CAATCCGTCA TCTCCAAACT 240  
 TATCCTGTCA TGTCAAACCG ACATAACATT TTAGCGTCTT AATACCATTG CCTCTTCATA 300  
 TACCCACGTA TATGATAACG TTTTCAATAA CTTTATATCT TTCGCCTTAT TTTCTTTTCA 360  
 TATCATATTT CAGACTACAA ATGCATCATA GTTAATTAAA 400

## (2) INFORMATION FOR SEQ ID NO: 4183:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4183:

AAAGTATGAA AGATGGTAGT GACGCGGTTG GTGATTGGGC TGTATTGAAT GCACTCATTG 60  
 ACACAGCTGC AGGTGGTTCA TGGATTTTCA TCCATCACGG TGGCGGTGTT GGCATGGGAT 120  
 ATTCACTTCA TCGCGGTATG GTTGTGTAG CAGATGGATC AGAGCGTGCT GAAGGAAGAT 180  
 TGGAACGTGT ATTGACGACT GACCCAGGTA TGGTGTGCCC CGACATGTTG nATGCTGGCT 240  
 ATGACATCGC TATTCAAACA GCTAAAGAAA AAGGTATTCA nATTCCAATG ATTGGTGAAA 300  
 GCAGGTGATA AGTAATGAAT GATTTAATAT TAATCAnATA GCAGAnTATT TTTACCGGGT 360  
 CCAACAGATA AACCTTTGAA GGGTTAGGTA TTAGATGCAT 400

## (2) INFORMATION FOR SEQ ID NO: 4184:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4184:

TTCCCTGTGC ATCGGCATCA CTATTATTAG CATGACTCAA TTATTGGCAT CACAATATGT 60  
 5 CATTGCAGTT ATCATTGGTT TCGTCATATG TCGGATAGGT AATGGTTT TAG TCGCAACACC 120  
 TGGACTTACG ATTGCAATTT TCAGTATGCC TAATGAnAAA GTTGGTTT TAG CTACAGGATT 180  
 ATATAAAATG AGTGGTACAT TAGGTGGCTC CTTTGGTATA GCACTAAGTA CTACAGTTTT 240  
 10 CAGTATGTTA CAACTAAACT ATGCACCAAG TG TAGCTGCA ACCGTAACAT TTATAGTCAG 300  
 CATTGTATTG ATGnTCCTTG GGTnCATTTGT CTGCATACAT GA 342

## (2) INFORMATION FOR SEQ ID NO: 4185:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4185:

AAGCATACTC TGAAGCGGTG AACAAAAATA GAACAGATCA CATTAGACAT TTAATTGAAT 60  
 25 TTAAAGCATG TACACCGATT GACATCGACC AAGTTGAACC GGTAAGTGAC ATTGTCAAAC 120  
 GCTTTAATAC AGGGGCGATG AGTTATGGAT CGATTTTCAGC GGAACACATG AAACGTTAGC 180  
 30 ACAAGCCATG AACCAATTAG GTGGAAAGAG TAATAGTGGT GAAGGTGGCG AnATGCCAAA 240  
 CGTTATGAAG TACAAGTTGA TGAAGCAAC AAAGTAAGTG CGATTnAACA AGTTGCTTCT 300  
 35 GGGCGTTTTG GTGTACTAGT GATTATTTAC CACCTGCCAA GGAATTCCAA TTAnACTTGC 360

## (2) INFORMATION FOR SEQ ID NO: 4186:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4186:

CCCAAGCGGA ATTCTAAAAT GATCGTCGCT CCATTCTTCA TTTTAATAAA TCCAAACGCA 60  
 50 GAATCTTCAA CTGTAAATTC ATCTGGATTC CATGAACCCC AAGCGTTTGC CGCATGATGC 120  
 TGTTATTTA ATTTATGGAA TGTTGAACCC ATCACTGATT CTGGTTCATA ATTATCCATC 180  
 ATCCATAACG TTAAATCTAA AGCGTGTGTA CCGATATCGA TTAATGGTCC TCCACCTTGG 240

nCTTTCCGAA GTTAAATGTC TCCTAAGTCG CCACGTTGGC GCTGCCTGGA TGGAAAATTG 360  
 GACGATCTGC TCGGGAAACG AATTTGGATA AACnGATGGG 400

5 (2) INFORMATION FOR SEQ ID NO: 4187:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 349 base pairs  
 (B) TYPE: nucleic acid  
 10 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4187:

GAATCATCTG GCAACnCCC CCAAGAAGG TAATAATCCT GTAGTCGAAA ATGTTGTCTC 60  
 TCTTGAGTGG ATCCTGAGTA CGACGGAGCA CGTGAAATTC CGTCGGAATC TGGGAGGACC 120  
 20 ATCTCCTAAG GCTAAATACT CTCTAGTGAC CGATAGTGAA CCAGTACCGT GAGGGAAAGG 180  
 TGAAAGCAC CCCGGAAGGG ATGTGAAATA GAACCTGAAA CCGTGTGCTT ACAAGTAGTC 240  
 AGAGCCCGTT AATGGGTGAT GGCCTGCCTT TTGTAGAATG AACC GGCGAG TTACGATTTG 300  
 25 ATGCAAnGTT AAGCAGTACA TGTGGAGCCG TAGCGAAAGC GAnGTCTGA 349

(2) INFORMATION FOR SEQ ID NO: 4188:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 336 base pairs  
 (B) TYPE: nucleic acid  
 30 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4188:

TGGATCCTGA GTACGACGGA GCACGTGAAA TTCCGTCGGA ATCTGGGAGG ACCATCTCCT 60  
 40 AAGGCTAAAT ACTCTCTAGT GACCGATAGT GAACCACTAC CGTGAGGGAA AGGTGAAAAG 120  
 CACCCCGGAA GGGGAGTGAn ATAGAACCTG AAACCGTGTG CTTACAAGTA GTCAGAGCCC 180  
 GTTAATGGGT GATGGCGTGC CTTTGTAGA ATGAACCGGC GAGTTACGAT TTGATGCAAG 240  
 45 GTTAAGCAGT AAATGTGGAn CCGTAGCGAA ACGAGTCTGA ATAGGGCGTT TAGTATTGG 300  
 TCGTAGACCC GAAACCAGGT GATCTACCCT nGGTCA 336

50 (2) INFORMATION FOR SEQ ID NO: 4189:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 358 base pairs  
 (B) TYPE: nucleic acid  
 55 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4189:

5 CAAAGGATGT TAAGAAATAC AATTTATTAC CCAGCATTTA ATAATGGTGC TATAGAAGGA 60  
 ATTAATAATA AGATAAAATT AATCAAGTGA ATTCTTTTG GTTACAGAAA TTTCAACAAC 120  
 TTAAAGCAC GTATAATGAT GATTTTCAGC TTGTACAAAG GAGAAAAAAA GAAGACAACC 180  
 10 AAGCCCAATA ATGGACTGGC CGCCTAATAA TAAAAGCTCT AAAAGTTGTA TTTTAAAAAT 240  
 AGTTCTTTAA ATTATATACC CACCACATTT GGTGGAGGAC CTAAAAAAA GCACCTCCCC 300  
 AAAAATGGGA AAGTGCAAGT AGTGAGCCnT AGGAGGGTTC GGACCTCTn nCCCCTCT 358

## 15 (2) INFORMATION FOR SEQ ID NO: 4190:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 362 base pairs

(B) TYPE: nucleic acid

20 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

## 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4190:

TCACCAAGTT GAGCAAAGAA GATGTTCTGC GTACCTTGAA CTAAGTGCCC TTTGACTTCT 60  
 AAnGTACCAC CAAGTGCCGT CTGCCAAAAC GGTAAGTAAA AAATATGGTG TAAACCGAGT 120  
 30 GGACCTAACA ATCTTAAGAT GAAGCCATAA ACAAAGTAC CGATGGCACC TGTTTTCGTT 180  
 ACAAATCCAC CAACATGATA AATGCCGGCT TGTATGCTTG GCCAAATGAA AAACATCAAT 240  
 ACACCTAAAA AGATTGCGGC AAATGCTGTG ACAATAGGGA CAnATGTAGA GCCACCAAAG 300  
 35 AAACCTAAAT ACGGTGGTAA TACCATTTGT GnTATTTGTT GTGAAGTATT GCGGTCATAA 360  
 TA 362

## 40 (2) INFORMATION FOR SEQ ID NO: 4191:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 362 base pairs

(B) TYPE: nucleic acid

45 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

## 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4191:

TGATCACCCA TGTTCCTGGAC TCCCAATTGA AATTGAATTG GGCAATCGGA GTTTGTCTGG 60  
 nATTCCGTAA .CCCGnGCAGG GTCCCCTCGT GCCAAACAGT GCTCTACCTC CAATAATCAT 120

55

nATTTCTCCG CTAACCTCAG TTCATCCGCT CACTTTTCAA CGTAAGTCGG TTCGGTCCTC 240  
 CATTCA GTGT TACCTGAACT TCAACCTGAC CAAGGTAGAT CACCTGGTTT CGGGTCTACG 300  
 5 ACCAAATACT AAAGCCCTA TTCAGACTCG CTTTCGCTAA GGCTCCACAT TTA CTGCTTA 360  
 AC 362

(2) INFORMATION FOR SEQ ID NO: 4192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4192:

20 CGTGTATTAT GCCTTCTACA TTGGCCATTA TGAAACTTA TTATCAGGGT GCTGAACGTC 60  
 AGCGTGCCCTT AAGTTATTGG TCTATCGGTT CTGGGGTGG CAGTGGTATC TGTTC ACTCT 120  
 TCGGTGGTGC AGTTGCGACA ACTATGGGTT GGAGATGGAT TTTCATCTTC TCAATTATCG 180  
 25 TTGCCGTACT TTCAATGTTA CTCATCAAAG GGACGCCTGA AACGAAATCA GAAATTACCA 240  
 ATACACATAA ATTTGACGTT GCAGGGCTAA TTGTTCTAGT AGTATGTTGC TAAGTTAAAC 300  
 30 GTTGTCACTA CTAAAGGTGC AGCACTTGGn TACACATCAT TATGGGTCTT GGGTTGAATG 360  
 CCAATCGGAA ATTGTAGCAT CnTTAATTTT CTAAAAGGTG 400

(2) INFORMATION FOR SEQ ID NO: 4193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4193:

45 AATCCCATGG ACCCTCAAAT TCTTTATCTA AATAGTACCC TAATGAAGTT TTTCTGTGCA 60  
 TGTGATTAAT TTCATGTAAA CCGATGACAC CAACTAGCGT TCCTTCATAC CAAATGCCAC 120  
 ACTGAAATCC ATTACCATCA GCAAATTGCA AAAGTCCTCT TTTAATAAAT GCACGCGTAT 180  
 50 CTGATGGTTG CTCAGTTGCA TCTACCCAAG GTAACCATTC CCTAAGTGAA TTTCTTGAAC 240  
 GATTGACTAA ATTGAAAAGC GCTTCTGTGT CATGAGCTTC TAAAATTTTA ATGTTATTGT 300  
 TCAATCACTT TCATTCCAAA CATACnATCA CATCCTCATT CATnTCATA TAATCCGGnA 360



## (2) INFORMATION FOR SEQ ID NO: 4194:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4194:

ACAAAGGACG ACATTAGACG AATCATCTGG AAAGAGAATC AAAGGTAATA ATCCTGTAGT 60  
 CGAAAATGTT GTCTCGAGTG GATCCTGAGT ACGACGGAGC ACGTGAAATT CCGTCGGAAT 120  
 CTnGGAGGAC CATCTCCTAA GGCTAAATAC TCTCTAGTGA CCGATAGTGA ACCAGTACCG 180  
 TGAGGAAAGG TGAAAAGCAC CCCGGAAGGG AGGTGTAAAT AGAACCTGAA ACCGTGTGCT 240  
 TACAAGTAGT cAGAGCCCGT TAATGGGTGA TGGCGTGCCT TTTGTAGAAT GGAACCGGCG 300  
 AGTTtACGAT TTGgATTgCA AGGTTAAGCA GTAAATGTGG GAGCCGTA 348

## (2) INFORMATION FOR SEQ ID NO: 4195:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4195:

AAGGCAGATG CTCTCCCAGC TGAGCTAATT CTCCGATTTA AAACCTGCCTG GCAACGTTCT 60  
 ACTCTAGCGG AANTAAGTng GACTACCATC GACGCTAAGG AGCTTAACTT CTGTGTTCGG 120  
 CATGGGAACA GGTGTGACCT CCTTGCTATA GTCACCAGAC ATATGAATGT AATTTATACA 180  
 TTCAAAATA GATAGTAAGT AAAAGTGATT TTGCTTCGCA AAACATTTAT TTTGATTAAG 240  
 TCTTCGATCG ATTAGTATTC GTCAGCTCCA CATGTCACCA TGCCTCCACC TCGAACCTAT 300  
 TAACCTCATC ATCTTTGAGG GATCTTATAA nCGAGTTGGG 340

## (2) INFORMATION FOR SEQ ID NO: 4196:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

TTTGCAGGTG GCGGTGCGAC TGCAGAAGAC GTTAAATTAA TGAAAGATAC AGTAGGTGCT 60  
 GATGTAGAAG TAAAAGCATC AGGTGGCGTA CGTAATTTAG AAGATTTCAA TAAAATGGTT 120  
 5 GAAGCAGGTG CGACACGTAT TGGTGGCAGC GChGTGTTC AATTATGCAA GGTTTAGAAG 180  
 CAGATTCAGA TTACTAATAT ATAThAAThT TGGGAGTGAT AGCTATGACA AGACCATTTA 240  
 10 ATCGTGTACA TTTAATCGTA ATGGATTGAG TAGGTATTGG TGAAGCGCCA GACGCAGCTG 300  
 ATTTTTAAAG ATGGAGGTTT ACATACTTTT A 331

## (2) INFORMATION FOR SEQ ID NO: 4197:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 371 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4197:

GTAGACGTCC CGATAGCCGT TACGCATGGT TACGATGTGT ATTGGTGTGC GCATGGGTGC 60  
 25 AGCTGCTATA TTTGAATATG TCGGTTAGAA TGGTTGATTT TGGATGAAGC GGATTCGTTT 120  
 TGTATTGAA TGAAGTAGGC TGAAGTTGAA GCCAGTTGAA GTTGAAGCGG GTTGAAGCAA 180  
 30 TTTCGTTTTA TTGAATGAAG CTGTGTGAAA TATAGTGATT GAACAAAAAA AGTGGTTTAA 240  
 TGGGATGGTG GTTATTTCCG TTTTAGAATT TAACATTTAC ACGTCTAATT TTAAATCATT 300  
 GTTTTAAATT TTATGAATCG AAGCCCTTTG GATTTAATAn TATTGCTAAT GChAGTAACT 360  
 35 nATCTGATTG T 371

## (2) INFORMATION FOR SEQ ID NO: 4198:

40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4198:

GCGACCCCAA CCTTGGCAAG GTTGTnATTC TACCGCTGAA CTACTTCTGC ATATGCCGGT 60  
 50 GAAGGGAGTC GAACCCCCAC GCCGTAAGCT nAGnATCCTA AGTCTAGTGC GTCTGCCAAT 120  
 TCCGCCACAC CCGCAAATGG TGAGCCATAG AGGATTCGAA CCTCTGACCC TCTGATTAAA 180  
 AGTCAGATGC TCTACCAACT GAGCTAATGG CTCTTCCATG GTGCCGGCCA GAGGACTTGA 240

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TAAGAATAAA TGGTGGAGAA TGACGGGTTG GnACCGTCGA CCCTGTGCTT GTTAAGGCAG 360  
 ATGGTTTTCC CACTGGGGTA AATTTTCCGA TTTAAAAATG 400

(2) INFORMATION FOR SEQ ID NO: 4199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4199:

ATCAGTTGCT GTTGC GCCTT GTGTAATGA ATTTACTAGT CGTACACCAA TAACCTCTGG 60  
 AATTGGGAAA TAAGAAGGTT GTCCAAGCAT TCCAGCTTCA GCTTCAATAC CACCAACACC 120  
 CCATCCTAGT ACGCCAATAC CATTATCAT TGTGTATGT GAATCAGTAC CAACTAATGT 180  
 ATCTGGAAAT GCAGTTTTTT CACCATCTAC ATCACAACA TGTACAACAC TTGCTAAATA 240  
 TTCTAAGTTA ACTTGGTGAA CTATTCCAGT TGCAGGAGGG AACTGCATTG TAATTATCAA 300  
 ATGCTTTTCG TTGGCCCAAT TAAAAAACT GGATAACGTT CATnGTTACG TTCCAATTCC 360  
 TAATTTCCnA ATTACGGTTC CAnGAGCTTC TGGGATTTTG 400

(2) INFORMATION FOR SEQ ID NO: 4200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4200:

CAACCTTTAT TGGTAAAAAC ACCCCAGCCA GGCACCTTAC GCCTACGCAT CGCTTGTACA 60  
 CGTGCTACTA nAGGTTTACC AACCACACCT GATTCAATTG CTTTTTTAGC AGTAATTGCC 120  
 ACATCTGTGT GACGATAATG ATATGCGACA GTTAATAATT TGTGATTTTT ATTAGCCGCT 180  
 TCAATCATGC GATCACACTC TTCCGTCGTC ATCGCCATTG GCTTTTCACA CAATACATGG 240  
 CACACCATGG TTCAATGChT CTATAGAAAG ATCAGCAGGA ATTTATTAGG TGTACAAATG 300  
 ACCCATCAAC AAGTTTAAAC AGCTCGCTAG GTGnC 335

(2) INFORMATION FOR SEQ ID NO: 4201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4201:

ATGATGTGGC GGTGGTGAAA TCAGACCGAT ACCTGGCGTT GACCCTCTTG TCTTCGCAAT	60
CCACGGATAT ACCTTAGTAC CAGGTAATTG ACCACCTTCA CCAGGCTTTG CACCTTGCGC	120
AACTTTAATT TGAATTTCTT TGGCATGTTG TAAATAATCA CTAGTTACAC CAAAACGCCC	180
AGAAGCAACT TGTTTAATCG CACTTACTTT GTTGCTTCCA TCAACTTGTA CTTCATAACG	240
TTTTGCATCT TCGGCAACTT CACCACTATT ACTCTTTCCA nCTAATTGGG TCATGGGCTG	300
TGCTAACGTT TCATGTGCTT CCGnTGnAAT CGATCCATAA CTCATCGGCC CCGTATTAAA	360
GCGGTTGGAC	370

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(2) INFORMATION FOR SEQ ID NO: 4202:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 380 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4202:

CAGCTAGCGA CTTACCTTGA CGTTTTGnGT ATTCAATCCA GCTTTGnGG AATGAGtCGG	60
gATATAAGCA TCTTTAGATA ATGCACCATC AACTAATGGA TATTTATGTC CAGTTGGaGC	120
CAGAAATCAT AAACGTCTTC AGTGTAAGCA ACAGCATCTT CaTTTAATGC CAAAATGCTT	180
GGaTTAgTGC AATAACCATC GCAACTGnGC CAnACCTTGT GTTGGCTCGC CGCCTGAATT	240
CAATCCATAA CGTGCTGTAT CTGTAGCAAT AACTAATACT TTTTCATTCG GTCTAGTTGC	300
TAAATAATCT TTAGCTAATT GAATTGCTGG TGTTCAGCA TAACAAGCTT CTTTCATTTT	360
AAAGCAGCGT GCAAAAGGTT	380

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(2) INFORMATION FOR SEQ ID NO: 4203:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4203:

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GACATGTCAC CAAGAGCATT AGAAGAAGTT ATTTACTTTG CTTCTTATGT TGTGTAGAT 120  
 CCAGGTCCAA CTGGTTTAGA AAAGAAACT TTATTATCTG AAGCTGAATT CAGAGATTAT 180  
 5 TATGATAAAT ACCCAGGTCA ATTCGTTGCA AAAATGGGTG CAGAAGGTAT TAAAGATTTA 240  
 CTTGGAAGAG ATTGATCTTG ACGAGGAACT TAAATTGTGA CGCGATGAGT TGGGAATCAG 300  
 CTACTGGGTC CAAAGACTTA CTCCGTGGCA ATTAACGGTT TAGAAGTTGT TnGAATCATC 360  
 10 CCGTAATCCA GGGTACCACC CTCCnnGGnT GGATTTAGGA 400

## (2) INFORMATION FOR SEQ ID NO: 4204:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4204:

AAATTCITCC GCCCTGTAAT TCCTTAACCG CTTCAACGGC ATCGTnAATn TCTTACATTT 60  
 25 AGATAAAGAT GCATTGCAAG ATATCGTCAA CTTATTATTA GACGATGTAC AAGTTACATT 120  
 AGACAAAAAA GGTATTACGA TGGACGTTTC TCAAGATGCG AAAGATTGGT TAATTGAnGA 180  
 AGGCTATGAT GAAGAATTAG GTGCACGTCC ATTAAGACGT ATTGTTGAAC AGCAAGTACG 240  
 30 TGACAAAATT ACAGATTACT ATTTAGATCA TACAGACGTT AAACATGTGG ATATAGATGT 300  
 TGAGGATAAC GAATTAGTCG TAAAAGGTA 329

## (2) INFORMATION FOR SEQ ID NO: 4205:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4205:

GGTAAACAAA AAACCTCCCT TTGGAAGCGA ATTATGGAGC GGAAGATAGG ATTTACACCT 60  
 ATACCTCGTT CCGGGAAGGG CTGTTTCTAA AAGTTGAACT ACTCCCGCAA ATATTAAATT 120  
 50 ATGGAGCGGA AGATAGGATT TACACCTATA CCTCATTCCA GGAAGGAATG TATTCTAAGA 180  
 GTTGAAATAC TCCCGCATTa TTATTAAATT ATGGAGCGGA AGTAGGATTT GCACCTATAC 240  
 CTCGTTCCGG GAAGGAGCTG TTTCTAAAAG TTGAACTACT ACCGCATAAA CCTGGTGGCG 300

## (2) INFORMATION FOR SEQ ID NO: 4206:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4206:

TACTTTGTGA ATCCAGAAAA CTTTGAGGAT GTCACATAA GTGTGAATAT TACATTCCCA 60  
 AATCCAAATC AATATAAGT AGAGTTTAAT ACGCCTGATG ATCAAATTAC AACACCGTAT 120  
 ATAGTAGTTG TTAATGGTCA TATTGATCCG AATAGCAAAG GTGATTTAGC TTTACGTTCA 180  
 ACTTTATATG GGTATAACTC GAATATAATT TGGCGCTCTA TGTCATGGGA CAACGAnnAG 240  
 CATTTAATAA CGGATCAGGT TCTGGTGACG GTATCGATAA ACCAGTTGTT CCTGAACACC 300  
 TGATGAGCCT GGTGAAATTG AACCAATCCA GGGATCAGAT CTGACCCAGG TCAGATCTGG 360  
 CAGCGATCTA ATCAGnAGCG GTCAGATCGG GnAGGATCAC 400

## (2) INFORMATION FOR SEQ ID NO: 4207:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4207:

AAAAAGTTGA GAAAAATGTT TGAATCAGCA AACGTTGTGC AATCGAAATT TCCACACCAT 60  
 CAAAACCTGC TTTAATCGCG CGTAATGTAG CATCGCnGwk ACTGCTGAAT GATGCTATTG 120  
 ATTTTCTCAT GAGACATGGC GATAACATCG TGTTtCAATC GGTGAATGCA ATGWCATAGG 180  
 GCTTGGTCCA TACACCTTTC CAAAATTTAA AATGGCTTGA TTTGAAAAAC GACCAGCATG 240  
 CGCTACTGGG ATAATAGCGA GGCTACCATG TTGTTTCATC GTAGATCCCA TGTTAGTTAA 300  
 TCCAGGGATA CAACCATCAT GATCAATATT AAAnCATATC CAACCATTGA CCATAAGGTC 360  
 AATGTAACAC GCCGGTGACT TCATCCAGCT GAATAGACGC GT 402

## (2) INFORMATION FOR SEQ ID NO: 4208:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4208:

5 GAAGAGTTGC AGCAGCAGAT ACAATTTATC CATTCACTCA AGCTGAAAAT GTTTGGTTAC 60  
 CAAACAAAAA TGACATCATC GAAAAAGCAA AAGAACTTT AGAATTTTAA TACATTTTAA 120  
 AAGTTAACGA ATTAGCCGTG ATTTTAGTCT CATTGATTAA AATGAAATnG TTAATTTACG 180  
 10 AAATCTTAGG AGGGCAAAAA CGTGGGCATT TGAATTTAGA TTACCCGATA TCGGGGGAAG 240  
 GTATCCACGA AGGTGAAATT GTAAAATGGT TTGTTAAAGC TGGAGGATAC TATnGGAAGA 300  
 AGACGATGTT TTAGCTGGAG GTACAAAACC GATAAATCAG TAGTAGAAAT CCCCATCCAC 360  
 15 CAGCATCTGG TACnGGTAAG 380

## (2) INFORMATION FOR SEQ ID NO: 4209:

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4209:

25 AATAAACCTC AGGCTATTCA ATGGCATACA AATTTAACGA ATGAGCGATT CACTACTATC 60  
 30 GCACATCGTG GCGCAAGTGG CTATGCACCC GAGCATACGT TTCAAGCATA TGATAAGAGT 120  
 CATAATGAGT TAAAAGCATC TTATATCGAA ATTGATTTAC AACGTACCAA AGATGGCCAT 180  
 TTAGTTGCTA TGCATGATGA AACTGTTAAC CGTACAACAA ATGGACACGG TAAAGTTGAG 240  
 35 GATTATACCC nTGATGAATT AnAACAGTTA GATGCAGGAA GTTGGTTAAT AAAAAATATC 300  
 CnAAATACGC CAGAGCAGTA TTAAAATGCT AAGTACCAC TTAGGTGGAA TTTAGGACGT 360  
 ATTGGCCCGA TGCCAAAnTT TATATTGAAC CAAGCACCTG 400

## (2) INFORMATION FOR SEQ ID NO: 4210:

## (i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 330 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4210:

50 GCCCCAACC ACAAAGGCTG TAGGCTACAA ATATGGAGAC GGCGGGATTT GAACCCGCGT 60

AAAAGTGATA AACACCAAC ATGATGCTAG TTTGATTAAG TTTCTTCTAA ACAGACTTCA 180  
 AACGGCAtnG TTAGCATATC CTATTAAGGT TGAATCGCGT TAACAGCACA TAGGAAATGC 240  
 5 TGTTAGGCGA TGCAGAGTGC GATTAGGCAG CTACTGCGAA ATTATTGTnt GATTTGCCAG 300  
 TTATTATnAA CTGTGTGGTG TTGATGACGA 330

## (2) INFORMATION FOR SEQ ID NO: 4211:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 339 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4211:

AAATCATCTT ATGACTGCTT TTTATTATAC TTTACATTTT TCGTTTCGTC AGATTCAAAC 60  
 GTTTTCACTT CGCCAAGCCA TCTTCTTTG TGTTTGCTTT TATTTTGACG TTTTAGACAT 120  
 AAAAAAGAG ACCTTGCGGT CTCAATGnGG CTCATCGCAT CCACTTTTTG CCTGGCAACG 180  
 25 TTCTACTCTA GCGGAACGTA AGTTCGACTA CCATCGACGC TAAGGAGCTT AACTTCnGTG 240  
 TTCGGCATGG GAACAGGTGT GACCTCCTTG CTATAGTCAC CAGACATATG AATGTAAATT 300  
 ATACATTCAA AACTAGATAG nAAGTAAAG TGATTTTGC 339

## (2) INFORMATION FOR SEQ ID NO: 4212:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 334 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4212:

GCGATGGTTG AACATTGAC TGATATTAAAGAGTTTATGA ACCAAGTTGA GTCGCATAGC 60  
 TAGTATGAAA CGTGGTGTGC GCATGGGAAC TATCAAGCTT TGAAGATGTG GTACTACATG 120  
 45 CGTTGAATTG GGGATCGGTA CTTTATATGA AGACGTGCTG CTTCCATTAA ATGAGTGATG 180  
 CGATTTTGGC ATGAAGGTCA CCTnAAATGT ACATTGTTGT AATAAAATTG CCTATAAAAT 240  
 TTTTAGCACA TAAATAAGA GGGGCCAnCC ATTTTAGACT ATAACAACGG TTGGCTCTTT 300  
 50 GAATTGTAAA AAGAAAACCA TACGCTATGn TATT 334

## (2) INFORMATION FOR SEQ ID NO: 4213:



(A) LENGTH: 332 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4213:

10 CTATGATTTC ACCGAGTCTC TCGTTGAGAC AGTGCCCAAA TCGTTACGCC TTTCGTGCGG 60  
 GTCGTTACCC GACAAGGAAT TTCGCTACCT TAGGACCGTT ATAGTTACGC CGCCGTTTAC 120  
 TGGGGCTTCG ATTTCGTAGCT TCGCAGAGTA nACCCACTCC TCTTAACCTT CCAGCACCGG 180  
 15 GCAGGCGTCA CCCTATACAT CACCTTACGG TTTAGCAGAG ACCTGTGTTT TTGATAAACA 240  
 GTCGCTTGGG CCTATTCACT GCGGCTCTTC TGGGGCGTTA ACCCTAAAGA GCACCCCTTC 300  
 TnCCGAAGTT TACGGGGTCA nTTTGCCGAG TT 332

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(2) INFORMATION FOR SEQ ID NO: 4214:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 363 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4214:

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CGCCTGGCAA CGTTCTACTC TAGCGGAACG TAAGTTGGCT ACCATCGTCG CTAAGACCT 60  
 TTCTTGACTT GTGACAATCG CTTGCTTCTT TCCTCTCCTT CGGCTCTCGC TTACTCATTT 120  
 35 AGCTCTACTA AACTCGTTGC GCTCTTTTCT CGTTTCGTCA GATTCAAACG TTTTCACTTC 180  
 GCCAAGCCAT TTTTCTTTGT GTTTACTTTT TAnTTTGACG TTTTAGACAT AAAAAAAGA 240  
 GACCTTGCGG TCTCAATGCG GCTCATCGCA TCCATTTTTT GCCTGGGCAA CGTTCTACTC 300  
 40 TAGCGGAACG TAAGTTGGGT ACCATCGACG CTAAGAACCT TCTTGGA nTG TGGACAACGn 360  
 TGG 363

40

(2) INFORMATION FOR SEQ ID NO: 4215:

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(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 338 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4215:

55

TTATTTGTAT TGTATAGAGA GAAATAAAAA GAAACCTTGT TTTACAAGGT TTCTAATACG 120  
 TTATGTTATG TAAATAACAG TTAATTATAC CGGTGGTCCG GGTGGAACCG AACTCCACA 180  
 5 AGTGAACCG GATTTTTGTAG TCCCGCGCGT CTGCCAATTC CGCCACACCG GCTTAATGGT 240  
 AAACAAAAAA CTTCCTTTG GAAGCAATTA TGGAGCGGAA GATAGGATTT ACACCTATAC 300  
 CTCGTTCCGG GAAGGACGTG TTCTAAAAGT TGACTACC 338  
 10

## (2) INFORMATION FOR SEQ ID NO: 4216:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear  
 15

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4216:

ACGGTGATCC CATAATGCTT GAACATCAAT TTCATCCATT AATGTTACAT GAGGTGCAGT 60  
 ATGCTTAGAG TTAACCATTG CTTTCGCAAT TGCTCTACGC ATAGCAGGGA TTTTTCAGT 120  
 25 TGTTTCTGGG AAGTCGCCCTT CTAATGTTAC TGCTGCAGGT GCTGCAGGAG TTTCAGCAAC 180  
 TTCTTCACTT GTAGCTGAAG CAGCTGATTC ATTTGAAGCT GTTGGTGCAC CACCATTTAA 240  
 GTATGCATCT ACATCTTCTT TTGTAATACG ACCATTTTAA CCAGATCCAG AAATGCTTT 300  
 AATGnTAACA CCTnTTTCAC GTGCGTATTA CGACTGAAGG CATGCCTTAA CAGTCnGGTT 360  
 CACCACTCTC AGTTGAGAGC ACAGGGCTGC nCGCTGGCGC 400

## (2) INFORMATION FOR SEQ ID NO: 4217:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear  
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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4217:

AGGGAATCGA ATTTTCTTTC TCTTCCTCCG GGTACTAAGA TGTTTCAGTT CTCCGGGTGT 60  
 GCCTTCTGAT ATGCTATGTA TTCACATATC GATAACATGA CATAACTCAT GCTGGGTTTC 120  
 50 CCCATTCGGA AATCTCTGGA TCAAAGCTTA CTTACAGCTC CCCAAAGCAT ATCGTCGTTA 180  
 GTAACGTCCT TCATCGGCTT CTAGTGCCAA GGCATCCACC GTGCGCCCTT AATAACTTAA 240  
 TCTATGTTTC CATCCTACAG GAAACGCGTT ATTAATCTTG TGAGTGTrCT TTCGAACATA 300  
 55

## (2) INFORMATION FOR SEQ ID NO: 4218:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4218:

```

GGCGCCCTCG TGCCAAACAG TGCTCTACCT CCAATAATCA TCACTTGAnG CTAGCCCTAA      60
AGCTATTTCG GAGAGAACCA GCTATCTCCA GGTTCGATTG GAATTTCTCC GCTACCCTCA      120
GTTTCATCCGC TCACTTTTCA ACGTAATCGG TTCGGTCCTC CAnTCAGTGT TACCTGAACT      180
TCAACCTGGA CCAAGGGTAG ATCACCTGn TTCGGGTCTA CGACCAAATA CTAAACGCCC      240
TATTCAGACT CGCTTTTCGCT GACGGCTCCA CATTTACTGC TTAACCTTGC ATCAAATCGT      300
AACTCGCCGG TTGCATTCTA CAAAAGGCAC GCCATGCACC CATTA                        345

```

## (2) INFORMATION FOR SEQ ID NO: 4219:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4219:

```

TCTTATGACT GCTTTTTATT ATACTTTACA TTTCTCGTTT CGTCAGATTG AAACGTTTTT      60
ACTTCGCCAA GCCATCTTTC TTTGTGTTTG CTTTTATTTT GACGTTTTAG ACATAAAAAA      120
AGAGACCTTG CGGTCTCAAT GCGGCTCATC GCATCCACTT TTTGCCTGGC AACGTTCTAC      180
TCTAGCGGAA CGTAAAGTTC GnACTACCAT CGACGCTAAG GAGCTTAACT TCTGTGTTTG      240
GCATGGGAAC AGGTGTGACC TCCTTGCTAT AGTCACCAGA CATATGGAAT GTAAATTATA      300
CATTCAAAAC TAGATAGTAA GTAAAGTGn TTTGCTTCGC AAACnTTAT TTTGGTTAGT      360
CTTCGTC                                                                367

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## (2) INFORMATION FOR SEQ ID NO: 4220:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4220:

5 AAGAGCCTTT CTTGACTTGT GACAATCGCT TGCTTCTTTC CTCTCCTTCG GCTCTCACTT 60  
 ACTCATTTAG CTCTACTAAA CTCGTTGCGT TCTTTTCTCG TTTCGTCAGA TTCAAACGTT 120  
 TTCACTTCGC CAAGCCATTT TTCTTTGTGT TTGCTTTTTA TTTTGACGTT TTAGACATAA 180  
 10 nAAAAAGAGA CCTTGCGGTC TCAATGCGGC TCATCGCATC CATTTTTTGC CTGGCAACGT 240  
 TCACTCTAGC GGAAnTAAGT CGAACTACCA TCGACGCTAA GGAGCTTAAC TTTCTGTGTT 300  
 CGGCATGGGA ACAGGTGTGA CCCCnTGGC TATAGTCACC AG 342

## (2) INFORMATION FOR SEQ ID NO: 4221:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 20 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4221:

25 ACCGGATGAC AGCCCCAGGA TCGATGAGC CGACATCGAG GTGCCAAACC TCCCCGTCGA 60  
 TGTGAACTCT TGGGGGAGAT AAGctGTTAT CCCCggGGTA GCTTTTATCC gTTGAGCGAT 120  
 30 GGCCCTTCCA TCGGGAACCA CCGGATCACT AAGTCCGTCT TTCGACCCTG CTCGACTTGT 180  
 AGGTCTCGCA GTCAAGCTCC CTTATGCCTT TACACTCTAT GAATGATTTC CAACCATTCT 240  
 GAGGGAACCT TTTGAGCGCC TCCGTTACCT TTTAnGAGGC GACCGCCCCA GTCAAACCTGC 300  
 35 CCGCCTGACA CTGTCTCnCA CCACGATAAG TGGCGnG 337

## (2) INFORMATION FOR SEQ ID NO: 4222:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 40 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4222:

45 GGCGCTTGAC TAAAAAGAAA TTGTACATTG AAAACTAGAT AAGTAAGTAA AATATAGATT 60  
 50 TTACCAAGCA AAACCGAGTG AATAAGAGT TTAAATAAG CTTGAATTCA TAAGAAATAA 120  
 TCGCTAGTGT TCGAAAGACA TCCACCAAGn TTAATAACGC GTTTAAATCT TTTTATAAAA 180  
 GAAAACGTTT AGCAGACAAT GAGTTAAATT ATTTTAAAGC AGAGTTTACT TATGTAAATG 240

55

ACATAGATTA AGTTATTAAG GCGGCACGGT GGGTGCCnTG GCACTTAGAA GCCGCTGAAG 360

G 361

5 (2) INFORMATION FOR SEQ ID NO: 4223:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4223:

CGGTAGAATA CAACCTTGCC AAGGTTGGCG TCGCGGGTTC GAATCCCGTC TTCTGCTCCA 60  
TTATTTTGCC GGGGTGGCGG AACTGGCAGA CGCACAGGAC TTAAAATCCT GCGGTGAGAG 120  
20 ATCACCGTAC CGGTTGATT CCGGTCCTCG GCACCATTTT AGCGCCCGTA GCTCAATTGG 180  
ATAGAGCGTT TGACTACGGA TCAAGAGGTT ATGGGTTTCA CTCCTATCGG GCGCGCCATT 240  
TTTAAATTAA TTGAATAACG GGAAGTTAGC TCAGCTTGGT AGAGCACTTG GTTTGGGGAC 300  
25 CAAGGGTCGC AGTTCGAATC CTGTCTTCCC GATTACTCnT AAnTCCATTT AnGGGGGCTA 360  
GCTCAGTGGG GAGAGCGCTG CTTGCACGCA GGAGGTCACG 400

30 (2) INFORMATION FOR SEQ ID NO: 4224:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4224:

40 CATAATATAC TCCTAAGTGT AAAGGGGAAT TTCCTGGGTA ATAATTCGCG TGTGCACCTT 60  
GAGTGACTTC TACCATTTTA TAGTCAAATT GCTTTAGTTC GTTTGGTTTA ACGCCGACAC 120  
TCGCAAATGT ATAATCAAAG AACTTCACAA TATTGTTGCC TAAGAAGCCT TTGAATTCAA 180  
45 TAGTGTCAAT TCCAGCAATT TGTTGCGCAA CAATACTTGC TGCACGGGTG AGCGCCCCCA 240  
GnCAAAAGGA CCACTAGCCG GTAGAATCGA CATGTCGATA ATGTGATGGT TGCCAATAAT 300  
CGCCTATTGC ATAATGTTTG GACCATTGGT TCCAAATTTA TCGTTACCGG TATGAAACCT 360  
50 TTCGATCCAG TTGGATAATT GAACTTCGnA AATTTGATTG 400

(2) INFORMATION FOR SEQ ID NO: 4225:

55

- (A) LENGTH: 328 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4225:

GGGTTCAATT TCTGCATACC AATCGATGCC AGCTCTATTT CTGACAATAT CCATATATTT 60  
 TGAAATTTTC TCTAATTCTT TGCCACTAAC CTTTTACCA TTCAACCAA ATTGATCCTG 120  
 TGTTAACTGG TCGTTAAAAG TGACTTTCGT TTCAGTGTA AATTTTCTA ATGTAACAGA 180  
 TATGCTATTA TTCAATTGAA TGATTAGTGC TTCATCTTTT TTACCCCAAT ATTTTATnAG 240  
 TGCAATATTC GTATGTGCAC GTGCTTTGCC ACTnnTAATC AACGCATTAA CCTCCTAAAT 300  
 TCTCAATCCA AGTATGTGCT GCACCAGC 328

20

## (2) INFORMATION FOR SEQ ID NO: 4226:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 325 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4226:

30

TGACGGGTTC GAACCGCOGA CCCTCTGCTT GTAAGGCAGA TGCTCTCCCA GCTGAGCTAA 60  
 TTCTCCGATT TAAACTGCC TGGCAACGTT CTA CTCTAGC GGAAnGTAAG TTCGnACTAC 120  
 CATCGACGCT AAGGAGCTTA ACTnCTGTGT TCGGCATGGG AACAGGTGTG ACCTCCTTGC 180  
 TATAGTCACC AGACATATGA ATGTAATTTA TACATTCAA ACTAGATAGT AAGTAAAAGT 240  
 GATTTTGCTT CGCAAAACAT TTATTTTGAT TAAGTCTTCG ATCGATTAGT ATTCGTCAGC 300  
 TCCACATGTC ACCATGCTTC CACCT 325

40

## (2) INFORMATION FOR SEQ ID NO: 4227:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 331 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4227:

50

GCGCAACTCA CACAACAAGG TGGCAATCAC TCTGAACAA GTGCGGCAAn TnTTCAACA 60

55

AACCTTACGC AAGAAGCACG TGACGGTTTA TTAGATCCAG TCATTGGTCG TGGATAAAGA 180  
 AATTCAAGnA ACTGCTGAAG TTTTAAGTAG ACGAACTAAA AACAATCCTA TATTAGTTGG 240  
 5 AGAAGCTGGT GTTGGTAAAA CTGCCATTGT TGGGAAGGTTT AGCACAGGCA ATCGTTGGAA 300  
 GGAAATGTAC CAGCAGCAAT CAAAGACAAA G 331

## (2) INFORMATION FOR SEQ ID NO: 4228:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 333 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4228:

AGAGGTCCGT TGCCTTACCG CTTGGCTATA GCCATTAATA ATAAGGGCGG CTGAAGGGGA 60  
 TCGAACCCCTC GAATGTCCGA ACCACAATCC GATGTGTAA CnCTTCACCA CAGCCGCCAT 120  
 GGCAGGGGCA GTAGGAATCG AACCCACACC AAAGTTTTGG AGACCTCTAT TCTACCGTTG 180  
 25 AACTATGCCC CTATTAAAAA TAATAAATGG AGGGGGGCAG ATTCGAACTG CCGAACCCGA 240  
 AGAGCGGATT TACAGTCCGC CGCGTTTAnC CACTTCGCTA CCCCTCCATA AATGGTGCCG 300  
 GCCAGAGGAC TTGnAACCCC CAACCTAATG GTT 333

## (2) INFORMATION FOR SEQ ID NO: 4229:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4229:

CTCTTACTTT GTAAACCAAA TCTTAAATTA AAATATTGAA AATGCAATGn ATCCTTAATA 60  
 TTTTATTAAA CCTATAATTA CTTATTAAAA ATAACACACA ATATTCATAA AGTTTTAAAA 120  
 45 ATATTCTGTT TTATCACCTA CTATTAGTGG AAAAGTACAA TTGCAATTGT ATATAGTTTG 180  
 CATAACGCTT CAAAAGTAAT TTCTTTTTTG TTTAGTTCAA AAAAAATTAG AGGTGATGTT 240  
 ATATGAATAA CGGTTTTTTC AATAGCGACT TTGATTCAAT TTTTCGAGGA TGATGAAAGA 300  
 50 TATGCAAGGT TCAAATCAAG TCGGAAACAA AAGTACTATA TThATGGTAA GGAGTTTCAC 360  
 CTGAGGACTG GCGCAACTnC ACACACCAGG TGGCCATCAC 400

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 339 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4230:

```

CATTAAACGGG CTCTGACTAC TTGTAAGCAC ACGGTTTCAG GTTCTATTTT ACTCCCCCTTC      60
CGGGGTGCTT TTCACCTTTC CCTCACGGTA CTGGTTCAC TACGGTCACT AGAGAGTATT      120
TAGCCTTAGG AGATGGTCCT CCCAGATTCC GACGGAATTT CACGTGCTCC GTCGTACTCA      180
GGATCCACTC AAGAGAGACA ACATTTTCGA CTACAGGATT ATTACCTTCT TTGATTCACT      240
TTTCAGATG ATTCGTCTAA TGTCGTCCTT TGTAAGTCCG TATAGAGTGT CCTAAsAACCC      300
CAACAAGCAA GCTTGTGGT TTGGGnTCTT GCCGTTTCG      339
  
```

(2) INFORMATION FOR SEQ ID NO: 4231:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 349 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4231:

```

GAAGTCATAT GCATACACTT GGTATCATT ATTCATACGT TCAATCGCAT CTGTAACTG      60
AATTCGTTA CCTGCGCCTT CTTTTGCGT TTTAAATAA TCGAAAATTT CAGGCGTTAA      120
TACATAACGT CCCATAATAG CTAGGnTTGA TGTTGCCGTA CCTTGTGCTG GCTTTTCAAC      180
AACTTTTTTC ACTTCAGACT GACGTCCGTh TTTAGTTAAT GGGTCAATAA TTCCATAACG      240
ATGAGTATCT GCTTCCGGAA CTCTTGAC ACCTATAACT GAGTGCCCTG ThTCTTCATA      300
AACGTCAATC AACTGTTTCA CTGCTGGCAC TTCAGAGTCA ACAATATCG      349
  
```

(2) INFORMATION FOR SEQ ID NO: 4232:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 377 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4232:



CCAGGATGCG ATGACCGACA TCGAkGTGCC AAACCTCCCC GTCGATGTGA ACTCTTGGGG 120  
 GAGATAAGCC TGTtATCCCC GGGGTAGCTT TTATCCGTTG aGCGATGGCC CTTCCATGCC 180  
 5 GAACCACCGG ATCACTAAGT CCGTCTTTTCG ACCCTGCTCG ACTTGTAGGT CTCGCAkTCA 240  
 AGCTCCCTTA TGcCTTTACA CTCTATGAAT GATTTCaAC CATTCTGAGG GAACTTTGaG 300  
 10 CGCCTCCGTT ACCTTTTtAGG AGGCGACCGC CCAGTCAaAC TGCCCGCCTG ACACTGTCTC 360  
 CCACCACGAT AAGGTCG 377

## (2) INFORMATION FOR SEQ ID NO: 4233:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 355 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4233:

GGCTAGCCTC AAGTGATGAT TATTGGAGGT AGAGCACTGT TTGGACGAAG GGCCCCCTCTC 60  
 25 GGGTTACCGA AGTTCAGACA AACTCCGAAT GCCAATTAAG TTAACTTGG GAGTCAGAAC 120  
 ATGGGTGATA AGGTCCGTGT TCGAAAGGGA AACAGCCCAG ACCACCAGCT AAGGTCCCA 180  
 AATATATGTT AAGTGGAaaa GGATGTGGCG TGGCCCAGAC AACTAGGATG TTGGCTTAGG 240  
 30 AAGCAGCCGT CATTTAnAGA GTGCGTAATA GCGCACTAGT CGAGTGACAC TGGGGGGAAA 300  
 GGGTACCGGG GCTGAACATA TTACCGAAGC TGGTGGGTTG TCCTTTGGAC AnTTn 355

## 35 (2) INFORMATION FOR SEQ ID NO: 4234:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 40 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4234:

45 ATCCGCCTCC CGCAATATTT TATAGGTCTC GTAGTGTAGC GnTTAACACG CCTGCCTGTC 60  
 ACGCAGAGAT CGCGGGTTCG ATTCCCGTCG AGACCGCCAT CATTACATTT TTATTATGGT 120  
 TCAGTAGCTC AGTTGGTAGA GCAATGGATT GAAGCTCCAT GTGTCCGCAG TTCGACTCTG 180  
 50 TCCTGAACCA TTTCTTAGCC GGCCTAGCTC AATTGGTAGA GCAACTGACT TGTAATCAGT 240  
 AGGTTGGGGG TTCAAGTCCT CTGGCCGGCA CCATTtATGG AGGGGTAACG AnTGGGCTAA 300

55

TTAATAATTT TAATAAGGGG CATAnTTCAA CGGTAnAATA

400

## (2) INFORMATION FOR SEQ ID NO: 4235:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 341 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4235:

ATGCCATGTT CACCTTGTTT AAAATCAAGG TTTGTAATGT TTCCTTGTGT CACGATAATA 60  
 GCGTAATAT CACTCTTTC ATGATTGCGG ATGTAGTCTA AATCAAAGTT GATTAATAAA 120  
 TCACCTTCTT TAACTnnTTG ACCTTCCTCA ACATGTAAAG TAAAGCCTTC TCCGTTTAAAT 180  
 TTAACAGTGT CTAAACCGAT GTGGATTAAT AGTTCATAAC CACTATCTGA TACAAGACCA 240  
 ATTGCATGnT TTGTTGGGAA AATCATTTGT ACTTTACCGT TGAATGGTGC ACGAACTTCA 300  
 CCTTGTGAGG TTTGATAGCG ATACCGTCAC CCATGCATTT T 341

## (2) INFORMATION FOR SEQ ID NO: 4236:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4236:

GTTGATGCAG CCCGTTGAGC TCTAAACCAA CTGAGCTAAA GGTCTCTAAAT ATAATTTTAC 60  
 AACTAATAAA TAGTGGCGGT GGAGGGGATC GAACCCCCGA CCTCACGGGT ATGAACCGTA 120  
 CGCTCTAGCC AGCTGAGCTA CACCGCCTTA TATAGTTTGT AAATAATATG GTGGAGACTA 180  
 GCGGGATCGA ACCGCTGGAC CTCCTGCGTG CAAAGCAGGC GCTCTCCCAG CTGAGCTAAG 240  
 CCCCCATAAT AATTACAGTA TATCGGGAAG ACAGGATTCG AACCTGCGAC CCCTTGGTCC 300  
 CAAACCAAGT GCTCTACCAA GCTGAGCTAC TTCCCGTATA ATTAACGnGC CCGTAGGAGT 360  
 TGAACCCATG AACCTnTTGA TCChTAGTnC AAACGGTCTA 400

## (2) INFORMATION FOR SEQ ID NO: 4237:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 376 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4237:

5     nAntTTCTTGA CCTGACATCA CCTGAAATTG AATGGACATG GTCCACCAGG TCATATACTC     60  
       TAATCCATGG GTCGCCGATA CCTTCAACGn ACAACATCTA CACCACTATT TCTAATACAG     120  
       AATCTTTCTC CTGCACTACC GTTAATAAAT GCCTTACCAC TTGTGCGACC ATAGAATGAG     180  
 10     ACGTTACCAG CAATAATTTT ATTTTGTCTG TCTTCAAAAG GTGCTTTGAC AATGACCGTA     240  
       CCACCAGATA ATCCTTTACC AACATAGTCA TTCGCATCTC CAGTATGATG AATCATTAAAG     300  
       CCTTTGCGTG CATATGCTGC AAGACTTTGA CCAGCATGAC CATTCGTATA AACATTAAAT     360  
 15     GTATTTTCAG GAAGTC     376

## (2) INFORMATION FOR SEQ ID NO: 4238:

## (i) SEQUENCE CHARACTERISTICS:

20     (A) LENGTH: 335 base pairs  
       (B) TYPE: nucleic acid  
       (C) STRANDEDNESS: double  
       (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4238:

25     CGATTTAAAG CTAAGCCCAT TTTCGCTCTT TCTCCATAGC CTAACCAAGC AATACGTGAT     60  
       GGTAGTCCTT GATATGAAAT TTTTCTTCA GCTAAATCAA GCCATCTTAA TAACTTTTCA     120  
 30     TTTTCTGGGA AAAGTTTGCG CATTTCTTCA TCCGCACGCT CGATATCTTT TGGATCACCA     180  
       CTCAACGCAG CAAAGCGGAA TGGCCCTTTA CCTTCACAGA ATAATGGTCT AATGTAAGCT     240  
 35     GGTACAAAAG CTGGGAAGTC AnAAAGCATT TTTCACTCCG TATTGAAGGC TACTTGACGA     300  
       TATGnTACCA TAATCAATGC TACAGCGCCA CGTTG     335

## (2) INFORMATION FOR SEQ ID NO: 4239:

## (i) SEQUENCE CHARACTERISTICS:

40     (A) LENGTH: 348 base pairs  
       (B) TYPE: nucleic acid  
       (C) STRANDEDNESS: double  
       (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4239:

45     CCACAnTTAC AAGCAACTAC TGAAGGCGCT GTATTTATTA AAGGTGGCGA CGGTTTTGAT     60  
 50     TTCGGACACG TAGAAAGATT TATTCAAAAC CCGCCACATG GGGCAACGGT TGCATGGCAT     120

55

TTACCTAATG GTCAAGGTAC GCGTAATGTT GAAGTTCCAG TCAAAGTTTA TCCAGTTGCT 240  
 AATGCAAAGG CGCCATCAGC TGATGTGAAA GGTCAAATT TGCTGTTGGA CGGATGCGAT 300  
 5 GAACTACATT ACATTTGTCC ANTACAACAC AGATnGTATC ACTGCAGC 348

## (2) INFORMATION FOR SEQ ID NO: 4240:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 395 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4240:

TTGATGTTAA AGATTTAGCA AGGGGCGAGA GAACTGGAGA AGAGGTTGCC AAACGAATGG 60  
 AACGTGCTTC TGTATTGGCC CAAGTAGATA TTCATCGTGC AGCAACACAT AATAAAGGTG 120  
 TTATGAATGG CATACTGCT GTTGTMTTAG CAACAGGAAA TGATACGCGT GGTGCAGAAG 180  
 CAAGTGCACA TGCATTACGC GAGTTCGTGA CGGACAGTAT CGTGGTATTG CTACATGGCG 240  
 TTACGATCAA GATCGTTCAA CGATTGATT GGTACATTGG AAGTGCCTAT GACATTGGCA 300  
 ATCGTTGGCG GTGGGTACAA AAGTATTACC AATTGCTAAG CCTTCATTAG GAGnTACTAA 360  
 ATGGTAGAGT CCGCCCCAAG AATTAnGnCC CTGTA 395

## (2) INFORMATION FOR SEQ ID NO: 4241:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4241:

ACTAATGATT TATTATGTAG TGGTCTTTG TCATTAGCCA CAGCTATTGT GTACTTAAAA 60  
 ATAGGAATGC ATGAGTGCAA CTCTAnAnGn AGCATACTAA TTTCTAAAGA AAAAGTATTT 120  
 CTTTATGTTG GGGCCCCGCC AACTTGCAAT GTTGTAGAA TTTCTTTTCG AAATTCTTTA 180  
 TGTGGGGGCC CCGCCAACTT GCATTGTTTG TAGAATTTCT TTTGAAATT CTTTATGTTG 240  
 GGGCCCCGCC AACTAATTCC AATATATCAT TGTAGAGCTT AGGTCATTGA TTTTGGCTC 300  
 50 GGACTTTTAT GCGGATATGA ACCATGTAAA T 331

## (2) INFORMATION FOR SEQ ID NO: 4242:

- (A) LENGTH: 389 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4242:

10 TGCATTGCAT TATTGTACTG CGTAATTGTA CCTGGCTTTT TACCTTCAGT GCTTACTGGA 60  
 TCATCTAAAT GATTTTTAGC TGTGATTAAAC TCACGTTTAT CCGCTTTTGT GAAAATGGAC 120  
 TCTTGTA CTTTCTTACT ACCATCATTG TAAGTTACTG TCACAGGAAT CGTCGTTGTG 180  
 15 CTACCACCAG CTAAATTAGT AGGCATTGCT GTGCCATTTT TAATCGTTGC AGTACGTTTA 240  
 TTAGCAACTT GAACTGCATT GTTAATTTCA GCTGCTGTTA CATTGAACC ATAATCTTTC 300  
 ACAATTn CAG TTGTGTTGAC AGATGAGnGG CCGTGCAGTA AGGACTGGAT ACACTACGAG 360  
 20 TGACCGGACT GCTTCGGGnA ATGTGATGA 389

(2) INFORMATION FOR SEQ ID NO: 4243:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4243:

ATACGCATGT TAACGATCGA ATGCTTAATG TCCCGGGAAA TAAATCTATC ATAAGTTACT 60  
 35 TTAATGAAGT TGTCTCACGA CAAGGTAATC ATGTTGCGCT ATCATGAATG ATTTGACAAT 120  
 GACGTATGAA CATTACGCAA CTATGTGGAT GCCATTGCGC ACATGCTCCT ATCAAATGGT 180  
 40 GTGGGCAATG GTCAACGGGT TGCCTTGTTT ACAGAACGn TTTTGAAAT GATTGCGGCG 240  
 ATGTTGGCGA CAGTTAAAGT AGGTGCATCT TATATACCTA TCGATATTGA TTTTCCGAAT 300  
 AAACGACAAG GTGCAATTTT GG 322

45

(2) INFORMATION FOR SEQ ID NO: 4244:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4244:

55

CAGTTCTCCG GGTGTGCCTT CTGTATATGC TATGTATTCA CATATCGATA ACATGACATA 120  
 ACTCATGCTG GGTTCCTCCA TTCGGAAATC TCTGGATCAA AGCTTACTTA CAGCTCCCCA 180  
 AAGCATATCG TCGTTAGTAA CGTCCTTCAT TGGCTTCTAG TGCCAAGGCA TCCACCGTGC 240  
 GCCCTTAATA ACTTAATCTA TGTTCCACC ATTTTATAA GTCAAACGTT AACATGAAGT 300  
 TACGTTCTTT TATAAAAAGA TTAAACGCG TTATTAATC 339

## (2) INFORMATION FOR SEQ ID NO: 4245:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4245:

CCATTAAACGG GCTCTGACTA CTTGTAAGCA CACGGTTTCA GGTTCTATTT CACTCCCCTT 60  
 CCGGGGTGCT TTTCACCTTT CCTCACGGT ACTGGTTCAC TATCGGTCAC TAGAGAGTAT 120  
 TTAGCCTTAC GAGATGGTCC TCCCAGATTC CGACGGAATT TCACGTGCTC CGTCGTACTC 180  
 AGGATCCACT CAAGACAGAC AACATTTTCG ACTACAGGGA TTATTACCTT CTTTGGATTG 240  
 ATCTTTCCAG ATGATTCGTC TAATGTCGTC CTTTGTAAGT CCGTATAGAG TGTCTACAA 300  
 CCCCACAAG CAAGCTTGTT GGTnTTGGGC nACTTCCCGG TTTCGGTTCG GCCGnAA 358

## (2) INFORMATION FOR SEQ ID NO: 4246:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4246:

AAAGAGACCT TGCGGTTAGA TGCGGCTCAT CGCATCCATT TTTGCTTG CAACGTTCTA 60  
 CTCTAGCGGA ACGTAAGTnG AnCTACCATC GACGCTAAGG AGCTTAACTT CTGTGTTCCG 120  
 CATGGGAACA GGTGTGACCT CCTTGCTATA GTCACCAGAC ATATGAATGT AATTTATACA 180  
 TTCAAAATA GATAGTAAGT AAAAGTGATT TTGCTTCGCA AAACATTTAT TTTGATTAAG 240  
 TCTTCGATCG ATTAGTATTC GTCAGCTCCA CATGTCACCA TGCTTCCACC TCGGAACCTA 300  
 TTAACCTCAT GCATCTTTGA GGGGnGCTTG ATAACCGA 338

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4247:

CCCCGGGTAG CTTTTATCCG TTGAGCGATG GCCCTTCCAT GCGGAACCAC CGGATCACTA 60  
 AGTCCGCTCTT TCGACCCTGC TCGACTTGTA GGTCTCGCAG TCAAGCTCCC TTATGCCTTT 120  
 ACACTCTATG AATGATTTCC AACCATTCTG AGGGAACTTT GAGCGCCTCC GTTACCTTTT 180  
 AGGAGGCGAC CGCCCAGTCA AACTGCCCCG CTGACACTGT CTCCCACCAC GATAAnGGCG 240  
 GGGGTTAGAA AGCCAACACA GCTAGGGTAG TATCCCACCA GCGCTCCACG TAACTAnCGC 300  
 TCACGTTTCA AAGnTCTACC TATCCTGTAC A 331

## (2) INFORMATION FOR SEQ ID NO: 4248:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4248:

ATAATCATAC AGATGGCAAT ACAACAGCAA CTGAGACAGT GTCAAACGCT AATAATAATG 60  
 ATGTAGTGTC GAATAATACC GCATTAAATG TACCAACTAA AACAAATGAA AATGGTTCAG 120  
 GAGGACATCT AACTTTAAAG GAAATTCAAG AAGATGTTCTG TCATTCTTCA AATAAACCAG 180  
 AGCTAGTTGC AATTGCTGAA CCAGCATGCT AATAGACCGA AAAAGAGAAG TAGACGTGCG 240  
 GCACCGGCAG ATnCCTAAAT GCAACTTCCA GCCAGATCCA GCGGCTGCAG CGGTAnGGAA 300  
 ACGGTGGTGC CACCAGTTTG CCAATTTACA GCGCCCATAT TACGCCAACA ACTGGTnCCC 360  
 TAATGCCCAA T 371

## (2) INFORMATION FOR SEQ ID NO: 4249:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

AATTGCATGG CATAACATCG GCGATTAAAA GATGGACGTT TTGATGATGT ACAACAAGAC 60  
 ATTGAAGCAG TGGTGAAAGC TGCGAAGGTC ACACAGTAAA AGTGATTATT GAGACGGTAT 120  
 5 TGTGGACCA TGACGAAATT GTAAAAGCGA GTGAATTAAC AAAAGCGGCT GGTGCGGACT 180  
 TCGTTAAAAC TTCAACAGGT TTTGCAGGTG GCGGTGCGAC TGCAGAAGAC GTTAATTAAT 240  
 10 GAAAGATACA GTAGGTGCTG ATATAGAAGT AAAAGCTCAG GTGGCGTACG TATTnTAGAA 300  
 GTTTCATGA AnGGTTGAAG CAGGTGCGAC ACGTAnTGGT GCGAGCGCAG CGTTCAA 357

## (2) INFORMATION FOR SEQ ID NO: 4250:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 352 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear  
 20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4250:

25 GAGCCCAAAC CAACAAGCTT GCTTGTGGG nGTTGTAGGA CACTCTATAC GGAGTTACAA 60  
 AGGACGACAT TAGACGAATC ATCTGGAAAG ATGAATCAAA GAAGGTAATA ATCCTGTAGT 120  
 CGAAAATGTT GTCTCTCTTG AGTGGATCCT GAGTACGACG GAACACGTGA AATTCCGTCG 180  
 30 GAATCTGGGA GGACCATCTC CTAAGGCTGA ATACTCTCTA GTGACCGATA GTGAAGnAGT 240  
 ACCGTGAGGG AAAGGTGAAA AGCACCCCGG GAAGGGGAAG TGAAATAGAA GCTGGAAACC 300  
 GGTGTGCTTA CAAGGTAGTC AnAGCCCGTT AATGGGTGAT GGCGTGCCTT TT 352

## (2) INFORMATION FOR SEQ ID NO: 4251:

35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 331 base pairs  
 40 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4251:

45 CATTTACTGC TTAACCTTGC ATCAnATCGT AACTCGCCGG TTCATTCTAC AAAAGGCACG 60  
 CCATCACCCA TTAACGGGCT CTGACTACTT GTAAGCACAC GGTTTCAGGT TCTATTTTAC 120  
 50 TCCCCTTCCG GGGTGCTTTT CACCTTTCCC TCACGGTACT GGTTCACTAT CGGTCACTAG 180  
 AGAGTATTTA GCCTTAGGAG ATGGTCCTCC CAGATTCCGA CGGAATTTCA CGTGCTCCGT 240  
 55 CGTACTCAGG ATCCACTCAA GAGAGACAAC ATnTTCGACT ACAGGATTAT TACCTTCTTT 300



## (2) INFORMATION FOR SEQ ID NO: 4252:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4252:

TATTTGATAT TTTGTGCATT GCAGTCAAAC CATGGCGGAA ATTGAACCAA TACCATTGCT 60  
 AATTTTTTCT GTGTATGTAA GGGCTCTAAC ATATTCTTAA ATTGATCAAA TAGTTCTnGC 120  
 CTTGTATCTG CAAATGTTTT GTAGTCTGCA TGCAATGTGA GTGCTTGATG AATTTTGACC 180  
 ACAAATTCAA ATGTATCAGG CGTTTCTTTT ATCCATTTCA ATATATTTCT TTCCGGTTGT 240  
 ATCGCATAGT ATGTCGCATC TAATTCGCAA CCGGAAAATG TCCAGCATAT GTTTTAAGGT 300  
 TATCGGTTTG GCGTTCTAAA TCTGCATATA ATGAATAGTG ATCACCCEAA CCTGTTAAAT 360  
 CCGATGGTTA TCCAnATGAT GATCACCATG TCATCANACC 400

## (2) INFORMATION FOR SEQ ID NO: 4253:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4253:

AAAGGTATCA AAGATGTTAA AGTTACTTTA TTAAATGAAA AAGGCGAAGT AATTGGnACA 60  
 ACTAAAACAG ATGAAAATGG TAAATACTGC TTTGATAATT TAGATAGCGG TAAATACAAA 120  
 GTTATTTTTG AnAAGCCTGC TGGCTTAAAC ACAAACAGTT ACAAATACAA CTGAAGATGA 180  
 TAAAGATGCA GATGGTGGCG AGTTGACGTA ACAATTACGG ATCATGATGA TTTCACTT 240  
 GATAACGGAT ACTTCGAGGG GATGACATCA GACAGCGATT CAGACTCCAG ATAGTGACTC 300  
 AGnCACGCGAC TCAGACTTCA GACAGCG 327

## (2) INFORMATION FOR SEQ ID NO: 4254:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4254:

5 AGATGACATT AAATAGCATC TCCTCGTGTT GATTATTTTG GTTGGCTGAC CAATATTTAT 60  
 TCTAGCACGT AGAGATGCAT TTTTGTGAC AATGGTAGAA CCTTTTCTGA ACCATACGCA 120  
 TAGGATTGTn CnTTTTTACA ATTAAAGAGC CAACCGTTGT TATAGTCTAA CAATGGTTGC 180  
 10 CCTCTTATTT TATGTGGCTA AAAATTTATA GGCAATTTTA TTACAACAAT GTACATTTAA 240  
 GGTGACCTTC ATGCCAAAAT CGCATCACTC ATTTAATGGA AGCAGCACGT CTTCATATAA 300  
 AGTACCGATC CCTAATTCCA ACGCATGTnG 330

## 15 (2) INFORMATION FOR SEQ ID NO: 4255:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 344 base pairs  
 (B) TYPE: nucleic acid  
 20 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4255:

ATTAGTGATT GTAAAAAGT AAAACTATTC TTGGGAGTCG GACATAAATC AATGTCTAGA 60  
 CTCTATAGTG TTGTATTTGG CAGTAGTTGA CGGGGCCCCA ACATAAAGAA ATACTTTTTTC 120  
 30 TTTAGAAATT AGTATTTCTT ATACATGAGT TTTACTCAGG ATATCCTATT TTTAAATACA 180  
 CATTAGCTGT GTTTAATGAT AAAGAACCAC TACATCATAA ATCTTTAATG GTTCTTTATC 240  
 AATTCCTTCC CCCCTCTCAT GTTTTGTATC TTTAAATCAA TATAATTCAA AAAAGGGTCG 300  
 35 AAGATATGAn ATCATCTTT CGACCCTTnn TTGTACTAAT TTAA 344

## (2) INFORMATION FOR SEQ ID NO: 4256:

## 40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 323 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4256:

CCAGTAATAT CTAAATGAGT TGGATATTTA ACTTTGCGAT TAATTTCAAT ATTAAATTGC 60  
 50 GTTACCGCGA CAAGnCATnA CACAACATAC ATAATAAGAT TGGCTAAAAA GATATAGTTA 120  
 AAGCTAAATT CTGCGACAAA GCCGCCCAT TGCAGCACCGA CAGCCACACC AATATTTTGC 180  
 55 GCTAAGTATA TCGCATTAAA CGTTTGTCTT CCGCCATTTG GCCACACTGC TCCAGCCATA 240

TACCAAGGCC ACCCGTGGAn AGA

323

## (2) INFORMATION FOR SEQ ID NO: 4257:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 369 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4257:

GCTGACTTTC CACCAGCCTC TGTGTTGGGG CCCCAGCTAT TTTTGAAAAG AGCGTGTTAC 60  
 ACGGTCATTG TTTTACAGTC AACTACTGCT AAAATAAAAT TAACGAGCTT AGGGCTTTGT 120  
 TTTCTGTCCC AAGCTCGTTA AATCACATAT GATAATTAAT TATGCCCAAC CACGATATCT 180  
 AGCTGCTTCT GCTGTACGTT TAATACCTAT GGATATATGC TGCAnTCTGC ATATCTATTT 240  
 TTCGGTTTTG AGACAATTCT TAAATCGTAT CAAATGCCGC TTCTAATTTT TnCACGTGGC 300  
 TTTTGCATTG AACTTCTTCT nGCAGGACCA ATAATAACCT TGGATTATTT TGTGACCCAT 360  
 GCGGAGTGA 369

## (2) INFORMATION FOR SEQ ID NO: 4258:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 335 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4258:

CCTTTTTCAA AATCATTGGA TGCATCGATA AATAGTACGT TGTCGTCTTG TTGGCGACAT 60  
 TTTTAAATA CTAAATACA TGTTGGAATA CTTGTCCCAT AGAAATATT GGCTGGTAAC 120  
 CCAATCACGG CTTCTAAGTA GTTCTTTTCT TCTATTAAAT AGCGACGAAT CACACCTTCT 180  
 GCGGCACCAC GAATAATACA CCATGnGGAG TACGACGCCA nGTACCTTCA TCGTCTAGTA 240  
 ATGTACCACT GTTGAATAAA GCAAAGTCTG CTTTGATTTT GGCGCAACTT GCCGTAACCA 300  
 CTGAATCGTT CATCATTTCA AATTTGAACT GCTGT 335

## (2) INFORMATION FOR SEQ ID NO: 4259:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 324 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4259:

5 ATTTGCTAC CTTACGACCG TTATAGTTAC GGCCGCCGTT TACTGGGGCT TCGATTTCGTA 60  
 GCTTCGCAGC nACAACCACT CCTCTTAACC TTCCAGCACC GGGCAGGCGT CACCCTATAC 120  
 ATCACCTTAC GGTTTAGCAG AGACCTGTGT TTTTGATAAA CAGTCGCTTG GGCCTATTCA 180  
 10 CTGCGGnTCT TCTGGGCGTT AACCTTAAAG AGCACCCCTT CTCCCGAAGT TACGGGGTCA 240  
 TTTTGCCGAG TTCCTTAACG AGAGTTCGCT CGCTCACCTT AGAnTTCTCA TCTTGACTAC 300  
 CTGTGTCGGT TTGCGGTACG GGCA 324

## (2) INFORMATION FOR SEQ ID NO: 4260:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 20 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4260:

25 AAGCGGTTGT TAGACAATGC ATTAAGAAAA ATTAAAGCGG AGTTTACTTT TGTAAATGAG 60  
 CATTTGATTT TTTGAAAATA AAGCAGTATC GGGCGCTTGA CTAAAAAGAA ATTGTACATT 120  
 30 GAAACTAGA TAAGTAAGTA AAATATAGAT TTTACCAAGC AAAACCGAGT GAATAAAGAG 180  
 TTTTAAATAA GCTTGAATTC ATAAGAAATA ATCGCTAGTG TTCGAAAGAC ACGAGCAAGA 240  
 TTAATAACGC GTTTAAATCT TTTTATAAAA GAAAACGTTT AGCAGACAAT GAGTTAAAnTT 300  
 35 ATTTTAAAGC AGAGTTTACT TATGTnAATG GAGCATTGAA AATnATGAAA ACGAGCCCGT 360  
 ATGTGGAGCG TTTGGACTTA TAAAAATGGT GGGAAACATA 400

## (2) INFORMATION FOR SEQ ID NO: 4261:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 334 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 45 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4261:

50 AATTAATGTG CGAGTTGGGG TGGGACGACG ATAAAGAAAT ACTTTTTCTA TAGAAATTAG 60  
 TATTTCTTAT GCATGAGTTT TACTCAGTAA TTCCTATTTT TAAGnACACA TTAGCTGTGG 120

55

CTCCCCTGAG AAGTTTAAAA TTTTATATGT TGGCTTGTTA TGTTAAGGGA ATTAACATGG 240  
 TTGTCTTGTT TATATTATGT GATTCAAACA TTACTAGTCT TGGTAAATCT AATTTCGTAAA 300  
 5 ATGCTAAATC TAACCATCTA TTAAATTTAA AACC 334

(2) INFORMATION FOR SEQ ID NO: 4262:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4262:

TTTCGGTCAT ATTCAAACGT TTTCACTTCG CCAAGCCATT TTTCTTTGTG TTTACTTTTT 60  
 20 ATTTTGGACGT TTTAGGCATA AAAAAAAGAG ACCTTGGCGG TCTCAATGCG GCTCATCGCA 120  
 TCCATTTTTT GCCTGGCAAC GTTCTACTCT AGCGGnAGTA ATTGGGCTAC CATCGTCGCT 180  
 25 AAAGACCTTT CTTGACTTGT GACAATCGCT TGChTCITTC CTCTCCTTCG GCTCTCGCTT 240  
 ACTCATThAG CTCTACTAAA CTCGTTGCGC TCTTTTCTCG TTTCGTCAGA TTCAAACGTT 300  
 TTCACTTCGC CAAGCCATT TTCTTTGTGT 330

(2) INFORMATION FOR SEQ ID NO: 4263:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4263:

GAGGTATACC CCGGGACGGC TGAAGGGGAT CGAACCCCTAC GnaATGTCGG AACCACAATC 60  
 CGATGTGTTA CCACTTCACC ACAGCCGCCA TGGCAGGGGC AGTAGGAATC GAACCCACAC 120  
 45 CAAAGGTTTT GGAGACCTCT ATTCTACCGT TGAACATATGC CCCTATTAAA AATAATAAAT 180  
 GGAGGGGGGC AGATTGGAAC TGCCGAACCC GAAGAGTCGG ATTTACAGTC CGCCGCGTTT 240  
 AGCCACTTCG CTACCCCTCC ATAAATGGTG CCGGCCAGAG GACTTGAACC CCCAACCTAC 300  
 50 TGATTACAAG TCAGTTGCTC TACCAATTGA GCTAGGCCG 339

(2) INFORMATION FOR SEQ ID NO: 4264:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4264:

	GTATTTCAAA GTAAAATTAC ATGTTAATAC GTGnTTAATG GGCGAGACTC CTGAGGGAGC	60
10	AGTGCCAGTC GAAGCCGAGG CTGAGACGGC ACCCTAGGAA AGCGAGCATT CAATACGAGA	120
	TtTnATGAAA TAGAGAACAG CAGTAAGATA TTTTCTAATT GAAAATTATC TTACTGCTGT	180
	TTTTTAGGGA TTTATGTCCC AGCCTCTTAC TCTAATTATA TTCACTATCA ATTAGACAAA	240
15	ATGGCCATTT TCAAATATCA CGCGTTGTTT CTGACCTTGA ATATATTTAT TATAATTCTC	300
	TTTTTGGAAT ATCAGTTAAC ATTAATTTAG ATGTACCGTA TTTTAAACAC T	351

20

(2) INFORMATION FOR SEQ ID NO: 4265:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 346 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4265:

30	ATTTTCACTT TAAACCTGC TTCTTTGGCT TTTTGCATAT AATGTTGCGA TTGTTCTATT	60
	GTAAATACAC CTGTTTCACA GAAATATCC GCAAAGTCTG CATATTGTTT TACTTCCGGA	120
	AGTAACGCAA TCATTCTTTC TAAAAATGCC TCATTTGAAC TTGCCTCTTT AGGTACAGCA	180
35	TGAGGCCCTA GGAAAGTATG TTTCATGTCT AAATCATATT TCTCAGCTAA ACGnTTAGAC	240
	ACTTTCAATT GCTTCAGTTC ATTTTCTCTA TCTAATCCAT AAACCACTCT TGACTTTCAA	300
40	CTGCAGTCAC GCCGTGTTTn AATCCATAGT AAGACAAAnC ATGACT	346

(2) INFORMATION FOR SEQ ID NO: 4266:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 347 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4266:

	TCAAACGCTC TATCCAATTG AGCTACGGGC GCATATGTTT TTATTGAAAA TGGTGCCGAG	60
55	GACCGGAATC GAACCGGTAC GTGATCACTC ACCGCAGGAT TTTAAGTCCT GTGCGTCTGC	120

CCAACCTTGG CAAGGTTGTA TTCTACCGCT GAACTACTTC TGCATATGCG GGTGAAGGGA 240  
 5 GTCGAACCCC CACGCCGTAA GGnTGAGATC CTAAGTCTAG TCGTCTGCC AATTCCGCCA 300  
 CACCCGCCAA TGGTGAGnCA TAGAGGnTTC GAACCTCTGA CCCTCTG 347

## (2) INFORMATION FOR SEQ ID NO: 4267:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4267:

GACTTGTTCT CTTGGACCTA TATCATGTTT TTTATTTTCT AATGCAGGAT CTTTAATTGC 60  
 20 ATCTTTAAGT GATTCATCCG CTGCAGGATA GTTTTTCGCA GTGTTTGCTG GTTGCGTGAG 120  
 GTnTGTTT GATTTGTATC CTTAGGTGGC TGAGTTGTAG TTGCATTATT ATTTTGATTT 180  
 25 TCCGAGATTT TATCTGAAGT ATTTGTATTT TCTGCTGCTT GTGCTTGATG TTGAGAAGTA 240  
 ATTAAAAATA GTGTACTGAC AATGACCGAT GCAACGCCTA GAGTTGATTT TCTAATAGAA 300  
 TAGGAAAGAC CnTnAATTTT GGGTGGATGT TTGTTCA 337

## (2) INFORMATION FOR SEQ ID NO: 4268:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4268:

ATACATGTTG GAATACTTGT CCCATAGAnA ATATTGGCTG GTAACCCAAT CACGGCTTCT 60  
 AAGTAGTTCT TTTCTTCTAT TAAATAGCGA CGAATCACAC CTTCTGCGGC ACCACGGAAT 120  
 45 AATACACCAT GTGGGAGTAC GACTGCCATG GTACCTTCAT CGTCTAGGTA ATGTACCATG 180  
 TGTGAATAA AGGGCAAAGT CTGCTTTGGG ATTTTGGCGC AACTTGGCCG TTAACCACTG 240  
 GAATCGTTCA TCATTTTCA nATTTTGGAA TCTGGCTGGT TCCATTTTCG GCACTGGTAT 300  
 50 GGTGGGGGTT TCGGCAATAA ACGGCATTCA AATGGTATTT GGCCTAAACA AGGCCGGGAT 360  
 TTTTCCAATG GGGGTCATCA TTAAnGGGAT CnTCGAAGTT 400

## (2) INFORMATION FOR SEQ ID NO: 4269:

(A) LENGTH: 345 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4269:

10 GGCTCATCGC ATCCTGGGGC TGTAAGCGGT CCCAAGGGTT GGGCTGTTCG CCCATTAAAG 60  
 CGGTACGGAG CTGGGTTTCAG AACGTCGTGA GACAGTTCGG TCCCTATCCG TCGTGGGCGT 120  
 AGGAAATTG AGAGGAGCTG TCCTTAGTAC GAGAGGACCG GGATGGACAT ACCTCTGGTG 180  
 15 TACCAGTTGT CGTGCCAACG GCATAGCTGG GTAGCTATGT GTGGACGnGA TAAGTGCTGA 240  
 nAGCATCTAA GCATGAnGCC CCCTCAAGAT GAGATTCCCA ACTTCGGTTA TAAGATCCCT 300  
 CAAAGATGAT GAGGATATAG GTCGAGGTTG GAGCATGGTA CATGT 345

20

(2) INFORMATION FOR SEQ ID NO: 4270:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 370 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4270:

30 AAGAATTAAT TATACATTTT ATTAACATTT AAGTCAATAA CTTTTTTTAT CTTGTCCATT 60  
 TTATTTTTTA ACCAAAATT GATTAAAAA CTGCCTGGCA ACGTTCTACT CTAGCGGAAn 120  
 35 TAAGTCGaCT ACCATCGACG CTAAGGAGCT TAACTTCTGT GTTCGGCATG GGAACAGGTG 180  
 TGACCTCctT GCTATAGTCA CCAGACATAT GaATGTAATT TATACATTCA AAAGTAGATA 240  
 40 GTAAGTAAAA GTGGATTTTG CTTGCGAAAc ATTTATTTTG ATTAAAGTCTT CGATCGATTA 300  
 GTATTCGTCA GCTCCaCATG GTCACCAGCT TCCACCTCGA ACCTATTGGn CGCATCATCT 360  
 CGCAGGGAnC 370

45

(2) INFORMATION FOR SEQ ID NO: 4271:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 327 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4271:

55



ATTAACAAAA GGCATTGATT TAGAAGGGCG GACATTTTTA CACAATTATG ATTGGCGTAA 120  
 AGATAAAGAT GGCACATTAT TAAATACCAT CATTTCTGGT CCGGCACCTG TGGCACAATG 180  
 5 GaTTAATTTA CAATATTATG CGTCGACAGT TGCGCCGCAT TTTTaCGGLA ATGGGAATAA 240  
 AGCGACACAA ACCGTCACGT CAGTGTGGT GTCATGCAAG GTAATGCGAG TGCATCTGAT 300  
 GTAGGGCTTA TCATGGCCAA TCTGTTA 327

(2) INFORMATION FOR SEQ ID NO: 4272:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4272:

CAITCTTTAA ACTCTGTAAG TACTTCTTCA ATCTCAGGGG CATCTACTAA CATATCATCA 60  
 GTAATATGCG TCAAATTGAT AATCGTTTCC GATAATCGTT CATGCGGATT ACTAAACCTT 120  
 25 TCAAATTAT CGATGATTTT ACCGTATGA ACTTTCACAG CTGCAATCG ATGATTTTAT 180  
 CATACTGATT TGATAAACCA GTTGTCTCAA CGTCGAACAC AACATAAGTA GCATCTTTTA 240  
 ATACGACATC TTGTGGGTTG TATGCAATCG GGAACACCAT CATCAACTAA CATACCTTCC 300  
 30 ATACCGGnAT ATCATTTTAA nGCCA 325

(2) INFORMATION FOR SEQ ID NO: 4273:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4273:

TCCGGCCTTG ACCTGAAGAA CACTGTCTTT GTCGTTAAGA TGA CTCTAGTA CTCTTATGTT 60  
 45 TATTATCAAC CGTTAATAAA CTTACCATCA AGAGTGCACC TACCCATACT GACAGTGCAG 120  
 TATAGAATGG TGCATACCT GAACCATAAT CCTTAACTGG GAAAACATCA ACAGTCTTCT 180  
 50 TATTAATAGG ATTTGCAATA ATACCGCCTT GCTTTTTCAA ATCATCTTTA AGTGTGTCGA 240  
 TnAATTTGTC GACTGCATCA TCTnTGTCTA ATTTCTTGAA AATTTTGATT CGCTTTTTTC 300  
 CAAATCCTTn TCCAACATCA GGCAATTTTA TTTTGAGAAA AATCAGCCAA ATCCGGA 357

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4274:

ACGTTAGCAC AAGCCATGAA CCAATTAGGT GGAAAGAGTA ATAGTGGTGA AGGTGGCGAA 60  
 GATGCAAAAC GTTATGAAGT ACAAGTTGAT GGAAGCAACA AAGTAAGTGC GATTAAACAA 120  
 GTTGCTTCTG GCGGTTTTGG TGTAAGTAGT GATTATTTAC AACATGCCAA AGAAATTCAA 180  
 ATTAAAGTTG CGCAAGGTGC AAAGCCTGGT GAAGGTGGTC AATTACCTGG TACTAAGGTA 240  
 TATCCGTGGA TTGCGAGGAC AAGAGGGTCA ACGCCAGGTA TCGGTCTGAT TTCACCACCG 300  
 CCACATCATG ATATTTnATT CCATAnGAGG ATTTAGCCGC CACCTGATAC CTGGATTTTG 360  
 GAAAAATGGC GAATTAAGGT TGCnGATTTT CCCCggGTAA 400

## (2) INFORMATION FOR SEQ ID NO: 4275:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4275:

AACGTCGTTA ATTGAATAAC GCTTATGTTA TAAGAGCACT CATACCAAAC CATAATCATC 60  
 TATAGATATA ACAATTCACG ATATAAGGGC TGTGTTTGGC ATAGCCTTTA GATATACACT 120  
 TAATTCCTAT TAAAATAGTA GGGATTAAAA GGGGGCTTGT CATGGATTAA AATTCAACAA 180  
 TTACAACATC ACTTTGGATC ACATAAAGTA ATTCATAACT TTAATTTGGA CATTAGCAAG 240  
 GGAGAAATAG TCACTTTCAT AGGGGAAAAG TG GTTGCGGA AAGTCTACTT TACTCAATAT 300  
 TATCGGTGGA TTTnTTCCAT CCATCGnCTG GTCGTGTCCA n 341

## (2) INFORMATION FOR SEQ ID NO: 4276:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

TAGTGATATA CGACATCACA GCATAATATT GCTTTAGAAA GTCGTGCCGA ACTGGAACCTT 60  
 ACAAGTCTAG TTCGAACACA CACTGATGTG AGTGGTTTTTC TTTATTTTAA ACATGAACAA 120  
 5 TCAGATAAGT TACTAGCATT AGCAAATATT ATTAAATCAA AGGGCTTCGA TTCATAAAAT 180  
 TTAAACAAT GATTAAATTT AGACGTGTAA ATTGTTAAAT TCTAAAACGG AAATAACCAC 240  
 CATTCCATTA AACCACTTTT TTGTTTCATCA CTATATTTCA CACnGCTTCA TTAATAAACG 300  
 10 GAATGCTTCA nCCGCTTCAA CTTCAACTGG CTTCAACTTC nGCCTACTTC ATCATACCAA 360  
 ACGGTCCG 368

15 (2) INFORMATION FOR SEQ ID NO: 4277:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4277:

25 ATGGAAGTAC GTGACGTTCA CTA CTCTCAC TATGGCCGTA TGTGTCCAAT TGAAACACCT 60  
 GAGGGACCAA ACATTGGATT GATTAACTCA TTATCAAGTT ATGCACGTGT AAATGAATTC 120  
 GGCTTTATTG AAACACCATA TCGTAAAGTT GATTTAGATA CACATGCTAT CACTGATCAA 180  
 30 ATTGACTATT TAACAGCTGA CGAAGAAGAT AGCTATGTTG TAGCACAAGC AAACCTCTAAA 240  
 TTAGATGAnA ATGGTCGTTT CATGGGATGA TGAAGTTGTA TGTCGTTTCC GTGGTAACAA 300  
 35 TACAGTnATG GCTAAAGn 318

(2) INFORMATION FOR SEQ ID NO: 4278:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 40 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4278:

CACTTGTA CT TTCTGATGTT GAGCCAGACT CTGATGTACT TACCGATGTA GATAAACTTG 60  
 50 CAATGGTCGA CATGCCGTTT GAAGTTGATG TACTTAGCGA ATCACTTAAT GATGCTGATG 120  
 TGCTTTGTGA ATCGGATTCG CTCGTGCTTG TACTTGTTGA GTTTGAGGCA CTTTGGCTTG 180  
 CTGAGTTTGA GTCTACTCCG CTTTGATTCA TTGAGGCACT TAGTGACAAT GATGTACTCG 240

55

TACTTATGCT CATTGGATGT TGAATCGGAT TTACTTTCAC TTGAATGATG TTGAGTCGGA 360  
 TTCACTTTC A CTTGTAGAAC CACTTAATGA TGTGGGATGT 400

5 (2) INFORMATION FOR SEQ ID NO: 4279:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 324 base pairs  
 (B) TYPE: nucleic acid  
 10 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4279:

TTTGTACTTC GATTTAAAAG ATATTAGACA TAAAATCTAA AAnCAGCAGT AAGATGATTT 60  
 ATGATTAAAA ACTATCTTAC TGCTGTTTAC TTTTATAAT ACTTCTGAAT GTCTTCACTT 120  
 20 ATACTTCTAG TCACAGATTT AAATAATCAA AAGTGCACAT TATTAAAATA TCAATTTTAC 180  
 ACTCAATGCG GCTCATCGCA TTCATTTCTT GTCTAGCAAC GTTCTACTCT AGCGGAAGTA 240  
 AGTTAGCTAC CATCCTCGCT AAGAACCCTT CTGACTTGT GACAATCGCT TGCTTCTTTC 300  
 25 CTCTCCTTCG GCTCTCGCTT ACTC 324

(2) INFORMATION FOR SEQ ID NO: 4280:

- 30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 326 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4280:

CTCACTAGTC GAGTGACACT GCGCCGAAAA TGTACCGGGG CTAAACATAT TACCGAAGCT 60  
 40 GTGGATTGTC CTTTGGCATG TGnTTAGGAG AGCGTTCTAA GGGCGTTGAA GCATGATCGT 120  
 AAGGACATGT GGAGCGCTTA GAAGTGAGAA TGCCGGTGTG AGTAGCGAAA GACGGGTGAG 180  
 AATCCCGTCC ACCGATTGAC TAAGGTTTCC TGnGGAAGGC TCGTCCGCTC TGGGTTAGTC 240  
 45 GnGTCCTAAG CTGAGGCCGA CAGTAGGGCG ATGGGATAAC AGGTTGATAT TCCTGTACCA 300  
 CCTATAATCG TTTAATCGAT GGGGGG 326

50 (2) INFORMATION FOR SEQ ID NO: 4281:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 370 base pairs  
 (B) TYPE: nucleic acid  
 55 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4281:

5 TCGAACATGA GCGATTATTT CTTATGAATT CAAGCTTATT TAAAACTCTT TATTCACTCG 60  
 GTTTTGCTTG GTAAATCTA TATTTTACTT ACTTATCTAG TTTTCAATGT ACAAATAATG 120  
 GTGGGCCTAA GTGGACTCGA ACCACCGACC TCACGCTTAT CAGGCGTGCG CTCTAACCAG 180  
 10 CTGAGCTATA GGCCCATTTT TTTGAATGTT AAATAAACAT TCAAACTGG AATACAATAT 240  
 GTCACGTTAT TCCGCATCTT CTGAAGAAGA TGTTCGAAT ATATCCTTAG AAAGGnAGGT 300  
 15 GATCCAGCCG CACCTTCCGA TACGGGCTGA CCTTGTTGAC GACTTGCACC CCAAGCATTT 360  
 GTGCCCAnCn 370

## (2) INFORMATION FOR SEQ ID NO: 4282:

20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4282:

GAGAGATGAC ACGGnACTGA ATTGGTTTGA CACCACGTGA TGAATGTGAT CGTCGGCCTT 60  
 30 CTTACAGATT GnAATACTTT TACATCAAGA ACGATACCGC CAGCGCCGTG AGGTACACGT 120  
 AATGAAGTAT CTCTAACTTC ACGTGCTTTT TCACCAAAGA TTGCATGTAA CAATCTTTCT 180  
 35 TCGGCAGTTA ACTCAGTTAC ACCTTTAGGC GTTACTTTAC CAACTAAAAT ATCTCCATCT 240  
 TTTACTTCTG CACCAATATA AACGATACCA CGATCGTCTA AGTTCTTAAG TGCACTTTCA 300  
 GAAACATTAG GnATATCTCT TGTGATTTC TCAGGGCCTA ACTTAGTATC ACGTGCCTCT 360  
 40 GAATCCATAC TCCTTCAATA TGAATAGAAG TATACACGn 400

## (2) INFORMATION FOR SEQ ID NO: 4283:

45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 324 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4283:

50 AATTCTACAG GCAATGCGAG TTGGGGTGTG GGCCCCAACA AAGAGAAATT GGATTCCCAA 60  
 55

TCTGTCCAC TCCCGATTAT CTCGTCGCAA TATTTTTTTC AAAGCGATT AAATCATTAT 180  
 CATGTCCAAT CATGATTAAA ATATCACCTA TTTCTAAATT AATATTTGGA TTTGGTGAAA 240  
 5 TGATGGACTC TTGCGCTCGT TTAATTGCCA TAATGTTAAT nCCATATTGT GCTCTTATAT 300  
 CTnAATCCAT GATAGACTGn CCCG 324

## (2) INFORMATION FOR SEQ ID NO: 4284:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4284:

20 AAATCGTAAC GAGTGAAC TTCTATTTAG GTGGCGAAGT AACTTACTAG CACCTGACGA 60  
 AACGGTTTTA GATCGTATTC AATTGAAAAG GCCGGTATTG AATGAATCAC ACTTAGCAGC 120  
 GATTGATCAG GAACATTTTA AATTAACCTA TTTATCAACG GTATATGAAG GGGATTTGGC 180  
 25 AAGATGCGTT ATAAGCATTG GGCCGTAGAA GCAGTGAAAT GCTGTnAAAC AAGGGCGCTC 240  
 AAATTCTAGT GTTAGATGAT AGTGGATTAG TTGGATAGCA ATGGCTTTGC AATGCCGATG 300  
 30 TTTACTCGCA ATGAAGTGCA TGTGCCATGC AATTGACTTC TTTAAAGCCA GATTTACGTG 360  
 ATGTCTAACA AGTTTTnTn GCTAAAATCh GGGTGGAGAC 400

## (2) INFORMATION FOR SEQ ID NO: 4285:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 560 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4285:

45 CATTTTTCTT TGTGTTTACT TTTATTTTG ACGTTTTAGA CATAAAAAA GAGACTCACG 60  
 GTCTCAACTT GCCTGGCAAC GTTCTACTCT AGCGGAACGT AAGTTGGCTA CCATCGTCGC 120  
 TAAAGACCTT TCTTGACTTG TGACAATCGC TTGCATCTTT CCTCAnCATC GGnTnTAGCT 180  
 50 TACTCATT TA GCTCTACTAA ACTCGTTGCG CTCTTTTCTC GTTTCGTCAG ATTCAAACGT 240  
 TTCACTTCG CCAAGCCATT TTTCTTTGTG TTTACTTTTT ATTTTGACGT TTTAGGCATA 300  
 AAAAAAGAG ACCTTGnCGG TCTCAATGCG GGCTCATCGC ATCCATTTTT TGCCTGGCAA 360

TGACAATCGC TTGCTTCTTT CCTCTCCTTC GGCTCTCGCT TACTCATTTA GCTCTACTAA 480  
 ACTCGTTGCG CTCTTTTCTC GTTTCGTGAG ATTCAAACGT TTTCACCTCG CCAAGCCATT 540  
 5 TTTCTTTGTG TTTACTTTTT 560

(2) INFORMATION FOR SEQ ID NO: 4286:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4286:

GTAACACTCG GnATAACCTA CCTATAAGAC TGGGATAACT TCGGGAAACC GTAGCTAATA 60  
 20 CCGGATAATA TTTTGAACCG CATGGTTAAA AGTGGAAGA CGGTCTTGCT GTCACCTATA 120  
 GATGGATCCG CGCTGCATTA GCTAGTTGGT AAGGTAACGG CTTACCAAGG CAACGATGCA 180  
 TAGCCGACCT GAGAnGGTGA TCGGCCACAC TGGAAGTGAG ACACGGTCCA GACTCCTACG 240  
 25 GGAGGCAGCA GTAGGAATC TTCCGCAATG GGCGAACTG GACGGAGCAA CGCCGCGTGA 300  
 TGnATGGAAG GTCTTCGGAT CGTAAACTC TGTTATT 337

(2) INFORMATION FOR SEQ ID NO: 4287:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4287:

CAATCGTGCT CAntGCGCAT CGTnACTCAT CTGTATGTGT TCCAGCATAT ACAATTTTGC 60  
 CATCTTTAAT GACAACTGTA CCATTTTTCA CAACATTTAA TTCATCTAAT TCCTTACCCT 120  
 45 TCAAAGGTTT ATCTGTTGAT CTCGGTAAAA TTAATTCTGG CTATATGATT AATTATTAAA 180  
 TCATCATTAC TTATCACCTG CTTTATCAAT CATGGAATAT GAATACCTTT TTCTTTAGCT 240  
 GTTTGAATAG CGATGTCATA GCCAGCATCA ACATGTCGGG CAACACCCAT ACCTGGGTCA 300  
 50 GTCGTCAATA CACGTTCCAA TCTTCTTTCA GCACGCTCTG AATCCATCTG G 351

(2) INFORMATION FOR SEQ ID NO: 4288:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4288:

CTATTCACCTG CGGCTCTTCT GGGCGTTAAC CCTAAAGAGC ACCCCTTCTC CCGAAGTTAC 60  
10 GGGGTCATTT TGCCGAGTTC CTTAACGAGA GTTCGCTCGC TCACCTTAGA ATTCTCATCT 120  
TGACTACCTG TGTCGGTTTG CGGTACGGGC ACCTATTTTC TATCTAGAGG CTTTTCTCGG 180  
CAGTGTGAAA TCAACGACTC GAAGACACAA TGTCTTCTCC CCATCACAGC TCAGCCTTAA 240  
15 CGAGTACCGG ATTTGCCTAA TACTCAGCCT TACTGCTTAG GACGTGCAAT CCAATCGCAC 300  
GGTTTnGCCT ATCCTA 316

20

(2) INFORMATION FOR SEQ ID NO: 4289:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 322 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4289:

30 TTnTTTATGT CTAAACGTC AAAATAAAAG CAAACACAAA GAAAGATGGC TTGGCGAAGT 60  
GAAAACGnTT GAATCTGACG AAACGAGAAA TGTAAGTAT AATAAAAAGC AGTCATAAGA 120  
TGATTTCAAT TAGAAATCAA TTTATGACTG TTTTCTTAC TATGTGTTAA ATTAACAATG 180  
35 AATATAACAT CTTATTTTCA TTAATATAAA TATTGGAAGG ATCGAATGA TTTACAGTT 240  
GTTTGAGTTG TATTAAATCA TCATGATCTT TAAGTTGAAT ACCAATAATG ACAGTACCTG 300  
TATTTTGAGA GATTTTTTAA GT 322

40

(2) INFORMATION FOR SEQ ID NO: 4290:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 338 base pairs  
45 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4290:

TCATTTAGCT CTAATAACT CGTTGCGCTC TTTTCTCGTT TCGTCAGATT CAAACGTTTT 60  
CACTTCGCCA AGCCATTTTT CTTTGTGTTT ACTTTTTATT TTGACGTTTT AGGCATAAAA 120

55



CTCTAGCGGA AATAATTGGC TACCATCGTC GCTAAAGACC TTTCTTGACT TGTGACAATC 240  
 GCTTGCTTCT TTCCTCTCCT TCGGCTCTCG CTTACTCATT TAGCTCnACT AAACCTCGTTG 300  
 5 CGCTCTTnTC TCGTTTCGTC AGATTTCAAA CGTTTTCA 338

(2) INFORMATION FOR SEQ ID NO: 4291:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4291:

AATTGGTTTA CACCAGGTGA TAATGTATCG TCGCCTTCTT CACGATTGAA TACTTTTACA 60  
 20 TCAAGAACGA TACCGCCAGC GCCGTGAGGT ACACGTAATG AAGTATCTCT AAC TTCACGT 120  
 GCTTTTTTAC CAAAGATTGC ATGTAACAAT CTTTCTTCGG CAGTTAACTC AGTTACACCT 180  
 TTAAGGCGTT ACTTTACCAA CTAAATATC TCCATCTTTT ACTTCTGCAC CAATATAAAC 240  
 25 GATACCACGA TCGTCTAAAG TTCTTGAAGT GCACTTTnCA GAAACATTGA GGGAAATGATC 300  
 TCTTGTGATT TCTTCCAGGT CCTAACTTGA GTGATCACGT GGCTTCTGGA TTGCAGACGC 360  
 TTGCAAGATG GAATGAGAAG TGAACACAGT GCATCCTTGC 400

(2) INFORMATION FOR SEQ ID NO: 4292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4292:

AAACGTTTTC ACTTCGCCAA GCCATTTTTT TTTGTGTTTA CTTTTTATTT TGACGTTTTA 60  
 45 GGCATAAAAA AAAGAGACCT TCGGTCTCA AATGCGGCTC ATCGCATCCA TTTTTGCCT 120  
 GGCAACGTTT TACTCTAGCG GAACGTAATT GGGCTACCAT CGTCGCTAAA GACCTTTCTT 180  
 GACTTGTGAC AATCGCTTGC TTCTTTCCTC TCCTTCGGCT CTCGCTTACT CATTTAGCTC 240  
 50 TACTAAACTC GTTGCCTCTT TTTCTCGTTT CGTCAGATTC AAACGTTTTC ACTTCGCCAA 300  
 GCCATTTTTT TTTGTGTnA CTTnT 326

(2) INFORMATION FOR SEQ ID NO: 4293:

(A) LENGTH: 356 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4293:

10 GGGGACAATT CCCTGGGGGT TCAAGTCCTC TCGGGCCGGC ATCAAAATTC TTAATTTAAA 60  
 TAAGCGGGTG TAGTTTAATG GCAAAACCTC AGCCTTCCAA GCTGATGTTG TGGGTTCGAT 120  
 TCCCATCACC CGCTCCATAG ATAATTTTAA TGAACATTGA AACTGAATG ACAATATGTC 180  
 15 AACGTTAATT CCAAAAACGT AACTATAAGT TACAAACATT ATTTAGTATT TATGAGCnAA 240  
 TCAAACATCA TAATTTTTAT GGAGAGTTTG ATCCTGGCTC AGGATGAACG CTGGCGGCGT 300  
 GCCTAATACA TGCCAGTCGA GCGAACGGAC GAGAAGCCTG CCTCnGnGAT GTTAGC 356

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(2) INFORMATION FOR SEQ ID NO: 4294:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 314 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4294:

30

TTATCACCCA TGTTCTGACT CCAAGTTAA ATTAATTGGC ATTCGGAGTT TGTCTGAATT 60  
 CGGTAACCCG AGAGGnCCCC TCGTCCAAAC AGTGCTCTAC CTCCAATAAT CATCACTTGA 120  
 35 GGCAGCCCTA AAGCTATTTT GGAGAGAACC AGCTATTTCC AGGTTTCGATT GGAATTTCTC 180  
 CGCTACCCTC AGTTCATCCG CTCACITTTT AACGTAATCG GTTCGGTCCT CATTTCAGTG 240  
 TTACCTGAAC TTCAACCTGA CCAAGGTAGA TCACCTGGTT TCGGGTCTAC GACAAATACT 300  
 40 AAACGCCCTA TTCA 314

40

(2) INFORMATION FOR SEQ ID NO: 4295:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 345 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4295:

AAGTGAAAGA ACTCGGCGTG ACACCTATTG CACGATTCGT TGGTTTTAAG GCAGTAGGCG 60

55

GCAATCTATC TGTTGAAGAC ATTGATTIGA TCGAATTGAA CGAAGCATTG GCTTCTCAAA 180  
 CGATTGCATC TATTAAAGAA GTAGGTCTAG ATATATCACG TACGAATGTG AATGGTGGCG 240  
 CTATTGCTTT AGGTCATCCA TTAGGTGCTA CAGGCGCCAA TGTTAACCCG CGCGTTTACC 300  
 TAATGAAATG GGGTAAACCG nCCCCGATAGn CCGTAnCGCA AGGGT 345

## (2) INFORMATION FOR SEQ ID NO: 4296:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 361 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4296:

TAAATTGATT TCTAATTGAA ATCATCTTAT GACTGCTTTT TATTATACTT TACATTTCTC 60  
 GTTTCGTCAG ATTCAAACGT TTTCACCTCG CCAAGCCATC TTTCTTTGTG TTTGCTTTTA 120  
 TTTTGACGTT TTAGACATAA AAAAAGAGAC CTTGCGGTCT CAATGCGGCT CATCGCATCC 180  
 ACTTTTTGCC TGGCAACGTT CTACTCTAGC GGAAnTAATT CnACTACCA TCGACGCTAA 240  
 GGAGCTTAAC TTCTGTGTTC GGCATGGGAA CAGGTGTGAC CTCCTTGGCT ATAGTCACCA 300  
 GACATATGAA TGThAATTGA TACATTGCAA AACTAGGATA GTGAAGTAAA AGTGATTTTG 360  
 C 361

## (2) INFORMATION FOR SEQ ID NO: 4297:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 337 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4297:

AACTCGTTGC GCTCTTTTCT CGTTTCGTCA GATTCAAACT GTTTTCACTT CGCCAAGCCA 60  
 TTTTCTTTG TGTTTACTTT TTATTTTGAC GTTTTAGACA TAAAAAAGA GACCTCACGG 120  
 TCTCAACTTG CCTGGCAACG TTCTACTCTA GCGGAACGTA AGTTGGCTAC CATCGTCGCT 180  
 AAAGACCTTT CTTGACTTGT GACAATCGCT TGCTTCTTTC CTCTCCTTCG GCTCTCGCTT 240  
 ACTCAITTAG CTCTACTAAA CTCGTTGCGC TCTTTTCTCG TTTCGTCAGA TTCAAACGTT 300  
 TTCATTTCGC CAAGCCATT TnCTTTGTGT nTACTnT 337

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4298:

GTATTCCTCC ATTATTATAG GTAAATCGCT ATTAATTATA AAATTAAATG GCGGTCTCGA 60  
 CGGGAATCCT GCGTGACAGn CAGGCGTGTT ACCGCTACAC TACGAGACCA TTAGTAAAC 120  
 GGAGGAAGAG GGATTCGAAC CCCC GCGAGC CGTTAAGCCC CTGTCGGTTT TCAAGACCGA 180  
 TCCCTTCAGC CGGACTTGGG TATTCCTnCA AAATTATATG GACCTnGCAG GACTCGAACC 240  
 TGC GACCGAA CGTTATGAGC CTTAGCTCTA ACCAACTGAG CTAAAGGTCC TAAATATAAT 300  
 TTTTACAAC TATAAAATAG TGG 323

## (2) INFORMATION FOR SEQ ID NO: 4299:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4299:

CTACATGCGT TGAATTAGG ATCGGTACTT TATATGAAGA CGTGCTGCTT CCATTAAATG 60  
 AGTGATGCCA TTTTGGCATG AAGGTCACCT TAAATGTACA TTGTTGTAAT AAAATTGCCT 120  
 ATAAATTTTT AGCACATAAA ATAAGAGGnG CCAACCATTG TTAGACTATA ACAACGGTTG 180  
 GCTCTTTAAT TGTA AAAAGA AAACCATACG CTATGnTGTT ACAAnGAAAA AGGTTCTACC 240  
 ATTGTCACAA AAAATGCATC TCTACGTGCT AGAATAAATA TTGGTCAGCC AACCAAAATA 300  
 ATCAACACGA GGAGATGCTA TTT 323

## (2) INFORMATION FOR SEQ ID NO: 4300:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 385 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4300:

TGAATCCAGA TAAAATTGGA ATGATTAACG CGAATCACTT TTACTACCAA TGTTCCAAAG 120  
 CTGCTCTGCA AACGCATTGT ACTCTGAGCT TTTTGGATTA AATGAATTTG CTCCAAATAA 180  
 5 AAATACAATT GCCATTAAAA TACCACCAGA TATTACAAGT GGCAACATGT TAGAAACACC 240  
 GTTnCATIGA AGTGTITGAT AGAATGCTTT ACCTGGGGCT TGAATTTTTT TTGGACTGTG 300  
 CATTGAGTT ACCTTTTCTT TGGACCATCA CGGGGCAACA AAAGGTTTGA CGACTTGTGA 360  
 10 GCTGAATGGC TnGnTGAAT GAATT 385

## (2) INFORMATION FOR SEQ ID NO: 4301:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 348 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4301:

TCCTGTACCA CCTATAATCG TTTTAATCGA TGGGGGGACG CATAGGAATA GGCGACGTGA 60  
 25 CGATTGGATT GCACGTCTAA GCAGTAAGGC TGAGTATTAG GCAAATCCGG TACTCGTTAA 120  
 GGCTGAGCTG TGATGGGGAG AAGACATTGT GTCTTCGAGT CGTTGATTTT AACTGCCGA 180  
 GAAAAGCCTC TAGATAGAAA ATAGGTGCCC GTACCGCAAA CCGACACAGG TAGTCAAGAT 240  
 30 GAGAATTCTA AAGTGAACGA ACGAACTCTC GTTAAGGGAC TCGGCAAAAT GAnCCCGTAA 300  
 CTTCCGGGAA AAGGGTnCTC TTTAnGGTTA ACGCCCCAAA AAACCGCT 348

35 (2) INFORMATION FOR SEQ ID NO: 4302:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 385 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 40 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4302:

45 AATGGAACGT GCTTCTGTAT TGGCCCAAGT AGATATTCAT CGTGCAGCAA CACATAATAA 60  
 AGGTGTTATG AATGGCATAc ATGCTGTTGT TTTAGCAACA GGGAAATGAT ACGCGTGGTG 120  
 CAGAAGCAAG TCGCATGCA TnACGCGAGT CGTGACGGGA CAGTATCGTG GTATTGCTAC 180  
 50 ATGGCGTTAC GATCAAGATC GTTCAACGAT TGATTGGTAC AATTGCAAGT GCCTATGGAC 240  
 ATTGGGCAAT CGTTGGCGGT GGTACAAAAG TATTACCAAT TGCTAAAGCT TCCATTAGGn 300

55

TTTTGAGCGG CAAAACTTT GnCAG

385

(2) INFORMATION FOR SEQ ID NO: 4303:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 374 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4303:

AGTGCGACGA TTGGTATTTT ACAAGAATTT TATCAACAAG ATTTAATTAG CTAAACGCA 60  
 GCAATCCCTG TGTTACTAGG CGATAACATT GGTACCACGA TTACAGCTAT CTAGCTAGT 120  
 TTAGCCGGCT CAATCGCTGC AAAACGTGCG GCGCTTGAC ACGTCATCTT TAACTTAATC 180  
 GGGGTAATTA TCTTCACAAT TTTCTTGCCA GTTGTGATTC ATTTGATTAG TTTGTTACAA 240  
 GATTTATGGG CACTTAAAC CAGCGATGAC GATTGCAGTA TCACATGGnA TCCTTCAACA 300  
 TAACCAATAC CTTGGATTCC ATTTACCAAT TTGTAGCCnG GTTTAGCATn GGATTGGTTA 360  
 CCAAGCCTTG TCCC 374

(2) INFORMATION FOR SEQ ID NO: 4304:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 314 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4304:

AAACAGGAT ACTTCGATAA GTTAATGATT TCTGTTGTGA ATCGCGCACC ACGTTTCTTA 60  
 ATTTTACCGA CTATTATATT AATTGGTATT TTAGGTAGTA CAGCCGGCGA TGCTGCGACA 120  
 ATTTCTTGCC GCCGCTTGCA GCAATGCTTT TTATTAAAT TGGCTATCAC CCTATCGCTG 180  
 GACTAACGAT GGCATATGCT TCCGCTGTTG GAGGATTTGC AGCAAATATA GTTGTGGTA 240  
 TGCAAGATGC TTTGGTCTAT TCATTACAG AACCGGCAAC ACGTATCGTT TCAGATTCTA 300  
 TTAAACAAA CGTT 314

(2) INFORMATION FOR SEQ ID NO: 4305:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 344 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4305:

5 CGTTGCAGAA TGTGTTGAAA TCATCAGAAA TATGCTTAGG CAAGCTAATA TCATTGTCAG 60  
 CCATTAATTT ACGGTTACCA ACCAATATAT GGTGATGATC AATCGTTGCT TCAATACCAT 120  
 GGCCAGGTAC TGCTTTAAAT GTTGTGTCT CAGTTAATAT TAATTGCTTT TCTTTTGCAT 180  
 10 AATTGACAAT GGCTTCTGCC AATGGGTGTT CAGAATCTTT TTCAGCAGTA GCAAGTAGTT 240  
 GTAGCGTTTG ATTGTCACCA TGATAATCTG TCACGACTGG GACGACCATT TGTAATGGnA 300  
 nCCGTCCTTA TCTAAAACGA TGGGTATCAA TTTGATGnGG GCGG 344

## (2) INFORMATION FOR SEQ ID NO: 4306:

## (i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 378 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4306:

25 AGTTTCCTTG AAAATTAATC AAGGACTTAA CATTGCGAGT CAAGGTATTG ATCAAGCTAA 60  
 TGGACAGTTA AATGATGCCA AAGCTTCGTC ACACAAGTTA GAAGTAGAGT CCGTGATTAT 120  
 30 CAAGATGCAA TTCGACGCGC GCAAGATTTA AATCGAAGAA ACCAGCAACA GATTCCTCAA 180  
 AATAGCGCGG CGAACAACGA AACATCAAAT AGTGCACCTG CAGCTGGTAA TGGTGTAGCA 240  
 35 TCAACGCCAC CAAGTGCACC AAGTGGCGAT ACTGCACCAA ATAATAATGT TACGCAAAAT 300  
 ACCGCACCAG ATGAGTGAAT AATGCGCCTG TATCGACTAC ACCACAAATG ACAnnCCGGG 360  
 GAAAnAGATGG TCAAATTT 378

## (2) INFORMATION FOR SEQ ID NO: 4307:

## (i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 318 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4307:

50 GGACTTGGGT ATTCCTCCAA AATTATATGG ACCTTGCAAG ACTCGAACCT GCGACCGAAC 60  
 GGTATGAGC CGTTAGCTCT AACCAACTGA GCTAAAGGTC CTAnATATAA TTTTACAACT 120

CTAGCCAGCT GAGCTACACC GCCTTATATA GTTTGTAAAT AATATGGTGG AGACTAGCGG 240  
 GATCGAACCG CTGGACCTCC TCGGTGGCAA AGCAGnCGCT CTCCAGCTG nGCTAAGCCC 300  
 5 CCATAATAAT TACAGTAT 318

(2) INFORMATION FOR SEQ ID NO: 4308:

(i) SEQUENCE CHARACTERISTICS:  
 10 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4308:

TGTACGTTTA ATACCTATGA TATATGCTGC AAGTCTCATA TCTATTTTTC GGTTTTGAGA 60  
 20 CAATTCGTAA ATCGTATCAA ATGCCGCTTC TAATTTTTC ACGTAGCTTTT CATTAACCTC 120  
 TTCTTCAGAC CAATAATAAC CTTGATTATT TTGTACCCAT TCGAAGTAAG AAACCGTTAC 180  
 ACCACCAGCA CTTGCTAATA CGTCTGGAAC TAATAATATA CCACGTTACG TTAAATACG 240  
 25 TGTGCTTCT GGTGTTGTAG GTCCATTAGC AGCTTCAACA ACGATACTAG CTTTAATATC 300  
 ATGTGCATTG TCCTCnGTAA TTGGGTTGAA TAGCGnGGGA CTAAATGCAC ATCnAATCAA 360  
 30 CAATCCTATT GGATGTCCCA AaAATTGTAC GACCAACACC 400

(2) INFORMATION FOR SEQ ID NO: 4309:

(i) SEQUENCE CHARACTERISTICS:  
 35 (A) LENGTH: 326 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4309:

CAAATAAACC AGAGCTAGTT GCAATTGCTG AACCACATCC TAATAGACCG AAAAAGAGAA 60  
 GTAGACGTGC GGCACCGGCA GATCCTAATG CAACTCCAGC AGATCCAGCG GCTGCAGCGG 120  
 45 GTAGGAAACG GTGGTGCACC AGTTGCAATT ACAGCGCCAT ATACGCCAAC AACTGATCCT 180  
 AATGCCAATA ATGCAGGACA AAATGCACCT AACGAATnGT TGTTCATTTG ATGACAATGG 240  
 50 TATTAGACCA AGTACCAACC GTTCTGTGCC ACnTnAAACG TTGTTAATAA CTTGCCGGGC 300  
 TTCACACTAA TCAATGGTGG CAAAGT 326

(2) INFORMATION FOR SEQ ID NO: 4310:

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(A) LENGTH: 313 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4310:

10 TCAAAGCGCC AATAACATCT TCTACTGAAG TTTCTTTAGA TTTAGCATTG AGTGATAATG 60  
 TTATTGTTGC TTTTCTTCC ATTGGAATAC TTTGATGAAT CGTTAATACA GATAGTTCTA 120  
 ACTTTGATAT AACATCTAGT ACACGTGCCA ACATACCAAC AATATCAGTT ACATATAAAA 180  
 15 TTAATGTAAA TTCTCGATGG TCAAGCATTT TATCGGCTAC TGGAAATATC GTTTCTCTAT 240  
 ATnTATAAnA AGCACTTCTA GATAGATCAA ACTGTTTAAC GGCATCATAA ATGGnCAATG 300  
 TCGGATCACT TTT 313

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(2) INFORMATION FOR SEQ ID NO: 4311:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4311:

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GGTTCGAATC CAGCTAGCCC AGCCATTAGA GCCATTAGCT CAGTTGGTAG AGCATCTGAC 60  
 TTTTAATCAG AGGGTCAGAG GTTCGAATCC TCTATGGCTC ACTACTTGCA CTTTCCATTT 120  
 35 TTGGGAAGTG CTTTTTTTTTA GGTCTCCAC CAAATGTGGT GGGTATATAA TTAAAGAAC 180  
 TATTTTTAAA ATACAACTTT TAGAGCTTTT ATTATTAGGC GGCCAGTCCA TTATTGGGGC 240  
 TGGTTGTCTT CnTTTTTTTCT CCTTTGTACA AGCTGAAAAT CATCATTATA CGTGCTTAAA 300  
 40 GTGGTGAATT CTGAACCAA GAATCACTTG ATAATTTATC TATATAATCC TcATAGACC 360  
 ATATAATGCT GGAATAATGG ATCTACAnCC TGAGTTCCAn 400

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(2) INFORMATION FOR SEQ ID NO: 4312:

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(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 318 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4312:

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ACTTACAGCT CCCCAAAGCA TATCGTCGTT AGTAACGTCC TTCATCGGCT TCTAGTGCCA 120  
 AGGCATCCAC CGTGCGCCCT TAATAACTTA ATCTATGTTT CCACCATTIT TATAAGTCAA 180  
 5 ACGCTCACAT ACGGCTTCGT TTTCAATTATT TTAAATGCTC ATTTACATAA GTAAACTCTG 240  
 CTTTAAATA ATTAACATCAT TGTCTGCnAA ACGTTTTChT TTATAAAAAG ATTAAACGCG 300  
 10 TTATTAAaCT GTGGAGTG 318

## (2) INFORMATION FOR SEQ ID NO: 4313:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4313:

ACGGTGATCA CTCACCGCAG ATTTTAAGTC CTGTGCGTCT GCCAGTTCGG CCACCCCGGC 60  
 ACTATAAAAA TGGAGCAGAA GACGGGATTC GAACCCGCGA CCCCAACCTT GGCAAGGTTG 120  
 25 TATTCTACCG CTGAACTACT TCTGCATATG CGGGTGAAnG GAGTCGAACC CCCACGCCGT 180  
 AAGGCATAGA TCCTAAGTCT AGTGCGTCTG CCAATTCCGC CACACCCGCA AATGGTGAGC 240  
 30 CATAGAGGAT TCGAACCTCT GACCCTCTGA TTAAAAGTCA GATGCTCTAC CAACTGAGCh 300  
 AATGGnTCTT CCATGG 316

## (2) INFORMATION FOR SEQ ID NO: 4314:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 356 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4314:

AGGAAAAGTC GTTGTGATAC ATCAACCAGC TGAAGAAGTA CCACCAGGTG GTGCTAAAC 60  
 45 AATGATTGAA AATGGTGTAT TAGACGGTGT TGATCATGTA TTAGGTGTAC ACGTCATGAG 120  
 CACAATGAAA ACAGGTAAAA GTGTATTACC AGACCTGGTT ATGTTCAAAC AGGACGCGCA 180  
 50 TnCTTCAAAT TGAAAGTCAA GGTAAAGTGG TCATGGTTCA TCACCACATA TGGCCAATGA 240  
 TGCCATTGTT GCAGGTAGCT ACTTCGTCAC AGCGTTACAA ACAGTGTATC TAGACGACTA 300  
 GGCCATTTGA ACCGGTGGTT TCACATCGGT CATTnCCGT AAAAGnCCAT TCCATG 356

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4315:

TATCAGCATT TGTAAGTGT ATTGTTTATA ACTTCTGTGT GAAGCGCAAT ATTACAATTA 60  
 AAATGCCGAA AGAAGTACCG CCGAATATTT CACAAGTATT TAAGGACTTA ATTCCATTTT 120  
 CAGCGGTAAT CATCATTCTT TATGCATTAG ATTTAGTCAT CGCAACAGCT TTAAATCAAA 180  
 TGTAGCGGAA GGAATTTTAA AATTATTCTA ACCATTATTT ACAGCAGCAG ATGGGATGGA 240  
 TTGGTGTCTC AATTATCCTT GGAAGGCTTT GCATATTCnG GGTGTAGGG AATCAGGTCC 300  
 GTCAATGTAG AGCCAGCAAT TGCAGCCATT ACATATGCGA TATCGGAGCG GACTTCAAGT 360  
 TGCCTCAGCG GAGGACACGC 380

## (2) INFORMATION FOR SEQ ID NO: 4316:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4316:

GCTCTAGGAT GACTGATTGA ATGTCCATGA ATGAACAACC CCTTTGTTTA ATATCGAGTT 60  
 TGGCAAATTT ACGTTTATCA GCGTTTCTAT GATCAGTACT TCTACGGGTA GCGTTTCTAT 120  
 GTAATTACA TCATCTTAAC ATATAAATAC TTCGCTATTT AATTGAAAAC ATATCCTATT 180  
 ATTCTTTGTC CGTTCTGACG TTAAATATCT AGCCTTAGGC ATTTCACTTG TTAATGAATT 240  
 TAACTTTCTT CCACTAACCG TCCCTAAACC CAATCCCGCA ACAGTTTTTA ACTTTTTCGT 300  
 TGTGTCTCTG ACATCTCATT AAGAAAGTTT ATTCTGCTTA AACTTATAA TCCACACCCT 360  
 GAGCAAACGn TnCTTATGAC AGAGTATTAA AATAAGCCGn 400

## (2) INFORMATION FOR SEQ ID NO: 4317:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4317:

CCTTATTGAT AATGGTATGA GAATATTTGT TCGAGATGGA TGAAGGTAAT GAGTGAGAAA 60  
 5 CTGGATTTTT AAAGTATGAG ACAATATTTT AAAAAGTTCA ATTATTAAC TATAAGCAAA 120  
 TAATTGCTAT AAAAAAGTTT GGACGTGTAC AATTGCAATA TGAAGATTTT AAATTAATTG 180  
 TAAAGTATCG TGGAGTGGGT AACGTGTCAG AACATGTATA TAATCTTGTG AAAAAGCATC 240  
 10 ATTCTGTTAG AAAATTTAAG AATAAACCTT TAAGTGAAGA CGTTGTTAGG AAATTGGTAG 300  
 GAGCTGGGCA AAGCGCTTCG ACGTCAAGTT TCCTGCCAGC ATACTCCATT ATTGGTTCGG 360  
 15 CCGTGGGAGG TTAAnGGAAT TTACGGGGAG GTTCTGGGCA 400

## (2) INFORMATION FOR SEQ ID NO: 4318:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 319 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4318:

TAACTACGTC TCCTGTTTCT GGATTCTTAA TTCCTGGTTT ACCTGGAAC TCTCTTTCT 60  
 30 CTCCTGTTGG TAACTTCGGA TCAAATTCGT CTCGATGACC TGGTGTATC GTTTCTGGTC 120  
 CGTATTCTGT TAATTCATTA ATCGGATCTn TTGTGATTTC TTCTTTTCGAT TCACCTGTAC 180  
 TAATAATTTT TCCAGTTAAT GGATTTTTTA GTGTGGCGT CGTTATTGTC TTCTCACCTn 240  
 35 TTTGTCCTTC TCTTGTAAC TTTTCTGTCC CGGTGCTAAA TnCGGATTAA ATTACGGTCT 300  
 TTCTTGAAGG AATCTCTTC 319

## (2) INFORMATION FOR SEQ ID NO: 4319:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 368 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4319:

AGGTGCATTG AGAGAATTTG TAAATGACGT ATTAGGACCT CAAGACGATA TTAATAAATT 60  
 55 TGAATACTTA AAAAAATCTT CTCAAATAC AGGTACTGTC AATTATTGGT ATTCAACTTA 120  
 AAGATCATGA TGATTTAATA CAACTCAAAC AACGTGTnAA ATCATTTTGA TCCTTCCAAT 180

ACAGTCATAA ATTGATTTCT AATTGAAATC ATCTTATGAC TGCTTTTAT TATACTTTAC 300  
 ATTTGCTCGT TTCGTCAGAT TGCAAACGTT TTCACTTCGC CAAGCCCATC TTTChTTGGn 360  
 5 GTTTGCCT 368

(2) INFORMATION FOR SEQ ID NO: 4320:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4320:

TAAGTTAGCT ACCATCCTCG CTAAGAACCT TTCTTGACTT GTGACAATCG CTGCTTCTT 60  
 20 TCCTCTCCTT CGGCTCTCGC TTAATCATTT AGCTCTACTA AACTCGTTGC GCTCTTTTCT 120  
 CGTTTCGTCA GATTCAAACG TTTTCACTTC GCCAAGCCAT TTTCTTTGT GTTACTTTT 180  
 TATTTTGACG TTTTAGACAT AAAAAAGAG ACCTCACGGT CTCAACTTGC CTGGCAACGT 240  
 25 TCTACTCTAG CGGAAnTAAA GTTGGnCTAC CATCGTCGCT AAAGACCTTT CTGACTTGT 300  
 GACAATCGCT TGCTTCTTTT CCTCTCCTnC GGCTCTCGGT TAACTCA 347

(2) INFORMATION FOR SEQ ID NO: 4321:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4321:

GGGCAAGTTA CAGTGGTGCA TGGTTGTCGT CACTCGTGTC GTGAGATGTT GGGTTAAGTC 60  
 CCnCAACGAG CGGCAACCCT TAAGCTTAGT TGCCATCATT AAGTTGGGCA CTCTAAGTTG 120  
 45 ACTGCCGGTG ACAAAACGTA GGAAGGTGGG GATGACGTCA AATCATCATG CCCCTTATGA 180  
 TTTGGcTACA CACGTGCTAC AATGGACAAT ACAAGGGGCA GCGAAACCGC GAGTCaAGCA 240  
 AATCCCATAA AGTTGTTCTC AGTTCGGATT GTAGTCTGCA ACTCGaCTaC ATGaAGCTGG 300  
 50 aATCGCTaGT aATCgTGGTC CAGCATGCTA CGGT 334

(2) INFORMATION FOR SEQ ID NO: 4322:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4322:

CTGTTAAACG ACTACAGGAA GTATTTACAA TCAAATAAG CAAAAGTATT CAGATGCCTC	60
AGATAAAGCT TGGGCGCATT CAAAATCTAT TTGGAGAGGC ACATCAAAAT GGTTTAGCAA	120
CGATATAAAA GTGCAAAGGG TTGGCTAATA GATATGGCTA ATAAATCGCG CTCGAAATGG	180
GATAATATTT CTAGTACAGC ATGGTCGAAT GCAAAATCCG TTTGGAAnGG AGCATCGAAA	240
TGGTTTAGTA nCTCATTACA AnTCTTTAAA GGGTTGGA CT GGGGATATGT ATTCAGAGCC	300
CACGATCGTT TTGATGCATT TCAGTTCGGC	330

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(2) INFORMATION FOR SEQ ID NO: 4323:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 337 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4323:

CAATGATGCC ATGAGCAGTG CCTCCTTTAA TAGCATTTTA GCACTGTTTT GTCGTATTTT	60
TAAATATAAA TTTGGAATGA ATAATAAGT AGTGATTAAA TTAAGTTGTG TGATAGGAAA	120
CTTGGACATC AATCAAAGTA ATAGGCACTA CAACGCTTAT TGGCGGGGCC CCAACAAAGA	180
AGCTGACGAA AAGTCACTTG CAATAATGTG CAAGTcnggg ATGGGCCCCA ACATAGAGAA	240
ATTGGGTCCG nAATTTCTAC AGACAATGCC AGTTGGCGGG GCCCCACAT AGAGAATTTT	300
GAAAAGGAAT TCTACCAGCA ATGCCAGTTG GGGGAnG	337

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(2) INFORMATION FOR SEQ ID NO: 4324:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 330 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4324:

TTACTTACTA TCTAGTTTTG AATGTATAAA TTACATTCAT ATGTCTGGTG ACTATAGCAA	60
GGAGGTCACA CCTGTTCCCA TGCCGAACAC AGAAGTTAAG CTCCTTAGCG TCGATGGTAG	120

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GCATTGAGAC CGCAAGnTCT TTTTTTTATG TCTAAAACGT CAAAATAAAA AGCAAACACA 240  
 AAGAAAAATG GCTTGGCGAA GTGAAAACGT TTGAATCTGC CGAACGAGAA AGAGCGnACC 300  
 5 GAGTTTAGTA GAnTAAATGA GTAAGCGAGA 330

(2) INFORMATION FOR SEQ ID NO: 4325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4325:

TTCATCCGCT CACTTTTCAA CGTAATCGGT TCGGTCTCC ATTCAGTGTT ACCTGAACTT 60  
 20 CAACCTGACC AAGGGTAGAT CACCTGGTTT CnGGTCTACG ACAAATACTA AACGCCCTAT 120  
 TCAGACTCGC TTTGCTACG GCTCCACATT TACTGCTTAA CCTTGACATC AAATCGTAAC 180  
 TCGCCGGTTC ATTCTACAAA AGGCACGCCA TCACCCATTA ACGGGCTCTG ACTACTTGTA 240  
 25 AGCACACGGT TTCAGGTTTC ATTTCCTCC CCTTCCGGGG TGGCTTTTCA nCTTCCCTC 300  
 ACGGnACTGG TTCAC 315

(2) INFORMATION FOR SEQ ID NO: 4326:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4326:

TATTTTGACG TTTTAGACAT AAAAAAGAG ACCTTGCGGT TAnATGCGGC TCATCGCATC 60  
 CACTTTTTGC CTGGCAACGT TCTACTCTAG CGGAACGTAA GTnGAACTAC CATCGACGCT 120  
 AAGGAGCTTA ACTTCTGTGT TCGGCATGGG AACAGGTGTG ACCTCCTTGC TATAGTCACC 180  
 45 AGACATATGA ATGTAAATTA TACATTCAA ACTAGATAGT AAGTAAAAGT GTTTTGCTTC 240  
 GCAAAACCAT TTATTTTGAT TAAGTCTTCG ATCGnTTAGT ATTCGTCAAC TCCACATGTC 300  
 50 ACCATGCTT 309

(2) INFORMATION FOR SEQ ID NO: 4327:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4327:

AAAGCTTATA AACGCTCATC TGACATTGTA GAATTCATGC TTTCAAAGA CGATATACTA	60
CGACACTCCT ACGAACTTGT CCAAGGATTA CGAAAAGACC TAAGGTTATG TAATTnGCCT	120
AAATTTATTA ATCGTTTAAA TTCAGTTAGT AAAAAGTCTG TGAGTAAGGG TGTATGGAAA	180
GTGGTTAAAT ATTATAGAAA ACATCAAAGG ATGTTAAGAA ATACAATTTA TTACCCAGCA	240
TTTAATAATG GTGCTATAGA AGGAATTAAT AATAAGATnA AATTAATCAA GTGAATTTCT	300
TTTGGTTnCA G	311

(2) INFORMATION FOR SEQ ID NO: 4328:

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(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 340 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4328:

TAGCTTCTGC GAGCTAGCGG AATCGAAGCC CCAGTAAACG GCGGCCGTAA CTATAACGGT	60
CCTAAGGTAG CGAAATTCCT TGTCGGGTAA GTTCCGACCC GCACGAAAGG CGTAACGATT	120
TGGGCACTGT CTCAACGAGA GACTCGGTGA AATCATAGTA CCTGTGAAGA TGCAGGTTAC	180
CCGCGACAGG ACGGAAAGAC CCCGTGGAGC TTTACTGTAG CCTGATATTG AAATTCGGCA	240
CAGCTTGTAC AGGATAGTAG GAGCTTTGAA ACGTGAGCGC TACTTACGTG GAGGCGCTGG	300
TGGGATACTA CCTAGCTGT TTTGGTnTCT nACCCGACCA	340

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(2) INFORMATION FOR SEQ ID NO: 4329:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 325 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4329:

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AATCCATAGC GAAATGTATA CCATCACCCA TCGCTCCTTC TAAAGGTAAA TCTCTACCTT	60
TTTGTGCACC AGTACATAAT ATAATGGCAT CATACTCAGA TTCTAACGTT GCTTTATCAA	120

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TACGACGTCG AACCACATCT TTATCAAGTT TCATATTCGG AATACCATAC ATTAATAAAC 240  
 CGCCTGATTC TCTAGCACGT TCATAAATAG TTAAGTTCTT 300  
 5 CAGCAGCAGT AATCCTGnTG GACCG 325

(2) INFORMATION FOR SEQ ID NO: 4330:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 327 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4330:

CAC TTCACCA CAGCCGCCAT GGCAGGnGCA GTAGGAATCG AACCCACACC AAAGGTTTTG 60  
 20 GAGACCTCTA TTCTACCGTT GAACTATGCC CCTATTAAAA ATAATAAATG GAGGGGGGCA 120  
 GATTGGAAT GCGGAACCCG AAGAGCGGAT TTACAGTCCG CCGCGTTTAA CCACTTCGCT 180  
 ACCCCTCCAT AAATGGTGCG GCGGnGnAGG ACTTGAAACC CCCAACCTAC TGATTACAAG 240  
 25 TCAGTTGCTC TGACCAATTG AGCTAAGGCC GGCTAAGAAA TGTTCCAGG ACAGAGTCGA 300  
 AACTGCCGAC ACATGGGAGC TTTCAAT 327

(2) INFORMATION FOR SEQ ID NO: 4331:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4331:

GCATCATTTT CAGCTTCCCA CTTCACATT TGGAAAATTT CTCCAGTAAC AATGAAAGAC 60  
 CATATACTTT TTCCTACAAG AGCAGGACCC GGTAACAATA CAGGTTGGTA ATGCCCAATA 120  
 ATAATGACCA TTTCCCAAAT GCCTAAGAAA ATAATAAATG TGATAATAGG TAATATAAAT 180  
 45 TTGTTATTTG TGGGACGTGT CATGAACGCG ATGCCTCCTT ATACAATGAC GGTTCACAA 240  
 AGTCATCATA TGCAGGTGGA TTAACAAAT GATGTTGTTT TACCAATGTC GTAATTTCTT 300  
 GGATAGCCGG ATGGnTTAAA TTGTTAAAAT CACCATAGGG TGTCCnGCC GTGGACTGTG 360  
 50 GTTAAAAACG TCACGGAATT TGTTTAAAAA GGTGCGTCAT 400

(2) INFORMATION FOR SEQ ID NO: 4332:

- (A) LENGTH: 366 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4332:

10 CTGGTATGCA GATTTACCAC CTGCCTCTCC ACAAnTnnGG GGAGAGCAAA CAGATGTGCC 60  
 TGAATCAAGT GACTGGTATA ACGCATCATA CATTATTATG TGGGGCTCTA ATGTACCTTT 120  
 AACACGTACT CCGGATGCAC ATTTTATGAC TGAAGTCCGC TATAAAGGTA CAAAAGTCAT 180  
 15 TTCAGTAGCA CCAGATTACG CAGAAAATGT GAAATTGCA GATAACTGGC TAGCACCGAA 240  
 TCCTGGTTCA GATGCTGCAA TTGCACAAGC AATGACGGCA TGTTATTTTA CAAGGAACAT 300  
 TATGTTAAAT CCAACCTGAA TGAACGGTTT TTATTAAATT ACGGTTAAAA CCATTATTAC 360  
 20 CAGGAT 366

## (2) INFORMATION FOR SEQ ID NO: 4333:

- 25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4333:

TATTATTTCA TTGAGCAGAA AGAAAATTAT GGCACCAAAC TTTAATATTT TTTTCAATGT 60  
 35 CATTCTTTTG AnGGGAGTGG GACAGAAATG ATATTTTCGC AAAATTATTT TCGTCGTCCC 120  
 ACCCCAACCTT GCATTGTCTG TAGAAATTGG GAATCCAATT TCTCTTTGTT GGGGCCCATC 180  
 CCCAACTTGG CACATTATTG TGAAGCTGAC TTTTCGTAC TTGCTGTGTT GGGGCCCTCA 240  
 40 CCCCAACTCG CATTGCCTGT AGAATTTCTT TTCGAAATTC TCTGTGTTGG GGCCCCCTGA 300  
 CTGAGAATTG GAAAAAAGCT TGTGACAAG CGnATTTTC GTTCCATGCA ACTGACTGCC 360  
 45 AAGAGAAcNt CGTGAGAGCn ATGAAGAAGA TTGGATTGTA 400

## (2) INFORMATION FOR SEQ ID NO: 4334:

- 50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 309 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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CGCCCTTAAT AACTTAATCT ATGTTTCCAT CCTACAGGAA ACGCGTTATT AATCTTGTGA 60  
 GTGTTCTTTC GAACnTATGC GATTATTCTT TATGAATTCA AGCTTATTTA AAACTCTTTA 120  
 5 TTCACTCGGT TTTGCTTGGT AAAATCTATA TnTTACTTAC TTATCTAGTT TTCAATGTAC 180  
 AATTTCTTTT TAGTCAAGCG CTCGCATAAG CAATATCACT TTAACCAAAA AATATTTGAA 240  
 10 TGTTAAATAA ACATTCAAAA CTGAATACAA TATGTCACAT TATTCGGCCA TCTTCTGnAA 300  
 GAAGATGTT 309

## (2) INFORMATION FOR SEQ ID NO: 4335:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 329 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear  
 20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4335:

nAGGACTTTT CTCGGTCAGT GTGAAATCA ACGCACTCGT AnACACAATG TCTTCTCCCC 60  
 25 ATCAGAGCTC AGCCTTAACG AGTACCGGTA TTTGCCTAAT ACTCAGCCTT ACTGCTTAGA 120  
 CGTGCAATCC AATCGCACGC TTCGCCTATC CTACTGCGTC CCCCCATCGA TTAAAACGAT 180  
 30 TATAGTGGT ACAGGAATAT CAACCTGTTA TCCATCGCCT ACGCCTGTG GnCTCAGCTT 240  
 AGGACCCGAC TAACCCAGAG CGGACGAGCC TTCCTCTGGA AACCTTAGTC AATCGGTGGA 300  
 CGGGATTCTC ACCCGTCTTT CGCTACTCA 329

## 35 (2) INFORMATION FOR SEQ ID NO: 4336:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 310 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 40 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4336:

45 CAAAGTGACA GGTGGTGCAT GGTGTGCGTC AGCTCGTGTC GTGAGATGTT GGGTTAAGTC 60  
 CCGCAACGAG CGCAACCCCTT AAGCTTAGTT GCCATCATT AATTGGGCAC TCTAAGTTGA 120  
 50 CTGCCGGTGA CAAACCGnnn GAAGGTGGGG ATGACGTCAA ATCATCATGC CCCTTATGCA 180  
 TTTGGGCTAC ACACGTGCTA CAATGGGACA ATACAAAGGG CAGCGAAACC GTGAGTGCAA 240  
 GCAAATCCCA TTAAAGTTGT TCTCAGTTCG GATTGTAGTC TGCAACTCGG ACTACATGAA 300

55

## (2) INFORMATION FOR SEQ ID NO: 4337:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4337:

```

CCAGCACCGG GGCAGGCGTC ACCCTCATAC ATCACCTTAC GGTTTAGCAG AGACCTGTGT      60
TTTTGATAAA CAGTCGCTTG GGCCTATTCA CTGCGGCTCT TCTGGGCGTT AACCTAAAG      120
AGCACCCCTT CTCCCGAAGT TACGGGGTCA TTTTGCCGAG TTCCTTAACG AGAGTTCGCT      180
CGCTCACCTT AGAATTCTCA TCTTGACTAC CTGTGTCGGT TTGCGGTACG GGCATTATTT      240
TCTATCTAGA nGGCTTTCTC GGCAGTGTGA AATCAACGAC TCGAAGACAC AntGGCTnCT      300
CCCATCAGAG CTCAGCCTTA ACGA                                             324

```

## (2) INFORMATION FOR SEQ ID NO: 4338:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4338:

```

CGGACATCAA ACGGATGCTG CTCGATTGGC AAATGCATAT AACTAGTAAC ATGATCATCG      60
ACATCAAATT TAGATGATCA AATGTcCCCA ATcATTAAATT TGATTGGGTT GTTTGCTCAA      120
TTGATTATAT GTTTTTCCCTA GCACTTCATG CGGCACCATA TCTTTACCTA GTAGCCACAA      180
AGATAAGTCT AACAAGTGGC AACCATAATC GATTAAACTA CCGCCACCTT GCAACGCTTT      240
ATTGGTAAAA ACACCCAGC CAGGCACTTT ACGCCTACGC ATCGCTTGTA CACGTGCTAC      300
TAAAGGTTTA CCAACCACAC CTGATTCAAT TGCTTTTTTA GCAGTAATTG CCACATCTGT      360
GTGACGATAA TGATATGCGC CAGTAATAnT TTGTGnTTT                             399

```

## (2) INFORMATION FOR SEQ ID NO: 4339:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4339:

5 TGAGGCGATT ATTTCTTATG AATTCAAGCT TATTTAAAAC TCTTTATTCA CTCGGTTTTG 60  
 CTTGGTAAAA TCTATATTTT ACTTACTTAT CTAGTTTTCA ATGTACAAAT AATGGTGGGC 120  
 CTAAGTGGAC TCGAACCACC GACCTCACGC nTATCAGGCG TCGCTCTAA CCAGCTGAGC 180  
 10 TATAGGCCCA TTTnTTTGAA TGTTAAATAA ACATTCAAAA CTGGAATACA ATATGTGCAC 240  
 GTTATTCCGC ATCTTCTGAA GAAGATGTTn CCGAATATAT CCTTAGAAAG GAGGTGATCC 300  
 AGCCGCACCT TCCGATACG GCT 323

15

## (2) INFORMATION FOR SEQ ID NO: 4340:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4340:

25

GGCTAGCCCT AAAGCTATTT CGGAGAGAAC CAGCTATTC CAGGTTTCGAT TGGAATTTCT 60  
 CCGCTACCCT CAGTTCATCC GCTCACTTTT CAACGTAAGT CGGTTCCGGTC CTCCATTTCAG 120  
 30 TGTTACCTGA ACTTCAACCT GACCAAGGGT AGATCACCTG GTTTCGGGTC TACGACCAAA 180  
 TACTAAACGC CCTATTCAGA CTCGCTTTTCG CTACGGCTCC ACATTTACTG CTTAACCTTG 240  
 CATCAAATCG TAACTCGCCG GTTCATTCTT ACAAAGGCA CGCCATCACC CATTACGGG 300  
 35 CTCTGAACTA ACTTGGTAAA GCnCCGGTTT nCnGGTCCAA TTTT 344

## (2) INFORMATION FOR SEQ ID NO: 4341:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

40

45

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4341:

TGTACCACCT ATAATCGTTT TAATCGATGG GGGGACGCAT AGnGATAGGC GAACGTGCGA 60  
 50 TTGGATTGCA CGTCTAAGCA GTAAGGCTGA GTATTAGGCA AATCCGGTAC TCGTTAAGGC 120  
 TGAGCTGTGA TGGGGAGAAG ACATTGTGTC TTCGAGTCGT TGATTTCACA CTGCCGAGAA 180  
 AAGCCTCTAG ATAGAAAATA GGTGCCCCGTA CCGCAAACCG ACACAGGTAG TCAAGATGAG 240

55

TTcNggGAAA AAGGGnTCCC CTTTAAGGGT TAACCGCCCC AAAAAACCCC C

351

(2) INFORMATION FOR SEQ ID NO: 4342:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 327 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4342:

AATAATGACT	CCTACGGGAC	TCGAACCCGn	GTTACCGCCG	TGAAAGGGCG	TGTACTTAAC	60
CGTATGACCA	AGGAGCCATG	GCTCACCAGG	TAGGACTCGA	ACCTACGACC	GATCGGTAA	120
CAGCCGATAG	CTCTACCACT	GAGCTACTGT	GGATTAATAT	TATGCCTGGC	AACGTTCTAC	180
TCTAGCGGAA	nTAAATTCGA	ACTACCATCG	ACGCTAAnGA	GCTTAACTTC	TGTGTTCCGC	240
ATGGGAACAG	GTGTGACCTC	CTTGCTATAG	TCACCAGACA	TATGAATGTA	ATTTATACAT	300
TCAAACTAG	ATAGTAAGTA	AAAGTGA				327

(2) INFORMATION FOR SEQ ID NO: 4343:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 360 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4343:

ACCGCTTGGG	CTGACATTTT	TGGCTTGTTA	AGCAGCTTGC	CTACTTTTTT	GGCAATAGCA	60
CCATACGTTG	TTAGAGTCCC	ATAAGGAACC	TGTCTTAATT	CATTCCAAAC	ACACTGTTGA	120
AAATGACTAC	CTGTTGGCTT	TAAAGGTATT	GTGATTTTCA	GATTGTCACC	TTTAAAATAC	180
GCGTCTAACC	ACTGTGTCGC	CTCTCTAAAT	ATCGCTAAAG	ACGTATTTTC	TTCCCTAGTA	240
CCATCACCTT	GTTGATTTTC	AAACAAAACA	GCGGTCAGAC	TTACCCCATC	ACTCAAAGT	300
TCCAAnCGTC	CTGACAGGCG	AAnCAGAGTG	AACGCTGAGA	CTCCAGAAAA	ATCCCCCTnT	360

(2) INFORMATION FOR SEQ ID NO: 4344:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 313 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4344:

5 ATTCCGACAT CTTCTGAAGA AGATGTTnCC GAATATATCC TTAGAAAGGA GGTGATCCAG 60  
 CCGCACCTTC CGATACGnCT ACCTTGTTAC GACTTCACCC CAATCATTTG TCCCACCTTC 120  
 GACGGCTAGC TCCTAAAAGG TTA CTCCACC GGCTTCGGGT GTTACAAACT CTCGTGGTGT 180  
 10 GACGGGCGGT GTGTACAAGA CCCGGGAACG TATTCACCGT AGCATGCTGA TCTACGATTA 240  
 CTAGCGATTC CAGCTTCATG TAGTCGAGTT GCAGACTACA ATCCGAACTG AGAACAACCTT 300  
 TATGGGATT T GCT 313

## (2) INFORMATION FOR SEQ ID NO: 4345:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4345:

25 ATTTTATCGT AAGATTTTTT CGCAATGAGA TTTGGATCGT TTTGTCCAC TACAATATCT 60  
 AATAGTTTTA CTTTAAGTCC AGCATTCACA AAAAGTGCTG CCAGTTGAGC GCCCATTGTG 120  
 CCTGCGCCAA GAACGGTTAC TTTATTAATT GTCATAGTGA TTCTCCAAT TTAGTTGAGG 180  
 30 ATAAGATAAC CATTAGATA ATTGGAATAA CGTTGCTATT TTATAAAATT AATTAAGTAT 240  
 CTTTGACAGT CATCTTAGCC TCTTATTTAA GGnAAAAGCh TTATGCTTAA nATAAGTCTT 300  
 35 TTTTA 305

## (2) INFORMATION FOR SEQ ID NO: 4346:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4346:

45 GTCAGTTATG GCAAGTGCAT CAACATTTTC AGACACAGCA AGTCTTACGG CATCTTCTAT 60  
 TTTTAAGCTT GAATTTAACA AATCATAAGC CGTATGAATA TTAAATATG CCACCATGAT 120  
 50 TGAATGGnCC CTTTCTATTA GTTAAGTTTG TCGTAAAGC TG TAGCAAGT TGCTCAAATT 180  
 CATCCCCAGC TGTCCACTGA AACTCCTGGA CGCATTTCGGA TGAnCAACGC CAACCAAAAT 240

AntACCTTCA TCGACTGCAA ATACCCATAA TTTCCAGCCT TGATGTCAGC AATGTAATAA 360  
 CCAACTGAGA TGCTCATTGG CTGATACGAT GntCCATACA 400

5 (2) INFORMATION FOR SEQ ID NO: 4347:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 337 base pairs  
 (B) TYPE: nucleic acid  
 10 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4347:

TCTGGGTTGA GTCGGGTCCT AAGCTGAGGC CGACACGTAG GCGATGGATA ACAGGTTGAT 60  
 ATTCCTGTAC CACCTATAAT CGTTTAAATC GATGGGGGGA CGCATAGGGA TAGGCGAnGT 120  
 20 GGCGATTGGA TTGCACGTCT AAGCAGTAAG GCTGAGTATT AGGCAAATCC GGTACTCGTT 180  
 AAGGCTGAGC TGTGATGGGG AGAAGACATT GTGTCTTCGA GTCGTTGATT TCACACTGGC 240  
 CGAGAAAAGC CTCTAGATAG AAATAnGTGC CCGTACCGCA ACCGACACAG GTAGTCCAAG 300  
 25 ATGAGATTCh TAAGGTGGAG CGACGAATCT CCGTTAA 337

(2) INFORMATION FOR SEQ ID NO: 4348:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 318 base pairs  
 30 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4348:

GTTAAGACAC CGCCCTTTCA CGGCGTAACA CGGGTTCGAG TCCCGTAGAG GTCACCATT 60  
 40 TTTAGGTCTC GTAGTGTAGC GATTAAACAG CCTGCCTGTC ACGCAGAGAT CGsGGGTTCG 120  
 ATTCCCGTCG AGACCGTACA AATGCCTATC CAAGAGGATA GnATTTTTTT TGCGTTTAAT 180  
 ATTATATTAA TAAAGATAT ATGGACGAAT GATAATCATA TTGATTTATC TGTTTCGTCCA 240  
 45 TTTTCTTTAA AATGTATGAA CCTCAAGTAA CTTAGTGGTT GGATATGAAA GATAAACGTh 300  
 GACAATAAAA TCTTTATT 318

(2) INFORMATION FOR SEQ ID NO: 4349:

- 50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 319 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

55



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4349:

CTTTAAAGCA CGTATAATGA TGATTTTCAG CTTGTACAAA GGAGAAAAAA AGAAGACAAC 60  
 5 CAAGCCCAAT AATGGACTGG CCGCCTAATA ATAAAAGCTC TAAAAGTTGT ATTTTAAAAA 120  
 TAGTTCTTTA AATTATATAC CCACCACATT TGGTGnAGnA ACCTAAAAAA AnGCACTTCC 180  
 CAAAATGGA AAGTGCAAGT AGTGAGCCAT AGAGGATTGC AACCTCTGAC CCTCTGATTA 240  
 10 AAAGTCAGAT GCTCTACCAA CTGAGCTAAA TGGCTCTAAA TGGCTGGGCT AGCTGGGATT 300  
 CGAACCAACG AGTGACGGA 319

## (2) INFORMATION FOR SEQ ID NO: 4350:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 346 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 20 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4350:

25 ACTTCGCTAC CCCTCCAGCT TATTCATATA ATTTAATAAT CAAAATGGTG GAGAATGACG 60  
 GGTTCGAACC GCCGACCCTC TGCTTGTAAG GCAGATGCTC TCCCAGCTGA GCTAATTCTC 120  
 CAAAATAATG ACTCCTACGG GACTCGAACC CGTGTTACCG CCGTGAAAGG GCGGTGTCTT 180  
 30 AACCGCTTGA CCAAGGAGCC ATGGCTCCAC AGGTAGGACT CGAACCTACG ACCGATCGGT 240  
 TAACAGCCGA TAGCTCTACC ACTGnAGCTA CTGTGGATTG AATCATTATG CCTGGCAACG 300  
 35 TTCTTACTAT AGCGGAAnGT CAAGTTCCGC ATnACCATAC GAAGCT 346

## (2) INFORMATION FOR SEQ ID NO: 4351:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs  
 40 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4351:

45 ACGTCCTTCA TCGGCTTCTA GTGCCAAGGC ATCCACCGTG CGCCCTTAAT AACTTAATCT 60  
 ATGTTTCCAC CATTTTTATA AGTnAAACGT TAACATGAAG TTACGTTCTT TTATAAAAAG 120  
 50 ATTTAAACGC GTTATTAATC TTGTGAGTGT TCTTTGGAAC ACTAGCGATT ATTTCTTATG 180

ACTTACTTAT CTAGTTTCA ATGTACAAAT AATGGTGGGA GACTAGCGGG ATCGAACCGC 300  
 TGACC 305

5 (2) INFORMATION FOR SEQ ID NO: 4352:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 302 base pairs  
 (B) TYPE: nucleic acid  
 10 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4352:

GTTTCATCAAT TGCTAATTCC AGTCCGCCTA ACGGATCAAT TTCATCCGCA TGTATTTTCA 60  
 CTTTAAAACC TGGCTTCTTT GGCTTTTTCG ATATAATGTT GCGATTGTTC TATTGTAAAT 120  
 20 ACACCTGTTT CACAGAAAAT ATCCGCAAAG TCTGCATATT GTTTTACTTC CGGAAGTAAC 180  
 GCAATCATTT CTTCTAAAAA TGCCTCATTT GAAGTTCCT CTTTAGGTAC AGCATGAGGC 240  
 CCTAGGAAAG TATGTTTCAT GTCTAAATCA TATTTCTCAG CTAAACGATT AGnCACTTTC 300  
 25 AA 302

(2) INFORMATION FOR SEQ ID NO: 4353:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 411 base pairs  
 30 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4353:

TCTACCGCTG AACTACTTCT GCGGGTGAAG GGAGTCGAAC CCCCACGCCG TAnnTGAGGA 60  
 TCCTAAGTCT AGTGCGTCTG CCAATTCCGC CACACCCGCA AATGGTGAGC CATAGAGGAT 120  
 40 TCGAACCTCT GACCCCTCTGA TAAAAGTCA GATGCTCTAC CAACTGAGCT AAtGGCTCTT 180  
 CCATGGTGCC GGCCAGAGGA CTTGAACCCC CAACCTACTG ATTACAAGTC AGTTGCTCTA 240  
 45 CCAATTGAGC TAGGCCGGCA ATATGTAAGA ATAAATGGTG GAGAATGACG GGTTCGAACC 300  
 GCCGACCCTC TGCTTGTAAG GCAGATGCTC TCCCAGCTGA GCTAATTCTC CGnTTTAAAA 360  
 CTGCTGGCnA CGGTCTAnTC TAAGGGGACG TAAGGTCGAC TACCATCGAC G 411

50 (2) INFORMATION FOR SEQ ID NO: 4354:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 367 base pairs

55

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4354:

TGCTTAGATG CTTCAGCAC TTATCCCGTC CACACATAGC TACCCAGCTA TGCCGTTGga 60  
10 CGACAACCTGG TACACCAGAG GTATGTCCAT CCCGGTCCTC TCGTACTAAG GACAGCTCCT 120  
CTCAAATTTTC CTACGACCAC GACGGATAGG GACCGAACTG TCTCAGCAGC TTCTGAACCC 180  
AGCTCGCGTa CCGCTTTAAT GGGCGAACAG ACAAGCCCTT GGGGACCGAC TACAGCCCCA 240  
15 GGATGCGATG AGCCGACATC GAGGTGCCAA ACCTnCCCGT CGATGTGAac TCTTGGGGGA 300  
GATAAGnCTG TTATCCCCGG GGTAACTTTT ATCCGTTGAG CGATGGGCCC TTACCATGCG 360  
GAAACCA 367

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(2) INFORMATION FOR SEQ ID NO: 4355:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 313 base pairs  
(B) TYPE: nucleic acid  
25 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4355:

GTATTTTAAA TCATAGTGGT TTATGCGTCT TTTTCAAATT CTATAAAAAA TCGGATGACG 60  
TGTAATCTGC CATAGATTAA CACATTCATC CGATTTATAA TAATAAGATA GACTAACATT 120  
35 TATTGAGAGC GGGACGGAAA TGATAAAGAA CGACTAATGA TTGATTATGT AGCGATTCTT 180  
TATCATTAGT CACAGCTAAT GTGTACTTAA AAATATGAAT GCATGAGTTA CACTCAaATT 240  
AGAGGAAATA CTAATTTCTA AAGAAAAAGT ATTTCTTTAT GTTGGGGnCC ACCCCAACCTT 300  
40 GnCATTGTCT GTT 313

(2) INFORMATION FOR SEQ ID NO: 4356:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 335 base pairs  
(B) TYPE: nucleic acid  
45 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4356:

GGGCTGGGTT CAGAACGTCG AGGCAGTTCG yTCCCTATCC GTCGTGGGCG TAGGAAATTT 60

55

TCGTGCCAnG CATAAGCTGG GTAGCTATGT GTGGACGGGA TAAGTGCTGA AGATCCTGAA 180  
 GCATGAAGCC CCCCTCAAGA TGAGATTTC CAACTTCGGT TATAAGATCC CTCAAAGATG 240  
 5 ATGAGGTTAA TAGGTTGAG GTGnGAAGCA TGGTGACAGT GGnAGCTGAC GAATACTAAT 300  
 CGATCGAGGA CTTAATCAAA ATAAATGTTT TGCGA 335

## (2) INFORMATION FOR SEQ ID NO: 4357:

10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 304 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4357:

20 GCTCTAAAAG TTGTATTTTA AAAATAGTTC TTAAATTAT ATACCCACCA CATTGGTGn 60  
 nGAACCTAAA AAAAAGCACT TCCCAAAAT GGAAAGTGCA AGTAGTGAGC CATAGAGGAT 120  
 TCGAACCTCT GACCTCTGA TAAAAGTCA GATGCTCTAC CAACTGAGCT AATGGCTCTA 180  
 25 ATGGCTGGGC TAGCTGGATT CGAACCAACG AGTGACGGAT nAAAGTCCGT TGCCTTACCG 240  
 CTTGGCTATA GCCCAATATA TAGATGTTGG AGGGGGGCGAG ATTGGAAGCTG CCGAACCCGA 300  
 AGAG 304

## 30 (2) INFORMATION FOR SEQ ID NO: 4358:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 302 base pairs  
 (B) TYPE: nucleic acid  
 35 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4358:

40 ATAATGGTGA CGTTGATGAT GCATTAAACAC AAGGTAAAGC AGCAATTGAT GCTATTCAAG 60  
 TAGATGCTAC TGTTAAACCT AAAGCGAACC AAGCTATTGA AGTTAAAGCA GAAGATACGA 120  
 AAGAATCTAT TGATCAAAGT GACCAGTTAA CTGCTGAAGA AAAAAGTGA GCATTAGCAA 180  
 45 TGATTAAACA AATTACAGAT CAAGCTAAAC AAGGTATTAC TGATGCAACA ACAACTGCTG 240  
 AAGTTGAAAA AGCGAAACTC AAGGACTTGA AGCATTGAT AACATTCAAn TCGACTCAnC 300  
 50 AG 302

## (2) INFORMATION FOR SEQ ID NO: 4359:

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- (A) LENGTH: 350 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4359:

10 GGTGTTGGGAAA TCATTGCATG AGAGTGTGAA AGGGCATAAG GGGAGCTTGG ACTGCGAGAC 60  
 CTACAAGTCG AGCAGGGTCG AAAGAGGACT TAGTGATCCG GTGGTTCCGC ATGGAAGGGC 120  
 CATCGCTCAA CGGATAAAAG CTACCCCGGG GATAACAGGC TTATCTCCCC CAAGAGTTCA 180  
 15 CATCGACGGG GAAGTTTGGC ACCTCGATGT CGGCTCATCG CATCCTGGGG CTGTAGTCGG 240  
 TCCCAAGGGT TGGGCTGTTT GCCCATTAAG GCGGTACAG GCTGGGTTCA GAACGTCGTn 300  
 AGAAAGTTCG GTCCTATCC GTCCTGGGGC GTAGGAAATT TnGAGAGGAG 350

20

(2) INFORMATION FOR SEQ ID NO: 4360:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 329 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4360:

AGCTCCTAAA AGGTTACTCC ACCGGCTTCG GGTGTTACAA ACTCTCGTGG TGTGACGGGC 60  
 GGTGTGTACA AGACCCGGGA ACGTATTCAC CGTAGCATGC TGATCTACGA TTACTAGCGA 120  
 35 TTCCAGCTTC ATGTAGTCGA GTTCGAGACT CACAATCCGA ACTGAGAACA ACTTTATGGG 180  
 ATTTGCTTGC ACCTCGnGGT TCGCTGTCC CTTTGTATTG TCCATTGTCA GCACGTGTGT 240  
 AGCCCAAATC ATAAGGGGCA TGATGATTG GACGTTTCATC CCCAnCTTCC TCCGGnTTGT 300  
 40 ACACCGGCAG TTCAACTTAG AGTGCCCAA 329

40

(2) INFORMATION FOR SEQ ID NO: 4361:

45

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 424 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4361:

55 AGACATAAAA AAAGAGACCT CACGGTCTCA ACTTGCTGG CAACGTTCTA CTCTAGCGGA 60

CTnTCCTCTC CTTCGGCTCT CGCTTACTCA TTTAGCTCTA CTAAACTCGT TGGCTCTTTT 180  
 TCTCGTTTCG TCAGATTCAA ACGTTTTTAC TnCGnCAAGC CATTTTTCTT TGTGTTTACT 240  
 5 TTTTATTTTG ACGTTTTAGG CATAAAAAAA wGAGAcCTTG CGGTCTCAAT GCGGCTCATC 300  
 GCATCCATTT TTTGCCTGGC AACGTTCTAC TCTAGCGGAA CGTAAGTTGG GCTAACAACG 360  
 10 TCGCCAAAGA CCTTTCTTGA CTTGTGACAA TCGGCTTGCT TCTTTCCTCT CCTTCGGCTC 420  
 TCGC 424

## (2) INFORMATION FOR SEQ ID NO: 4362:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 316 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear  
 20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4362:

25 CACAACAAGT ATCTAAGATA CTGGCCGAAG ATTGTCACAG ACGGTAGGGG AAGGGGGTCA 60  
 CGTGTCAGAC CCAACATGTG GTTCCGGTTC ATnGTTGTTA CGTGTGTTGTA AAGAAACGCA 120  
 ATnAnTCGT TATTTCCGAC AAGAACGTAA CAATACTACA TACAACCTAG CACCATGAAT 180  
 30 ATGTTATTAC ATGATGTGCG TTATGAGAAC TTCGAGATCC GTAATGATGA CACATTGGAA 240  
 AATCCAGCCT TTTTAGGCAA TACATTTGAT GCGGTTATTG CGAACCATAC AGTGCGAAAT 300  
 TGGACAGCAG ATTCCA 316

## 35 (2) INFORMATION FOR SEQ ID NO: 4363:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 318 base pairs  
 40 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4363:

GGGTACTAAG ATGTTTCAGT TCTCCGGGTG TGCCTTCTGA TATGCTATGT ATTCACATAT 60  
 CGATAACATG ACATAACTCA TGCTGGGTTT CCCCATTCCG AAATCTCTGG ATCAAAGCTT 120  
 50 ACTTACAGCT CCCCAAAGCA TATCGTCGTT AGTAACGTCC TTCATCGGCT TCTAGTGCCA 180  
 AGGCATCCAC CGTGCGCCCT TGAATAACTT AATCTATGTT TCCATCCTAC AGGAAACGCG 240  
 55 TTGATTAATC TTGTGGAGTG TTCTTTCGAA CATAGCGATT ATnTCTTATG GAATTCAAGC 300

## (2) INFORMATION FOR SEQ ID NO: 4364:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4364:

NTGCACTTAA GAACTTAGAC GATCGTGGTA TCGTTTATAT TGGTGCAGAA GTAAAAGATG 60  
 GAGATATTTT AGTTGGTAAA GTAACGCCTA AAGGTGTACT GCAGTTAACT GCCGAAGAnA 120  
 GATTGTCACA TGCAATCTTT GGGTGAAAAA GCACGTGAAG TTAGAGnATA CTTCATTACG 180  
 TGTACCTCAC GCGCTGGCG GGTATCGTTC TTGCATGTTA AAAGTATTCC AATCGTGCAA 240  
 GAAGGGCGAC GATACATTAT CCACCTGGTG TTAACCAAT TTTAGTACGT GGTATATATC 300  
 GTTCCAAAAA CGT 313

## (2) INFORMATION FOR SEQ ID NO: 4365:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4365:

AACCATTGCA TGCAATAGCG TCATTCTTGG ATATTAATCC CTAAATTGCC GTGATATCCC 60  
 GCGTCTATCT TGGCCTGTTT CAATCACTAA ATGCGTTTTA CTACTTACAC CACTACGGGC 120  
 TAGTTAATAG TCCGACATAG CCCTCTGGTA TGCTTACAGC TACATCTGTh TTAATCACTG 180  
 CCTTTTCTTG TGGCTCAAGT ACGACAGTTC AGCTGAGAAT ATGTCATAAC CTGCATCCGn 240  
 CTTATGATTT CGTTCGGGCA TTCTAGCATT TTCTGATAAT AGCCTTACTT GTAATGTGTh 300  
 AGTCATTTTC 310

## (2) INFORMATION FOR SEQ ID NO: 4366:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

AGTGGTACTT CTGTTAATTG GTGAATTTGG ATACTGGTTA TATTCAGCTG CACCGCAAGC 60  
 AACTTCTATT GATGGCCTAA CTGCCTTTTT ACCTCAAGCA ATGGGTATGG TAATTGTTGC 120  
 5 AGTCATTTAT GGCTTTATGA ATATGAAAGC AGAGAATCCA TTCCGTAATA AAATTACGTG 180  
 GTTACAAATT ATTTCAGGTT TCTTCTTTGC ATTTGGTGCT TTAACATATC TTATTTTCAGC 240  
 10 ACAACCTAAT ATGAATGGTT TAGCACTGGA TTTATCCTTC TCAACATCCG TGGTGCTGCT 300  
 ACATTAAngG TATTAATTCT TAAACCACAT AAACGTCAAA GAATGGTAAT ACAATCACGG 360  
 CTAGTACCAT TTAGTAGCCG CTCCGTACCG nAATTATAAA 400

15 (2) INFORMATION FOR SEQ ID NO: 4367:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 326 base pairs  
 (B) TYPE: nucleic acid  
 20 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4367:

CACCTGGACG AAACGGTTTT AGATCGTATT CAATTGAAAA GGCCGGTATT GAATGAATCA 60  
 CACTTAGCAG CGATTGATCA GGAACATTTT AAATTAACCT ATTTATCAAC GGTATATGAA 120  
 30 GGGGATTGG AAGATGCGTT AGAAGCATTG TGCCGAGAAG CAGTGAATGC TGTAACAAG 180  
 GCGCTCAAAT TCTAGTGTTA GATGATAGTG GATTAGTTGA TAGCAATGGC TTTGCAATGC 240  
 CGATGTTACT CGCnATAAGT CATGTGCATC AATTACTTAT TAAAGCAGAT TACGnATGnC 300  
 35 TACAAATTTA ATCGCTAAAT CTGGTG 326

(2) INFORMATION FOR SEQ ID NO: 4368:

(i) SEQUENCE CHARACTERISTICS:  
 40 (A) LENGTH: 307 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4368:

ATTATAGCCG AAATGCCCAA AATAGATTTT GACGAATATT ACGAATGGTT GCTTTACTTG 60  
 50 CATAAATGGC TTTAGGAATA AGCATCAAGT CGCCACCAAG AATAGTAATA TCAGCTGCTT 120  
 CAATGGCAAC TTCTGTACCT GTAnCAATGG CGATACCGAT ATCAGCTTTA ACTAATGCAG 180  
 GTGCATCATT TACACCGTCA CCAnCCATCG CAACCTTCTT ACCTTGTTGC TGTAGTTTCG 240

55



GTTTTGC

307

## (2) INFORMATION FOR SEQ ID NO: 4369:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 396 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4369:

15	TTCTTTCTCT TCCTCCGGGT ACTAAGATGT TTCAGTTCAC CGGGTGTGCC TTCTGATATG	60
	CTATGTATTC ACATATCGAT AACATGACAT AACTCATGCT GGGTTTCCCC ATTCGGAAAT	120
	CTCTGGATCA AAGCTTACTT ACAGCTCCCC AAAGCATATC GTCGTTAGTA ACGTCCTTCA	180
20	TCGGCTTCTA GTGCCAAGgC ATCCACCGTG CGCCCTTAAT AACTTAATCT ATGTTTCCAT	240
	CCTACAGGAA ACGCGTTATT AATCTTGTGA GTGTTCTTTC GAACAYTAGC GATTATTTCT	300
25	TATGAATTCA AGCTTATTTA AAACCTCCTTA TTCAATCGGT TTTGCTTGGG TAAAATCCTA	360
	TATTTTACnT ACCnTATCGA GTTTTCAATG TAACAA	396

## (2) INFORMATION FOR SEQ ID NO: 4370:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 315 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4370:

40	CAGTAAGATA ATTTTCAATT AGAAAATATC TTAAGTCTGT TCTCTATTTA TACAATACTT	60
	CGTATTGAAT GGCTTCGCTT TCCTAGGGTG CCGTCTCAGC CTCGGTCTTC GACTGGCACT	120
	GCTCCCTCAG GAGTCTCGCC ATTAATACTA CGTATTAAACA TGTAATTTTA CTTTACATA	180
45	CTTTTAAAAA ATAAGACACT TTGCCAAACT TGCACATAAA TGTTTAATTC AATAATTIGA	240
	ATTTTCTGTG TTGGGTCCCT TCGTATAATT TAATAAATAC CACTAAACTA AaTTA-TGAA	300
	GTGCCTTATG TATAA	315

## (2) INFORMATION FOR SEQ ID NO: 4371:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 322 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4371:

5 GTCGTCAAAT GTACCTTCAC CAAGTAGTGA TGTACATATT TACCGCCTTG TTCAACAGCA 60  
 CGTGTCGGCG CACCTGTAAT CGCAATGACA GGTATGCGTT CAnATATGAA CCTGCGATAC 120  
 CGTTGACGGC ACTTAATTCG CCAACACCAA ATGTAGTAAC TAATGCAGCG AGTCCATTAA 180  
 10 GACGGGCATA ACCGTCCGCT GCGTAACTTG CGTTTAATTC ATTTGTATTT CCTACCCAAT 240  
 CTACAATGGG GTTGCTGATA ATATCGTCTA GAAAAGCGAG ATTAAATCA CCAGGGnCAC 300  
 15 CAAAATTTTT ATCGACGGCn TG 322

## (2) INFORMATION FOR SEQ ID NO: 4372:

## (i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 327 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4372:

25 CcTAAGTCTA GTGCGTCTGC CAATTCCGCC ACACCCGCAA ATGGTGAGCC ATAGAGGATT 60  
 30 CGAACCTCTG ACCCTCTGAT TAAAnAGTCAG ATGCTCTACC AACTGAGCnA ATGGCTCTTC 120  
 CATGGTGCCG GCCAGAGGAC TTGAACCCCC AACCTACTGA TTACAAGTCA GTTTGCTCTA 180  
 CCAATTGAGC TAGGCCGGCA ATATGTAAAG AATAAATGGT GGGAGAATGA CGGGTTCGnA 240  
 35 ACGGCGGAAC CCTCTGCTTG TAAAGCAGAT GCTCTCCAGC TTGAGCTAAA TCTCCGATTT 300  
 AAAACTGCTG GGCAAGTTCT ACTCTAG 327

## (2) INFORMATION FOR SEQ ID NO: 4373:

## (i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 45 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4373:

50 CATTTTAATT TATTGTACAG AACGAAATGT GATGTTAGTA GATCATAGGG TTGATGATAA 60  
 TATTAAAGCT GAAAACGTTA TATTTATTGG CCTTTTGTGT AAACATGGAC ATTGGCATGC 120  
 AGTCATTTAT GACATTGCTC AAGACAAAAC TGCCGAACTC GAAATTGAAA ATATTATAGA 180

TCAATTTTTA AACCCCATCG ATTCCTAAAA AACAGCAGTA AGATGATTTT CAATTAGAAA 300  
 ATATCTTGCT GCTGTTCTCT ATTTATACAA TACTTCGTAT TGAATGGCTC GCTTTCCCAG 360  
 5 GGnGCCGCTC AGCCTGGGCC TCGACTGGCA ATGCTCCCTC 400

## (2) INFORMATION FOR SEQ ID NO: 4374:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4374:

TAATGGATTT TTTAGTGTTG GTGTCGTTAT TGTCTTCTCA CCTTTTGTG CTTCTCTTGT 60  
 20 TACTTTTTCT GTCCCTGGTG CTAAATCAGG ATTAAATTTA CGTTCTTTCT CGAATGGAAT 120  
 CTCTTCTTTT TCTACAATCG AGTCTCCTTT TACAGGTCCA TATTTTGTTA CGCTATCGAC 180  
 CGGTGGTCTA ACTACATCTC CTGTTTCTGG ATTCTTAATT CCTGGTTTAC CTGGGAACTT 240  
 25 CCTCTTCTC TCCTGTTGGT AACTTCGGGA TCAAATTCGT CTCGATGGAC CTGGTGTTGA 300  
 nCGTTTCTGG GTCCGnAAGT CTGnGAATT GCAG 334

## (2) INFORMATION FOR SEQ ID NO: 4375:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4375:

ATACATGCAA GTCGAGCGAA CGGACGAGAA GCTTGCTTnG TGAATGTTAG CGGCGGACGG 60  
 GTGAGTAACA CTGGATAACC TACCTATAAG ACTGGGATAA CTTCGGGAAA CCGnAGCTAA 120  
 45 TACCGGATAA TATTTTGAAC CGCATGGTnA AAGCTTGCAA AGACGGTCTT GCTGTCACTT 180  
 ATAGATGGAT CCGCGCTGCA TTAGCTAGTT GGTAAGGTAA CGGCTTACCA AGGCAACGAT 240  
 GCATAGCCGA CCTGAGAGGG TGATCGGCCA CACTGGAAct GAGACACGGT CCAGACTCCT 300  
 50 ACGGG 305

## (2) INFORMATION FOR SEQ ID NO: 4376:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4376:

	GATAAAGTGA AAGAACTCGG ACGTGACACC TATTGCACGA TTCGTTGGTT TTAAGGCAGT	60
10	AGGCGTTGAC CCGAAAATTA TGGGTATTGG GCCTGGCATA TGCGATTCTT GAAGTATTGT	120
	CACTCAGCAA TCTATCTGTT GAAGACATTG ATTTGATCGA ATTGAACGAn CATTGCTCT	180
	CAAACGATTG CATCTATTAA AGAAGTAGGT CTAGATATAT CACGTACGAA TGTGAATGnT	240
15	GGCGCTATTG CTTTAGGTCA TCCATTAGGT GCTACAGGCG CAATGTTAAC CGCGCGTTTA	300
	CTTAA	305

20

(2) INFORMATION FOR SEQ ID NO: 4377:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 324 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4377:

30	AATGTCTTCT ACCCCATCAC AGCTCAGCCT TGAACGAGTA CCGGGTTTGn CCTAATACTC	60
	AGACCTTGAC TGCTTAGACG TGACAATCCA ATACGACACG CTTGCGCTAT CCTACTGCGT	120
	CCCCCATCG ATTAAAACGA TTATAGGTGG TACAGGAAAT ATCAACCTGT TATCCATCGC	180
35	CTACGCTGT CGGCCTCAGC TTAGGACCCG ACTAACCCAG AGCGGACGAG CCTTCTCTG	240
	GAAACCTTAG TCAATCGGTG GACGGGATTC TCACCCGTCT TTCGCTACTC ACACCGGCAT	300
40	TCTCACTTCT AAGCGTCCA CATG	324

(2) INFORMATION FOR SEQ ID NO: 4378:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4378:

	CATCATGCTT AGAAAACGCT TAATTTAGGT TTTGACTTTT TAATCAGAGT ATATAAGCAA	60
55	AACTTATCAT ACAGGTAAGG TGTAATAAGT ATTTTTTATT AATTGAGAAT AATTATCAAT	120

TGGCACCAAA CTTTAATATT TTTTCAATG TCATTCTTTT GATGGGAGTG GGACAGAAAT 240  
 GATATTTTCG CAAAATTTAT TTCGTCGTCC CACCCCAACT TGCATTGTCT GTAGAAATTG 300  
 5 GGAATCCCA ATTCCTCCTT GGTGGGGGCC CATCCCCACC TTGCACATAA TGGnAGCnGG 360  
 ACCTTTCCGC CGCTCCGGGG TGGGGGCCTC nACCCCAATC 400

(2) INFORMATION FOR SEQ ID NO: 4379:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 345 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4379:

20 ATAAATATA TCACCTGAAA AATTTTCATGT AGAAAAGATG ATGGATAGGC TATAAAGTAA 60  
 TTGTGACTGA GATGAACCTT TATGTCTTAG AACTACAAC ACTATATTGG CAGTAGTTGA 120  
 CTGCGGGGCC CCAACATAGA GCAAATTGGA TTCCCAATTT CTACAGACAA TGCAAGTTGG 180  
 25 GGTGGGCCCC AACATGAAAG AAATACTTTT TCTTTAGAAA TTAGTATTTT TTATGCATGA 240  
 GTGTACTCAT GTTGCATTA TTTTnAGTA CACATTAGCT GTGGACTAAT GATAAAGGnn 300  
 TCGCTACATA ATCCATCCAT TAGGTCGTTT CTTGATTCAT TCCCT 345

(2) INFORMATION FOR SEQ ID NO: 4380:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 363 base pairs  
 35 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4380:

CTAAAGCTGn CATATGCGGC TTGCCGATGA AGCCAACCCT GCTGCTGTTG GTACAAAATT 60  
 45 GTCGCTTTCA ATTTCTGCAT ACCAATCGAT GCCAGCTCTA TTTCTGACAA TATCCATATA 120  
 TTTTGAAATT TTCTCTAATT CTTTGCCACT AACCTTTTCA CCATTCAACC AAAATTGATC 180  
 CTGTGTTAAC TGGTCGTTAA AAGTGACTTT CGTTTCAGTG TAAAATTTTT CTATGTAAC 240  
 50 AGATATGCTA TTATTCATGG AAGATTAGTG CTTCACTTTT TTTACCCCAA TATTTTATAA 300  
 GTGCAATATC GTAGTCAGG CTTGCCACTT TAACACGCAT AACTCCTAAA TCTCAACCAG 360  
 ATn 363

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4381:

ACCTGAATGA CTCAAAGTTG ACTTTnCGAC AATTGACTGT nCATTnTTGCA TAGTTGTATG 60  
 nCTCCATTnC GTAATTATTA GATTGTTCG CTTACGTCTA TTGAATCATA CAGCTTTATT 120  
 ATAGTTAGCG TATTGACACC TTGCACATT AAACCATGTT TAATAATCAT TGAATCATT 180  
 TTAAGTAAAT TAAGGAATCT ATAATGTTTCG TTAAATAAAA CTGATCCCGT TGTGGCTTCA 240  
 CACCCGATAG ATAGGGATTT ACAGATAAAT TCAGGTCTCT TCCACGTCCA TATTGGGGAC 300  
 CCATCGAAAA TCGGGTTCTC AAATCATCGA ACATAACAAA AGAAGCTAAG CAACAGTAGG 360  
 GCCGTTGTCA CTTAACTTCT GTTTTTCCGA TGACAGCTTC 400

## (2) INFORMATION FOR SEQ ID NO: 4382:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4382:

GnACTACAAA GCAATGGGGT TTGCCAGTTT CTTTATTTAC TGACGAATAC TGGCAATGAC 60  
 ATCAGATACA TGTGGCAnCA CCAATCCATT TCTTTTCACC ATTGATAACC CAAGTATCGC 120  
 CTTGGGTTGC AGGGACTGTT TCAAGACCTC CCGCAACGTC CGAACCGTGT TCTGGTTTCAG 180  
 TTAAAGCAAA GCATGTTACG CnTTCATGTG AACTGTAATT TAGGTACATA TTTCGCAATT 240  
 TGTTCCTTTC TACCTCCGAA ATAGAAAGTG TTATGCCCTA AACCTTGGTG AACACCGAGT 300  
 AGGG 304

## (2) INFORMATION FOR SEQ ID NO: 4383:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

GTGCATTATT TTGGAGAATT AGCTCAGCTG GGAGAGCATC TGCCTTACAA GCAGAGGGTC 60  
 GGCGGTTTGA ACCCGTCATT CTCCACCATT TTGATTATTA AATTATATGA ATAAGCTGGA 120  
 5 GGGGTAGCGA ATGGCTAAAC GCGGCGGACT GTAAATCCGC TCCTTCGGGT TCGGCAGTTC 180  
 GAATCTGCCC CCTCCACCA TCTATATATT GGGCTATAnC CAAGCGGTAA GGCAACGGAC 240  
 10 TTTGACTCCG TCACTCGTTG GTTCGAATCC AnCTAGCCCA GCCATTAGAG nCATTAACTC 300  
 AGTTGGTA 308

## (2) INFORMATION FOR SEQ ID NO: 4384:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 309 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4384:

AATTTTGGCC AAAACACCCA TCCGCTGTAA CTCAGAGTG TCATTGGCAT TTATTACACT 60  
 25 ATCTCCAAT CCTAGTGGAA CAACCACATC TCGTCCTTGG GGTGCATGGA ATGTTCCGTC 120  
 AGCCCTGTGA ATTATTTCTT GAACTCCACC ACCTGGGGCG TTTCCAGAAC CTCTATCATT 180  
 30 TAATACAGCA AATGTCGGTT GCGTTAATGC TCCTGAATTA TCGGkAGCTA CACCCTTTCC 240  
 TGCTAAAGTA CCAGTAGACA ATGTAGGTAT TGGCTTGATG AGATTTtTAT CAGTAATGGC 300  
 TTTAGAnAT 309

## 35 (2) INFORMATION FOR SEQ ID NO: 4385:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 308 base pairs  
 (B) TYPE: nucleic acid  
 40 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4385:

45 AAAGGTGAAA AGCACCCCGG AAGGnAGGTG AAATAGAACC TGAAACCGTG TGCTTACAAG 60  
 TAGTCAGAGC CCGTTAATGG GTGATGGCGT GCCTTTTGTA GAATGAACCG GCGAGTTACG 120  
 50 ATTTGATGCA AGGTTAAGCA GTAAATGTGG AGCCGTAGCA nAACAGGTCT GAATAGGGCG 180  
 TTTAGTATTT GGTGCTAGCC GAnAACCAGG TGATCTACCC TTGGTCAGGT TGAATTCAGT 240  
 AACACTGAAT GGAGGACCGA ACCGACTTAC GTTGAAAAGT GAGCGGATGA ACTGAAGGTA 300

55

## (2) INFORMATION FOR SEQ ID NO: 4386:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4386:

TAGAATCTTC ATCAATATGA TCTAACCAAT ATTGATAAAA CCTTGATGTG TTTCGTGTCA 60  
 ATGACATACC ATATCGACTA GGTACCTTTT TAGAATGTTG ATTAATCANG GCAAATATCA 120  
 TGGCAAGGTC ATCTTCAAAA TGATTGATT CAAGTGAAG GCATATGACG TCTCATCACT 180  
 ATACCCTTTT TCCATTCTG CAAATCCACC ATAAATACTA CGCGACGCGG AACCCGGACC 240  
 CATTGCGGGC AATCTCGGTn AATCCTTATC TGGACAGCTG GCATGTCTAG CGGCTGGATT 300  
 TACAAGCTGG CTGGCTAAAG CTGGCATATG CGCTTGCCGG TTGAAGCCCA ACCTGGCTGG 360  
 CTGGTGGGGn ACAAATTGGT CGCTTTTCAA TTTGnGGCAT 400

## (2) INFORMATION FOR SEQ ID NO: 4387:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4387:

TCAATTTATG GGGCATTATG ACTTTATATA CCTAAAATAC TATTAAGAAG TCCTGAAAAA 60  
 TTCACATTAG CAGTTGGATT GTTCAACTTT ATTAATGATA AGTATGCAA TAATTCACA 120  
 GTGTTTGCAG CAGGGGCAAT TATGATTGCA GTACCTATAG CAATCGTATT CTTGTTCTTG 180  
 CAACGCTATT TAGTATCAGG TTTAACAACA GGTGCGACAA AAGGTTAGTT TGAAATTCn 240  
 GnGTGGGGCA GAATTGATAA AGAACCACnA ATGACGATAA AGATTAAAAG GAGGACGTTA 300  
 TGGATGACGA 310

## (2) INFORMATION FOR SEQ ID NO: 4388:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4388:

AACATCATGC TGATGTTGTT GAATATGAAG AAGATACAAA CCCAGGTGGT GGTCAGGTTA 60  
 5 CTACTGAGTC TAACCTAGTT GAATTTGACG AGATTCTACA AAAGGTATTG TAACTGGTGC 120  
 TGTTAGCGAT nCATACAACA ATTGAAGATA CGAAAGAATA TACGACTGAA GTAATCTGAT 180  
 10 TGAAGTAGTA GATGAACTAC CTGAGGAACA TGGTCAAGCG CAAGGACCCA TTCGAGGAAA 240  
 TTACTGGAAA ACATCATCAT ATTTCTCATC nGGTTTAGGn ACTGAAATGG TCACGGTAAT 300  
 TTTGGCGTGG 310

## (2) INFORMATION FOR SEQ ID NO: 4389:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 302 base pairs  
 (B) TYPE: nucleic acid  
 20 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4389:

25 TTTACCATAT CATCCACTAT TTATTAAACC TAATAAAGAT GAATTAGAAG TGATGTTTAA 60  
 TACAACAGTG AACTCAGACA CAGATGTTAT TAAATATGGT CGTTTGTTAG TTGATAAAGG 120  
 30 TGCCTCAATCT GTTATTGTCT CGCTTGGCnG TGGATGGTGC TATTTATATT GATAAnGAAA 180  
 TCAGTATTAA AGCAGTTAAT CCACAAGGGA AAGTGTTAA TACAGTTGGC TCTGGTGATA 240  
 GTACAGTTGC AGGCATGGTG GCTGGGAATT GCTTCAGGTT TAACGnTTGA AAAGGCATTC 300  
 35 CA 302

## (2) INFORMATION FOR SEQ ID NO: 4390:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 333 base pairs  
 40 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4390:

AAAGAGTGCG TAATAGCTCA CTAGTCGAGT GACACTGCGC CGAAAATGTA CCGGGGCTAA 60  
 50 ACATATTACC GAAGCTGTGG ATTGTCTTTT GGACAATGGT AGGAGAGCGT TCTAAGGGCG 120  
 TTGAAGCATG ATCGTAAGGA CATGTGGAGC GCTTAGAAGT GAGAATGCCG GTGTGAGTAG 180  
 CGAAAGACGG GTGAGAATCC CGTCCACCGA TTGACTAAGG TTTCCAGAGG AAGGCTCGTC 240

TnCCCTTACCA CCTATAATCG nTTAATCGTG GGG

333

## (2) INFORMATION FOR SEQ ID NO: 4391:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4391:

AGTGCGTTTG TGCACAnACT TGACTGnAAC TTAGTGCCAT TGCAGCACCA GCAACCCATG 60  
 GCGCAATAAG CCCAATGCAG CTATAGGGAT ACCGnCAATA TTATAGCCGA ATGCCCAAAA 120  
 TAGATTTTGA CGAATATTAC GAATGGTTGC TTTACTTGCA TAAATGGCTT TAGGAATAAG 180  
 CATCAAGTCG CCACCAAGAA TAGTAATATC AGCTGCTTCA ATGGCAACTT CTGTACCTGT 240  
 ACCAATGGCG ATACCGATAT CAGCTTTAAC TAATGCAGGT GCATCATTTA CACCGTCACC 300  
 AACCAT 306

## (2) INFORMATION FOR SEQ ID NO: 4392:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4392:

TACGGTATGC ATATCTTTTA AAACCTATTC TTTTGTATT AGGACATATA AATTCATCAT 60  
 TAAGTTCGTC ATATTTCCAA TTTTAAGTGT TGAAAATGTC ACTTTTAAAC TTTCTAGTTT 120  
 TATCTTTAAT AAACATGCCA TACGTAATAA GTGGCGTTTT ATTAAAATCA TCTATAATAG 180  
 CCATATAGTT TTGCTCACTA CCATAACCTG CATCAGCTAC AATATACTCC GGTAATAAAC 240  
 CGAAGGGATT TTGAATCATT GTTAAAAATG GAATTAAAGT TCTAGTATCT GTTGGGTTTT 300  
 GAATAGGGTC ATGGGATAAA CCAATGnGG AATTTGCCnC AATTnGTAAA TGGAA 355

## (2) INFORMATION FOR SEQ ID NO: 4393:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 364 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4393:

5 CATTCCGTAA TAAAATTACG TGGTTACAAA TTATTTTCAGG TTTCTTCTTT GCATTTGGTG 60  
 CTTTAACATA TCTTATTTCA GCACAACCTA ATATGAATGG TTTAGCAACT GGATTTATTC 120  
 TTTCTCAAAC ATCCGTTGTG CTTGCTACAT TAACTGGTAT TTATTTCTTA AAACAACATA 180  
 10 AAACGTCAAA AGAAATGGTT ATTACAATCA TCGGCTTAGT ACTCATTTTA GTAGCCGCTT 240  
 CTGTTACAGT ATTTATAAAA TAAGGAGTGT AGATGTCATG AAAAAATCAG CGGTTTAAAT 300  
 GGAACCTATT CCAAAGCCAT CGCGACCAAT GGGTCATTG GATTAnTAAC GATAATGGCG 360  
 15 nngg 364

## (2) INFORMATION FOR SEQ ID NO: 4394:

## (i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 315 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4394:

25 GATTAAAACG ATTATAGGTG GTACAGGAAT ATCAACCTGT TATCCATCGC CTACGCCTGT 60  
 CGGCCTCAGC TTAGGACCCG ACTAACCAG GAnCGGACGA GCCTTCCTCT GGAAACCTTA 120  
 30 GTCAATCGGT GGACGGGATT CTCACCGTC TTTGCTACT CACACGGCA TTCTCACTTC 180  
 TAAGCGCTCC ACATGTCCTT ACGATCATGC TTCAACGCCC TTAGAAGCT CTCCTAnCAT 240  
 35 TGTGCCAAAG GACATGCCAC AGCTTCGGTG AATATGTTTA GCCCCGGTAC ATTTTCGGCG 300  
 CATGTnCACT CGACT 315

## (2) INFORMATION FOR SEQ ID NO: 4395:

## (i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 322 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 45 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4395:

50 AGCCCCCAA TGGGTATTGA AATTGAATGG TGGGnCTGA AnTGGACTCG AACCACCGAC 60  
 CTCACGCTTA TCAGGCGTGC GCTCTAACCA GCTGAGCTAT AGGCCCATTA ATTTGAATGA 120  
 ACAAACATTC AAAACTGAAT ACAATATGTC ACGTTATTCC GCATCTTCTG AAGAAGATGT 180

TACGACTTCA CCCCAATCAT TTGTCCCACC TTCGACGGCT AGCTCCTAAA AGGTTACTCC 300

ACCGGCTTCG GGTGTTACAA AC 322

(2) INFORMATION FOR SEQ ID NO: 4396:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 303 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4396:

TCGGCTCTCG CTTACTCATT TAGCTCTACT AAACCTCGTTG CGCTCTTTTC TCGTTTCGTC 60

AGATTCAAAC GTTTTCACCT CGCCAAGCCA TTTTCTTTG TGTTTACTTT TTATTTTGAC 120

GTTTTAGACA TAAAAAAGA nACCTCACGG TCCAACTTG CCTGGCAACG TTCTACTCTA 180

GCGGAAnTGA ATTGGCTACC ATCGnCGCTA AAGACCTTTC TTGACTTGTC ACAATCGCTT 240

GCTTCTTTCC TCTCCTTCGG CTCTCGCTTA CTCATTTAGC TCTACTAAAC TCGTTGCGCT 300

CTT 303

(2) INFORMATION FOR SEQ ID NO: 4397:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 377 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4397:

TAAGAATATA AATGATTTTG AAAGCATTTG AAAGCTACAA CATTCTATA AAATTTTCA 60

ATAACAATTG CGCCACTAAA ACTCAAAATT TCCACCACCA ACATCCAAAT TATCAACATC 120

GCAACATAAC CAAATGTTAT AATAAATCTA TTACACAAAG AGATAAATTA CTTATGCAAA 180

GGCGGAGGAA TCACATGTCT ATTACTGAAA AACAACGTCA GCAACAAGCT GAATTACATA 240

AAAAATTATG GTCGATTGCG AATGATTTAA GAGGGACATG GATGCGAGTG AATTCCGTAA 300

TTACATTTTA GGCTTGATTT TCCTATCGCn TCCTTATCTG GAAAAAnCCG ACCAGGATnT 360

GCAGATGCCT GGCCAGG 377

(2) INFORMATION FOR SEQ ID NO: 4398:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 313 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4398:

	TGCAATAACA GTATCTATGC CTACTTGTTT TGCAATGGCT TGAGCAGTGT TTTTATTATC	60
10	GCCAGTTAAC ATGGGCAACT TCAATGCCCA TATCATGGCA ATTGTTTTAT AGCATCTTTG	120
	GGCATGATnT TTGACAGTAT CTGCCACTGC GATGATACCA GTTAATGAAT AATTAACAGC	180
	AATGAGCATA nCAGTTTTAC CATCTCGTTC ATAATGTGTT AAATCATCAG AAATATGCTT	240
15	AAGCAACTAA TATCATTGTC AACCATTAAAT TTACCGTTAC CAACCAATAT ATGGTGATGA	300
	TChATCCTTC CTC	313

(2) INFORMATION FOR SEQ ID NO: 4399:

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(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 400 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4399:

30	TGGCTATGAT CATCCAAAT ATGGTGAATC AATTGCTGCA GCCATTATAC TTCGCGAAGA	60
	TGAACCTCAT TACGCTGAAA TTTTAAATCA ACATATGCGA AGTCGTTTAG CAGGTTATAA	120
	AGTCCCAAGA ATGTATGTAC CAGTGACACA TATGCCGTTA AACAGTACGC AGAAACCAGA	180
35	TAAACTTGCG ATTCGACAAA TGATGAATGA CAAAGTCTCG CAAACACTTT AAAGGTGATA	240
	AAAATTTTTG ACATTTAGTG TAAGCGTTTA CAAATAAAGC GTGTTGTTTT TGAATTAAAT	300
	GCATTTTACA TTAGTATTCA TATTATnTTT AGGAGGAATT TATATGACAT TTGAAAAAGA	360
40	ACGGGGCTTAA AACATTATTC CTGAGATGTA CTAGTATGCT	400

(2) INFORMATION FOR SEQ ID NO: 4400:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 409 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4400:

	CTCATTTAGC TCTACTAAAC TCGTTGCGCT CTTTTCTCGT TTCGTCAGAT TCAAACGTTT	60
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AAAAGAGACC TCgtCTCAAC TTGCCTGGCA ACGTCTACT CTAGCGGAAC GTAAGTTGGC 180  
TACCATCGTC GCTAAAGACC TTTCTTGACT TGTGACAATC GCTTGCTTCT TTCCTCTCCT 240  
5 TCGGCTCTCG CTTACTCATT TAGCTCTACT AAACTCGTTG CGCTCTTTTC TCGTTTCGTC 300  
AaATTCAAAC GtTTTCaCTT CGGCCAAGGC ATTTTCTTT GTGGTTACTT TTTAATTGG 360  
10 ACGGTTTTAG GCATAAAAAA AAAGGGGACC CTGCGGGCTC nAAAGGGGG 409

(2) INFORMATION FOR SEQ ID NO: 4401:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 base pairs  
15 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4401:

TCATGTAGAC TTTCAAGAAT CGACACATGA AAATTCAAAA CATCATGCTG ATGTTGTTGA 60  
ATATGAAGAA GATACAAACC CAGGTGGTGG TCAGGTTACT ACTGAGTCTA ACCTAGTTGA 120  
25 ATTTGACGAA GATTCTACAA AAGGTATTGT AACTGGTGCT GTTAGCGATC ATACAACAAT 180  
TGAAGATACG AAAGAATATA CGACTGACAT nnATCTGATT GAACTAGTAG ATGAACTACC 240  
30 TGGAGAACA TGGTCCAAGC GCAAGGnCCA ATCCGAGGAA ATTGACTGGA AAACAATCCA 300  
TCCATATTC C 311

(2) INFORMATION FOR SEQ ID NO: 4402:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs  
35 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4402:

TTAACGGATT ATTTGGCAAT TCGGTTAGTT GTCGAACAAT TGCTAGTTGG TGATGAGTTT 60  
45 AAGTCAGTCG CTAAAGATTG TGAAAGTAGA TCGGAAAATT GGTTTAAGCA AACTGTTGCA 120  
TCATGGTGTT ACTACAGTGA TATGCCTAGC GATGTATTAC TACAACATGG ACGTCAATGT 180  
AAATTnCAAA CGTTTATTCA TTTTGGCAGC AACTATGGAA TAAAAATGTA TTTAAAAATT 240  
50 TATGGCTAAT TGCTGGGGA AATGACATAC GAATCTCAGG TTAAAACAGA AAATTAAAGC 300  
AGGTCCATGT nAAGTGTGGG CGGGnCGCAT 330

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4403:

TGnTCACACA TAATTTGCGG CCATATGTTG TTGGCACTGG CCGTTTTGAT TATCTGGCAC 60  
 TTTGGGCCCCA TATGTTGnCA AAATACGCGC CAATTGCTTC TTTATAAGTT GTTATTTTTT 120  
 TACTTTTTTCC ATCGATAAGC CATACCTCTG GATGATACAT ATGATGCCCC ATCGCAGACC 180  
 AATAGCGAAA TTCACCCGTT AAAGTTTCGA GCTCTGATAA TTGTATAGAC CATTGATGAT 240  
 TTTGAGGTGG TACTTGATAT AAATTTCTT CTCTAAAATA TTCATTTAAA ATGCGTTCGA 300  
 TAGCCGCATA CGCTGCCATG TTGTATTAAT CnTTAATTTG 340

## (2) INFORMATION FOR SEQ ID NO: 4404:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4404:

TTAACATATA TTTTGGGACC TTAGCTGGTG GTCTGGGCTG TTTCCCTnnA CGAACACGGA 60  
 CCTTATCACC CATGTTCTGA CTCCCAAGTT AAATTAATTG GCATTGCGAG TTTGTCTGAA 120  
 TTCGGTAACC CGAGAGGGGC CCCTCGTGCC AAACAGTGCT CTACCTCCAA TAATCATCAC 180  
 TTGAGGCTAG CCCTGAAAGC TATTTGCGGA GAGAACCAGC TGATTTCCAG GTTCGATTGG 240  
 AATTTCTCCG CTACCCTCAG TTCATCCGCT CACTTTTCCA ACGTnAATCG GTTCGGTGCC 300  
 TGCCATT 307

## (2) INFORMATION FOR SEQ ID NO: 4405:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4405:

AnACTTGAGT GCAGAAGAGG AAAGTGAAT TCCATGTGTA GCGGTGAAAT GCGCAGAGAT 120  
 ATGGAGGAAC ACCAGTGGGC GAAGGCGACT TTCTGGTCTG TAACTGACGC TGATGTGCGA 180  
 AACGTGnGGG ATCAAACAGG ATTAGATACC CTGCTAGTCC ACGCCGTAAA CGATGAGTGC 240  
 TAAGTGTTAG GGGGTTTCCG CCCCTTGAGT GCTGnCAGCT AAACGCATTA AGCACTCCGC 300  
 CTGGGGGAGT GACGGACCGC AAG 323

## (2) INFORMATION FOR SEQ ID NO: 4406:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4406:

AATTATGGGA TGCAATGGGA TACGAACGTG TTAAACACG TATGGAAGAC GAACTTGGAG 60  
 ACTTACCACA ATGGATTAGT GATTAGATG GTGGCTTTTA TAAACAAGAT GAGACCATTG 120  
 AATATGCAAC ACCTATTTCT CACTTCGTAA AAGATGAACT TTGGGATAAA GGTGATGCCA 180  
 AACTTTCCGT AACTCATGAT GATCAACTGT TACTGAAATT ACAAAGTAAA AATAATGTCA 240  
 TTACCGATGA ATTCAACGGT GCGTTAGTTG ATGCGATTGA TTTACTGGGA AATGACCCTT 300  
 ACnChAGnAT GGGTA 315

## (2) INFORMATION FOR SEQ ID NO: 4407:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4407:

CACCACCTCC CTACCTACTC GCCCCCATC ATAAATAGG TGGACAGGAA TATCAACCTG 60  
 TTATCCATCG CCTACCCTGT CGCCTCAGCT TAGGACCCGA CTAACCCAGA GCGGACGAGC 120  
 CTCCTCTGG AAACCTTAnT CAATCGGTGG ACGGGATTCT CACCCGTCTT TCGCTACTCA 180  
 CACCGGCATT CTCATTCTA AGCGCTCCAC ATGTCCTTAC GATCATGCTT CAACGCCCTT 240  
 AGAACGCTCT CCTACCATTG TCCAAAGGAA TChCACAGCT TCGGTAATAT GTTTAGCCCC 300  
 GGTACATTTT CGGCGCATGT CACTCGACTA nTG 333



- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 393 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4408:

ATTTAATGAA	GTGCTTGTTA	ATGAACCAAG	CGCTAAAGAT	ACTGTTGAAA	TTTTAAAAGG	60
TATTCGCGAA	AAATTCGAAG	AACACCATCA	AGTAAAATTA	CCAGATGACG	TATTAAAAGC	120
ATGTGTTGAC	TTATCAATTC	AATATATTCC	ACAACGATTA	TTACCAGATA	AAGCAATCGA	180
TGTGTTAGAT	ATTACAGCAG	CACATTTATC	TGCGCAAAGT	CCCAGCTGTC	GATAAAGGTT	240
GAAACTGAAA	AACGGATTTC	TGGATTThGA	AAATGATAAA	CGTAAAGCAG	TAAGTGCTTG	300
AAGGGATTTT	AAAAAAGCTG	ACGGACCATT	CCAAAATTGG	AATCCAAATC	nnTTACCAGG	360
TTAAATTTGG	GAAAATGGTT	AATTGGTGGG	ACC			393

(2) INFORMATION FOR SEQ ID NO: 4409:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 319 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4409:

GACTTGTGAC	AATCGCTTGC	TTCTTTCCTC	TCCTTCGGCT	CTCGCTTACT	CATTTAGCTC	60
TACTAAACTC	GTTGCGCTCT	TTTCTCGTTT	CGTCAGATTC	AAACGTTTTT	ACTTCGCCAA	120
GCCATTTTTT	TTTGTGTTTA	CTTTTTATT	TGACGTTTTA	GGCATAAAAA	AAAGAGACCT	180
TGCGGTCTCA	ATGCGGCTCA	TCGCATCCAT	TTTTTGCCCTG	GCAACGTTCT	ACTCTAGCGG	240
AAGThAATTG	GGCTACCATC	GTCGCTAAAG	ACCTTTCTTG	ACTTGTGGAC	AATCGCTTGG	300
CnTCTnTCCT	CTCCTTCGG					319

(2) INFORMATION FOR SEQ ID NO: 4410:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 325 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

AATTAAACAT TTCATTTTAA TCAATGAGAC TAAATACGC CTAAC TTCGT TAACTTTTAA 60  
 AATGTATTAA AATTCTAAAG TTCTTTTGC TTTTTCnATG ATGTCATTTT TGTTTGGTAA 120  
 5 CCAAACATTT TCAGCTTGAG TGAATGGATA AATTGTATCT GCCTGCCTGA ACTCTTCCAA 180  
 TAGGTGCTTC TAATGAAAGG ATTGCACGTC ACTTAATTCA GCTAACAACT GCTGCACCAA 240  
 CACCAGCTTG CnGTTGTGCT TCTTGACTAC AAAGTGACGA CCAGTTTTTC AACTGAGCAC 300  
 10 AATTGTGCAC ATCGATTGGT GACAG 325

## (2) INFORMATION FOR SEQ ID NO: 4411:

(i) SEQUENCE CHARACTERISTICS:  
 15 (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4411:

GAGTTGGACA ATGCCGAAGC GTGAGCAAAG TTTTACCAT GCATGGTTGC ATTTAGCGCA 60  
 25 ACATGACCAT AGTTTTACTA AAGCACAGCG CCAAGTGATT AAAGGCTTAC CCAATGATCC 120  
 TGAAATGACG ATAGAGTCAG TATTAAGTCA TTTTCAATA GATCAGGAAG ACTanCAAGC 180  
 TTATGTTGAA GGACATCTTT TGGCGTTACC GGGTTnGGCA nGTATGTTGT ATTACCGTTC 240  
 30 ACCACAGCAT CACTTTGAAC CACCTTTGTT AACGGGTAA TTGGCCATTC GGGTAAGTTG 300  
 TCCGACCATT GCCAAGTGGG TGATGAGTn AGGCCAGTCC GCAAAAGATT GGGAAAGTAG 360  
 TCCGAAAAT GGGTTAAGCC AACCTGTTGC CATCCAGGGG 400

35

## (2) INFORMATION FOR SEQ ID NO: 4412:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 369 base pairs  
 40 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4412:

GATATATGGC AGCTCAAAGG AATGGGTTTC AGTTGAAGTG AAATTATCAC AGTCACTAGA 60  
 CCCGAGCACA TTATTTATC TCACTGACAA TGAGGCAGGA GATCGCTTTT ATATGCGTTT 120  
 50 GAATGATAAT CGAACGTCAT ATTTTGGCTA CAAAGCAATT CAATTATTCA AAAATAATTC 180  
 TAAAAATAAA CAATCTATTT TAAAAGACTG GGGAAATTA AACATAACCA TCACCATTTA 240

55

CCATAAATCA GATGATGAAT GGCGnGAGTT TGGCCTAAAn CATTGGAAT ACCCGGAGTT 360  
TTAATTCCA 369

5 (2) INFORMATION FOR SEQ ID NO: 4413:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 315 base pairs  
 (B) TYPE: nucleic acid  
 10 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4413:

TACCATCCTC GCTAAGAACC TTTCTTGACT TGTGACAATC GCTTGCTTCT TTCCTCTCCT 60  
 TCGGCTCTCG CTTACTCATT TAGCTCTACT AAACCTCGTTG CGCTCTTTTC TCGTTTCGTC 120  
 20 AGATTCAAAC GTTTTCACTT CGCCAAGCCA TTTTCTTTG TGTTTACTTT TTATTTTGAC 180  
 GTTTTAGACA TAAAAAAGA GACCTCACGG TCTCAACTTG CCTGGCAACG TTCACTCTA 240  
 GCGGAAGTAA GTGGGCTACC ATCGTCGCTA AAGACCTTTC TTGGACTTGT GGACAAnCGC 300  
 25 TTGCGTCCTT nCCTC 315

(2) INFORMATION FOR SEQ ID NO: 4414:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 309 base pairs  
 30 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4414:

GACCATCTCC TAAGGCTAAA TACTCTCTAG TGACCGATAG TGAACCACTA CCGTGAGGAA 60  
 AGGTGAAAAG CACCCCGGAA GGAGGTGAAA TAGAACCTGC AAACCGTGTG CTTACAAGTA 120  
 40 GTCAGAGCCC GTTAATGGGT GATGGCGTGC CTTTGTAGA ATGAACCGGC GAGTTACGAT 180  
 TTGATGCAAG GTTAAGCAGT AAATGTGGAG CCGTAGCAGA ACAGGGTCTG GAATAGGGCG 240  
 45 TTTAGTATTT GGTGCTAnCC GnaAACCAAG TGATCTACCC TTGGTCCAGT TGAAGTTTCA 300  
 GTTnACACT 309

(2) INFORMATION FOR SEQ ID NO: 4415:

- 50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 300 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

55

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4415:

5 TTTATTATAC TTTACATTTC TCGTTTCGTC AGATTCAAAC GTTTTCACTT CGCCAAGCCA 60  
 TCTTTCCTTG TGTTCGCTTT TATTTTGACG TTTTAGACAT AAAAAAGAG ACCTTGCGGT 120  
 CTCAAATGCG GCTCATCGCA TCCACTTTTT GCCTGGCAAC GTTCTACTCT AGCGGAANTa 180  
 10 AGTTCGGACT ACCATCGACG CTAAGGAGCT TAACTTCTGT GTTCGGCATG GGAACAGGTG 240  
 TGACCTCCTT GGCTATAGTC ACCAGnACAT ATGAATGTGA AATTTATACA TTCAAAACTn 300

## (2) INFORMATION FOR SEQ ID NO: 4416:

15

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 20 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4416:

25 AGAAAAATAA GCGAACTGnA ATAAATAAAG ATTCAATTAA CGCATCAGTA TTAGGATTCA 60  
 CTCTAAAACG ATTAAATAGTT TTATAAGAAG GTGTTTGATC TTGAGCTAAC CACATCATTG 120  
 GAATACTGTC ATGAAGTAAT TTCTCTATTC TACGACCAGA AAATACAGAT TGAGTATATG 180  
 30 CATATAAGAT GATTTTAAAC ATCATCTTTG GATGATAGGA TGTTCGCCCA CGATGATGTC 240  
 TGAATTCATC GAATTGCTA TCAGGTATCG TTTCAACAAT TTCATT 286

## (2) INFORMATION FOR SEQ ID NO: 4417:

35

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 40 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4417:

45 TTTGATAAAA ATGGGCCATC GTCACGAGCT TCAACAATTC GTTTCGCAAC GTTTTCGCCA 60  
 AGCCCAGCCT GATATATTAC ATGAGGAGCG GTGCAATGT TGTTAGAAAT TAAAGATTTA 120  
 GTGTATAAAG CGAGCGATAG AATCATACTA GATCATATCA GTCTAAAAGT AGATAAAGGC 180  
 50 GAGAGTATTG CCATTATAGG TCCATCAGGT AGTGGTAAAA GTACATTTCa AAAGCAAATA 240  
 TGAATTTGT TTAGTCCAAC TAGTGAGAA CTTTATTTTA AAGGTAAACC CTATAATGAT 300

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GTTTGGTGA ACGnATTGGA nGATAACCAT GGATAATTCC

400

## (2) INFORMATION FOR SEQ ID NO: 4418:

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- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 286 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4418:

15 GTATTACAA TCAAACTAAG CAAAAGTATT CAGATGCCTC AGATAAAGCT TGGGCGCATT 60  
 CAAAATCTAT TTGGAGAGGC ACATCAAAAT GGTTTAGCAA CGCATATAAA AGTGCAAAGG 120  
 GTTGGCTAAT AGATATGGCT AATAAATCGC GCTCGAAATG GGATAATATT TCTAGTACAG 180  
 20 CATGGTCGAA TGCAAAATCC GTTTGGHAAA GGAnCATCGA AATGGTTTATG TAACTCATACT 240  
 AAATCTTTAA AAGGTTGGAC TGGGGATATG TATTCAAGAG CCCACG 286

## (2) INFORMATION FOR SEQ ID NO: 4419:

25

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 300 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4419:

35 CTCACCTCTA AGCGCTCCAC ATGTCCTTAC GATCATGCTT CAACGCCCTT AGAACGCTCT 60  
 CCTACCATTG TCCAAAGGnA TGcncACAGC TTCGGTAATA TGTTTAGCCC CGGTACATTT 120  
 TCGGCGCATG TCACTCGACT AGTGAGCTAT TACGCACTCT TTAAATGATG GCTGCTTCTA 180  
 40 AGCCAACATC CTAGTTGTCT GGGCAACGCC ACATCCTTnT CCACTTAACA TATATTTTGG 240  
 GACCTTAGCT GGGTGGTCTG GGCTGTTTCC CTTTCGAACA CGGACCTTGA TCACCCCATG 300

## (2) INFORMATION FOR SEQ ID NO: 4420:

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- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 336 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4420:

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GGTGAGCGGA GCGAACTCnC GTTAAGGAAC TCGGCAAAAT GACCCCGTAA CTTGCGGAGA 120  
 AGGGGTGCTC TTTAGGTTAA CGCCCAGAAG AGCCGCAGTG AATAGGCCCA AGCGACTGTT 180  
 5 TATCAAAAAC ACAGGTCTCT GCTAAACCGT AAGTGATGTA TAGGGGCTGA CGCCTGCCCC 240  
 GTGCTGGAAG GTTAAGAGGA GTGGTTAGCT TCTGCGAACT ACGAATCGAA GCCCCAGTAA 300  
 10 ACGGcGGCCG TAACTATAAC GGTCTAGACG ATCTGC 336

## (2) INFORMATION FOR SEQ ID NO: 4421:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4421:

GGnCACCCCTC GTGCCAAACA GTGCTCTACC TCCAATAATC ATCACTTGAG GCTAGCCCTA 60  
 AAGCTATTTT GGAGAGAACC AGCTATCTCC AGGTTTCGATT GGAATTTCTC CGCTACCCCTC 120  
 25 AGTTCATCCG CTCACTTTTT AACGTAATCG GTTCGGTCCT CCATTCAGTG TTACCTGAAC 180  
 TTCAACCTGA CCAAGGTAGA TCACCTGGTT TCGGGTCTAC GACAAATACT AAACGCCCTA 240  
 30 TTCAGACTCG CTTTCGCTAC GGCTCCACAT TTACTGCTTA ACCTTGCATC AAATCGT 297

## (2) INFORMATION FOR SEQ ID NO: 4422:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4422:

GTACATCGTC TAATAATAAG TTGACGATAT CTTGCAATGC ATCTTTATCT AAATGTAAGA 60  
 ATTCAACGAT GCCGTTGAAG CGGTTAAGGA ATTCAAGGCG GAAGAATTTT TTCATTTTCGT 120  
 45 GCATAATATC TTTTTCTTCA GCGTCATTGC CATTGCCAAA GCCAGCATTT GATGTACAAA 180  
 TAATAATTGT ATTTTAAAG TTGATGACAT TACCTTGACC ATCAGTCAAA TTACCATCAT 240  
 50 CCATTACTTG TAATAACAAT GTTAAAATTG TGGATTGCTT TTCGATTCAa CAATAGAATG 300  
 ACTGAGaGG GATACGGCGA CTTTTAGTA AACGGATTGA ATGGCATCAT AnCCACATAC 360  
 CAGCGTGGAC CATCATTTTG GAACAGCGTG GGCACATATC 400

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4423:

AAGTTGAGTC GCATAGCTAG TATGAAACGT GGTGTGCGCA TGGGAACAT CAAGCTTTGA 60  
 AGATGTGGTA CTACATGCGT TGAATTAGGG ATCGGTACTT TATATGAAGA CGTGCTGCTT 120  
 CCATTAAATG AGTGATGCGA TTTTGGCATG AAGGTCACCT TAAATGTACA TTGTTGTAAT 180  
 AAAATTGCCT ATAAATTTTT AGCACATAAA ATAAGAnGnG CCAACCATTG TTAGACTATA 240  
 ACAACGGTTG GCTCTTTAAT TGTAAAAAGA AAACCATACG CTATGGTAGT T 291

## (2) INFORMATION FOR SEQ ID NO: 4424:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4424:

AACTGCCACC ACCTGGGGnG GTTCCAGAA CCTCTATGCA TTTCAATCAC AGnCAAATGT 60  
 GCGGTTGACG TTCAATGACT ACCTGCAATT CATCGGTCAG CTCACACCCT TTACCTGnCT 120  
 AAAGTACCAG TAGACAATGT AGGTATTGGA CTTGCATGAG CATTTTTATn CAGTAATGGG 180  
 CTTTAGATAT TTTATTAATA CCGGCCAATC ATGCTATTCA AACCGCCAAT AGCTTTATTA 240  
 GCAACATTTT TACCTAAATC AGCCGCAGCT CTTCCCATGT CTTTACCAAT ATCTCTAATC 300  
 CAATCATATG TTTTGCATA GCCATTTTCT AAAACCATT AATACTGATT TAGCGTTAGA 360  
 CCATGCCGAA CTTGAAATTG CATCAAAACG ATCGTGGGCT 400

## (2) INFORMATION FOR SEQ ID NO: 4425:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4425:

AGATGATAAA AGCAACAGGT GGTTTTGC GA AAAGTGAAGT ATGGCGTCAA ATGATGTCAG 120  
 ATATATTTGA CACAGAGTTA GTGGTTCCTG AAAGTTATGA AAGTTCATGC TTAGGTGCCT 180  
 5 GCGTGCTCGG ACTTAAAGCT GTAGGTGACA TTGAAGATTT TTCAATCGTT TCATCGATGG 240  
 TCGGTGCCAC AAACAATCAT ACGCCGATTG AAGAAAATGC ACTGTTACCA AGAnTCGAAT 300  
 10 CCATTnTTAT CATTAAAGCGT CTTAnCAGAG ATATGACAAT 340

## (2) INFORMATION FOR SEQ ID NO: 4426:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4426:

CTGAAGATGA TAAAGATGCA GATGGTGGCG AGTTGCACGT AACAAATTACG GATCATGATG 60  
 ATTTACACT TGATAACGGA TACTTCGAnG AATTATCATC AGACAGCGAT TCAGACTCAG 120  
 25 ATAGTGACTC AGACAGCGAC TCAGACTCAG ACAGCGACTC AGACTCAGAC AGTGATTTCAG 180  
 ATTCAGACAG CGACTCAGAT TCAGATAGCG ACTCAGATTC GGACAGCGAT TCAGACTCAG 240  
 30 ATAGCGACTC AGATTTCAGAT ACGGATTTCAG ACTCAGACAG CGACTCAGAT TC 292

## (2) INFORMATION FOR SEQ ID NO: 4427:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4427:

AACAGTGCTC TACCTCCAAT AATCATCACT TGAGGCTAGC CCTAAAGCTA TTTCGGAGAG 60  
 AACCAGCTAT TTCCAGGTTT GATTGGAATT TCTCCGCTAC CCTCAGTTCA TCCGCTCACT 120  
 45 TTTCAACGTA ATCGGTTTCG TCCTCCATTC AGTGTTACCT GAACTTCAAC CTGACCAGGG 180  
 TAGATCACCT GGTTCGGGT CTACGACAAA TACTAAACGG CCCTATTCAG ACTCGGCTTT 240  
 50 CGCTACGGTT CCCACATTTA CTGGCTAAAC CTTGCATCAA AATCGGTAAC TCGnCGGGTC 300  
 ATTCTAn 307

## (2) INFORMATION FOR SEQ ID NO: 4428:



- (A) LENGTH: 354 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4428:

GACCATACAT CGTCATCGTT TGCACCGTCA AATACTGGTG ATGCAACGTG AATACCAAGA 60  
 TTTTTCAGCAG CCATACCTAA GTGTAGCTCT AATACTTGTC CGATGTTTAT ACGAGATGGT 120  
 ACACCAAGAG GATTTAACAT GGATATCGAT CGGGACGTCC ATCTGGTGAA GTGAAGGCAT 180  
 ATCTTCTTCA GGGAAACAATC TTGAGGAAAT GGACACCTTT GTTGACCATG TCGGACCACA 240  
 CATGCTTATG CACCAACATG GAATTTTACG TTTTGGAAAT GATGATTATT ACACGTACT 300  
 AATTGGTTTA CACCAGGTGG AATAATGTTAT CGTCGGCCTT GCTTCACGAT TGGA 354

## (2) INFORMATION FOR SEQ ID NO: 4429:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4429:

GTGACTATC nGCTTGTCTA TGATAATATT ATTCTTTGTA CTTGTTTAAA AGATATTAGA 60  
 CTAATACTAA AAACAGCAGT AAGATGATTT ATGATTAAAA CTATCTTACT GCTGTTCAT 120  
 TTTTATAATA CTTCTGAATG TCTCACTTAT ACTTCTAGTC ACAGATTTAA ATAATCAAAA 180  
 GTGCACATTA TAAAATATC AATTTACAC TCAATGCGGC TCATCGCATT CATTTCTTGT 240  
 CTAGCAACGT TCTACTCTAG CGGAACGTAA GTAGCTACCA TCTCGCTAAG GAACTTTCTT 300  
 GACCTGGTGA CAACCGCTGC GACTTCTCT CTTGGCTCT CGCTTACTCC ATTTAGCTCC 360  
 ACTAACTCG TCGGGCCCTT CCGTTTCGGC AGATCCAACG 400

## (2) INFORMATION FOR SEQ ID NO: 4430:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4430:

ACCATTACACA CCTTGACAGC CACATAACAT AACTAAGTTT AAGATnGGGG GATAAATCGT 120  
 ATCTGAGTTA AACCAATGGT TAATACCCGC ACCCATGATA ATCATTGAAC GCCCTTCAGT 180  
 ATCGATAGCG TTTTGCGCAA ATTCTTTTCGC TACTTGAATG ACAACACTTT GTTTTACGCC 240  
 TGAAATGGCT TCTTGCCAAG CAGGTGTATA TTTTGATTCT GCATCGTCGT AA 292

(2) INFORMATION FOR SEQ ID NO: 4431:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4431:

TGAGCCGnAC ATCGAGGTGC CAAACCTCCC CGTTCGATGT GAACTCTTGG GGGAGATAAG 60  
 CCTGTTATCC CCGGGGTAGC TTTTATCCGT TGAGCGATGG CCCTTCCATG CGGAACCACC 120  
 GGATCACTAA GTCCGTCTTT CGACCCTGCT CGACTTGTAG GTCTCGCATC AAGCTCCCTT 180  
 ATGCCTTTAC ACTCTATGAA TGATTTCCAA CCATTCTGAG GGAACCTTGA GCGCCTCCGT 240  
 TACCTTTTAG GAGGCGACCG CCCAGTCAAA CTGCCCGCCT GACA 284

(2) INFORMATION FOR SEQ ID NO: 4432:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4432:

TATCATTGTG GTACGATAAG GCATATGTTG TACCTATGnA TGGTGAAGA GCCTTCAGTT 60  
 GTCGCTGCAG CTAGTTATGG TGCAAAGCTA GTGAATCAGA CTGGCGGATT TAAAACGGTA 120  
 TCTTCTGAAC GTATTATGAT AGGTCAAATC GTCTTTGATG GCGTTGACGn TACTGGAAAA 180  
 TTATCAGCAG ACATTAAAGC TTTAGAAAAG CAAATTCATA AAATTGCGGn TGAGGCATAT 240  
 CCTTCTATTA AGCGCGTGTG GTGGTTACCA CGTATAGCGA TTGATACATT CCTGGCCACC 300  
 AGTTCTATCT TT 312

(2) INFORMATION FOR SEQ ID NO: 4433:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4433:

	CGGTACTCGT TAAGGCTGAG CTGTGATGGG GAGAAGACAT TGAGTCTTCG AGTCGTTGAT	60
10	TTCACACTGC CGAGAAAAGC CTCTAGATAG AAAATAGGTG CCCGTACCGC AAACCGACAC	120
	AGGTAGTCAA GATGAGAATT CTAAGGTGAG CGAGCGAACT CTCGTTAAG AACTCGGCAA	180
	AATGACCCCG TAACTTCGGG AAAAAAGGTG CTCTTTAAGG TTAACGCCCA GAAGAGCCGC	240
15	AGTGAATAAG CCCAAGCGAC TGTTTTATCC AAAACACAGG TCTCTGCT	288

(2) INFORMATION FOR SEQ ID NO: 4434:

(i) SEQUENCE CHARACTERISTICS:

20	(A) LENGTH: 336 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4434:

	GGACCGAACC GACTTACGTT GAAAAGTGAG CGGATGAACT GAGGGTAGCG GAGAAATTCC	60
30	AATCGAACCT GGAGATAGCT GGTCTCTCTn nAAATAGCTT TAGGGCTAGC CTCAAGTGAT	120
	GATTATTGGA GGTAGAGCAC TGTGTGGACG AGGGGCCCT CTCGGGTAC CAATTTCAGA	180
	CAAATCCGA ATGCCAATTA AATTAACTT GGAATTCAG AACATGGGTG ATnAAGTCCG	240
35	TGTTTCGAAA GGAAACAGCC CAGACCACCA GCCAAGTCCC AAAATATATG TTTAATGGGA	300
	AAAGGTGTGG CCTTTGCCCA GGACAACCAA GAAGTT	336

(2) INFORMATION FOR SEQ ID NO: 4435:

40

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 304 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
45	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4435:

50	ATTGACGCCG CATTTTTACG GAATGGGAAT AAAGCGACAC AAACCGTCAC GTCnGTGTTG	60
	GTGTCATGAC AAGGTAATGC GAGTGATCTG ATGTATGGCT TATCATGGCA ATCTGTTATG	120
	GnCTGACTGA TCGGACGATG TATCATTCGC CAATTCGTTT ACTTGTCGTT ATTCAGGCAC	180

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AATCATTGGC TGCCTTTTAA TGAGCGTAAT GAGGAAGGGG CGTTTAAAAA GTTGGATTTA 300

ACGA 304

5 (2) INFORMATION FOR SEQ ID NO: 4436:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 305 base pairs  
 (B) TYPE: nucleic acid  
 10 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4436:

AATATACTCC GGTAAATAAC CGAAGAGTTT TGAATCATTG TTAAAAATGG AATTAnAGTT 60  
 CTAGTATCTG TTGGGTTTTG AAATAGGTCA TAGGATAAAA CAAATnGAGA ATTTGTGCGCT 120  
 20 ATTTGTAAAT TGTATCCTGG CTTAAGTTGG CCATTTTTCA TATGGTCTTC CTTCATTCTC 180  
 ATAAAAGTTG CATCATGGAT CAGTTTTAGA AAAGCTATTT CTATCTTTAA GAATCGATT 240  
 TTGTTCTTCA TATTTATTTT TTCTTTCGGA ATAATCATCA AATTTATnTT TGGAACCTCT 300  
 25 TAATC 305

(2) INFORMATION FOR SEQ ID NO: 4437:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 359 base pairs  
 30 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4437:

ATCGTTTTAA TCAGTTAGTA AAAAGTCTGT GAGTAAGGGT GTATGGAAAG TGGTTAAATA 60  
 40 TTATAGAAAA CATCAAAGGA TGTTAAGAAA TACAATTTAT TACCCAGCAT TTAATAATGG 120  
 TGCTATAGAA GGAATTAATA ATAAGATAAA ATTAATCAAG TGAATTTCTT TTGGTTACAG 180  
 AAATTTCAAC AACTTTAAAG CACGTATAAT GATGATTTTC AGCTTGTTACA AGGGGGAnAA 240  
 45 AAGGAnGnCA ACCAAGCCCA ATAATGGACT GGCCGCCTAA TATTAAAAAC TCTAAAGTT 300  
 GTATTTTAAA ATAGTTCTTT AAATTATATA CCCACCACAT TTGGTGGAGA CCCGTTAAC 359

(2) INFORMATION FOR SEQ ID NO: 4438:

- 50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 286 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4438:

5 ACTTACAGTT ATTTTAACTT GGCAGAAATC CATCATCCAT AAGTTCGAAA TGTTGTAAAA 60  
 CATAAACCTT GAAAACGGCA ACATTTTGG GTCCTTCTCC ATCAATTTAT TTAAGCGC 120  
 ATTATGATCA ATATCATGCC CAATTAACCTT TCCAGCAATT TCCATAGTAT GTTCTGAGGT 180  
 10 ATTGTAAAA AGGAATCGCC CAGTATCACC GACGATACCA AGATATAAAA CGCTCGCGAT 240  
 ATCTTTATTA ACAATTGCTT CATCATTAAT ATGTGAGATT AAATCG 286

## (2) INFORMATION FOR SEQ ID NO: 4439:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 394 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4439:

25 TCGCTTGACT TCTTCTCTT CCTTCGGCTC TCGCTTACTC ATTTAnCTCT ACTAAACTCG 60  
 TTGCGCTCTT TTCTCGTTTC GTCAGATTCA AACGTTTTCA CTTGCCAAG CCATTTTCT 120  
 TTGTGTTTAC TTTTATTTT GACGTTTTAG ACATAAAAAA AAGAGACCTT GCGGTCTCAA 180  
 TGCGGCTCAT CGCATCCATT TTTGCTTG CAAcGTTCTA CTCTAGCGGA ACGTAAGTTG 240  
 30 GCTACCATCG ACGCTAAGAA CCTtTCTTGA CTTGTGACAA aTCGCTTGCT TCTTCTCTCh 300  
 TCTTCGGTCT CGCTTACTCA TTTAGCTCTA CTAAACTCGT TGCGCTCTTT TCTCGTTTCG 360  
 35 TCAGATTCAA CAGTTTTTCAT TCGCCAAGCC ATTT 394

## (2) INFORMATION FOR SEQ ID NO: 4440:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4440:

45 TAATAGGTTT GAGGTGGAAG CATGGTGACA TTGGCAGCTG ACGAATACTA ATCGATCGAA 60  
 GACTTAATCA AAATAAATGT TTTCGACAA TGCAACTTTT ACTTACTATC TAGTTTTGAA 120  
 50 TGTATAAATT ACATTCATAT GTCTGGTGAC TATAGCAAGG AGGTCACACC TGTTCCCATG 180

TAGAACGTTG CCAGGCAAAA AATGGATGCG ATGACCGCAT TGAGACCGCA GCnTn

295

## (2) INFORMATION FOR SEQ ID NO: 4441:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4441:

TTTCATAAAA AGATTTCAAA CGCGTTCATC AAnCCTCGTC GCAGGTCTTT CGAACACTAG 60  
 CGATTATTTT tTATGAATTC AAGCTTATTT AAAACTCTTT ATTCaCTCGG TTTTGCTTGG 120  
 TAAAATCTAT ATTTTACTTA CTTATCTAGT TTTCAATGTA CAATTTCTTT TTAGTCAAGC 180  
 GCTCGCATAC TGCTTTATTT TCATAAGCAA TATCACTTTA ACCAAAAAAT ATTTGAATGT 240  
 TAAATAACA TTCAAACTG AATACAATAT GTCACGTTAT TCCgCATCTT CTGAAGAAGA 300  
 TGTTCCGAAT ATATCCTTAG AAAGGAGGTG ATCCnGCCGn ACCTT 345

## (2) INFORMATION FOR SEQ ID NO: 4442:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4442:

AATCATTGTC AAAACTACGT TCTGGTAAAC AAGGACAACC CGTTTGAACC ATTGGCCCCAC 60  
 ACCATTTGAT AGGCAGnCAT GTGCGCAATG GACATCCACA TAGTTGCGTA ATGTTTCATA 120  
 CGTCATTGCT CAAATCATTG ATGACTAGCG CAACATGATT ACCTTGTCGT GnGCACCTTC 180  
 ATTAAAGnAA CTTATGATAG ATTTATTTCC CGGGACATTA AGCATTGCA TCGTTAACAT 240  
 GCGTATTGCA CCCAATTTAG AAGTTCCTCC GTGCCGTTTG GTATATCACA AATTTGTAGT 300  
 GTATCTTGGA TGC 313

## (2) INFORMATION FOR SEQ ID NO: 4443:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4443:

AGCATGGTGT TTCTCAGATT GTCGGATGTA TAAATGTGTA TGTTATGTTT TAATTTTTC 60  
 5 CAGTCTTTAA AAATAGATTG TTTATTTTGA GAATTATTTT TGAATAATTG AATTGCTTTG 120  
 TAGCCAAAAT ATGACGTTTC ATTATCATTG AAACGCATAT AAAGCGTATC TnCTGCCTCA 180  
 TTGTCAGTGA GATGAAATAA TGTGCTCGGG GTCTAGTGAC TGTGGATAAT TTCACTTCAA 240  
 10 CTGAAACCCC ATTCCCTTTG AGCTGCCCCAT ATATCTCTTT GGACAATATC GGTCCCTCTA 300  
 ATACGGnCCG TAGnCCATTG CATTTCATT CTTTTC 336

## (2) INFORMATION FOR SEQ ID NO: 4444:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 20 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4444:

CAGACTGGGA TATTTATAAA ACGTTGGCAA AAGCATTTTC AGAAATGGCA AAAGACTATT 60  
 25 TACCTGGAAC GTTTAAAGAT GTTGTGACAA CTCCACTTAG TCATGATACA AAGCAAGAAA 120  
 TTTCAACACC ATACGGCGTA GTGAAAGATT GGTGGAAGGG TGAAATTGAA GCGGTACCTG 180  
 30 GACGTACAAT GCCTAACTTT GCAATTGTAG AACGCGACTA CACTAAAATT TACGACAAAT 240  
 ATGTCACGCT TGGGCCTGTA CTTGAAAAAA GGGGAAATTT GGAGCACCTG GGGGTAAGTT 300  
 35 TCCGTGTCCA GTTGAACCAT TATGGAGGAA TTA AAAAGT ATGTTAAGGG ACCTGGGAGT 360  
 TGAATACCCA ATGGATnGAT TCCCGTGAAG AGCCGAATCC 400

## (2) INFORMATION FOR SEQ ID NO: 4445:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 40 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4445:

TACGCCCACG ACGGATAGGG ACCGAACTGT CTCACGACGT TCTGAACCCA GCTCGCGTAC 60  
 50 CGCTTGTAAAT GGGCGAACAG CnATCGCCTT GGGACCGACT ACAGCCCCAG GATGCGATGA 120  
 GCCGACATCG AGGTGCCAAA CCTCCCCGTC GATGTGAACT CTTGGGGGAG ATAAGCCTGT 180

CACTAAGTCC GTGCTTTCGA CCCTGACTAC GGA CTGTGThA GGTCTGCGGC ATTCAAGCTT 300  
 CCCTTGATGG CCTTTGACAC TGCTTATGGA ATGnATTG 339

5 (2) INFORMATION FOR SEQ ID NO: 4446:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 318 base pairs  
 (B) TYPE: nucleic acid  
 10 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4446:

CAATTTTAAG TGTTGAAAAT GTCAC TTTTA AACTTTCTAG TTTTATCTTT AATAAACATG 60  
 CCATnCGTAA TAAGTGGCGT TTTATTAAAA TCATCTATAA TAGCCATATA GTTTTGCTCA 120  
 20 CTACCATAAC CTGCATCAGC TACAATATAC TCCGGTAAAT AACCGAAGGA ThTTTGGAAT 180  
 CATTGT TAAA AATGGAATTG AAAGTTCTAG TATCTGTTGG GTTTTGAAAT AGGTCATAGG 240  
 ATAAAACAGG GTGAGAATTT GTCGCTATTT GTAAATTGTA TCCTGGCTTA AGTTGGCCAT 300  
 25 TTTThCATAG GTCTTCCT 318

(2) INFORMATION FOR SEQ ID NO: 4447:

- (i) SEQUENCE CHARACTERISTICS:  
 30 (A) LENGTH: 279 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4447:

TTTTGAAATT CTCTATGTTG GGGCCCCGAC TATAATTGAA AAATGCTTGT TACAAGTGCA 60  
 40 TTTTATTTCA GTCAACTACT AACAAATATAA CATTGTGGAG CCCAGAnCTT TGATTAATGT 120  
 ATATGAAAAT CAAAGTAATG CTTATGTATG ATTATTTCAA ATATTTTACA TACATGAACT 180  
 TTCCAATGT ACGATACTAT TATTATAAAG CGCTCGCTAA GATTTTACGA TGATTAGAGG 240  
 45 GTAAAAAATG AACGATCAAT GGThTAACCA TTTAATTGG 279

(2) INFORMATION FOR SEQ ID NO: 4448:

- (i) SEQUENCE CHARACTERISTICS:  
 50 (A) LENGTH: 302 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

55



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4448:

5 GACACCGGCA TTCTCACTTT CTAAGCGCTC CACATGTCCT TACGATCATG CTTCAACGCC 60  
 CTTAGAACGC TCTCCTACCA TTGTCCAAAG GACAATCCAC AGCTTCGGTA ATATGTTTAG 120  
 CCCCAGTACA TTTTCGGCGC AGTGTCACTC GACTAGTGAG CTATTACGCA CTCTTTAAAT 180  
 GATGGCTGCT TCTAAGCCAA CATCCTAGTT GTCTGGGGCA ACGnCACATC CTTTTCCACT 240  
 10 TAACATATAT TTTGGGACCT TTAGCTGGTG GTCTnGGGCT GTTTTCTGnA TTGAACACGG 300  
 GA 302

## (2) INFORMATION FOR SEQ ID NO: 4449:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4449:

25 CGTTGGTATA TAGAGGGCAA CCGTCACCTG ATAAATGTG GACACAGTTT TTACAAGAGG 60  
 TTAAGGAAAT GAGTTTGGAG GCATACGAGC ATCAAGAATA CCCATTGAA TGTTTAGTAA 120  
 ATGACTTAGA TCAATCACAT GATGCCTCAC GGAATCCATT ATTTGATGTC ATGTTAGTAC 180  
 30 TACAAAACAA TGAACGAAA TCATGCTCAT TTTGGGCATA GTAAATTTAA CACACATTCA 240  
 ACCCCAAATC AGTGACGGGC GGAAATTTGG ATTTnTCCTT TTCCATCATT GGAAGAAGGA 300  
 TCGCGGATGA CCTAATAnCA ATCCAATTAT CGGGGTATAA ATACCGGATT TTATAACCA 359

## (2) INFORMATION FOR SEQ ID NO: 4450:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4450:

45 GATGACAAAA TTTGCTTGAA AACCGAAATG GATGGTCATC ATTGACTGnA TCAAGGTACA 60  
 TCATTCTTTG GTGCTTATGC ATTTAGACAT TATACAAAAA CAATACTTTT ATAGGGCAAC 120  
 50 CTTATGGGGT TCTATCGGCT ATACATTACC TGCAACATTA GGTCACAAT TAGCAGACAA 180  
 AGATCGTCGn TAACTTATTA TTAATTGGTG ATGGCTCATT GCCAACTAAC TGTTCAGCT 240

GCTATACGGT AGAACGACTT ATTCCC

326

## (2) INFORMATION FOR SEQ ID NO: 4451:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4451:

5 GAAAACATCA AAGGATGTTA AGAAATACAA TTTATTACCC AGCATTTAAT AATGGTGCTA 60  
 15 TAGAAGGAAT TAATAATAAG ATAAAATTAA TCAAGTGAAT TTCTTTTGGT TACAGAAATT 120  
 TCAACAACTT TAAAGCACGT ATAATGATGA TTTTCAGCTT GTACAAAGGA GAAAAAAGA 180  
 20 AGACAACCAA GCCCAATAAT GGACTGGCCG CTAATAATA AAAACTCTAA AAGTTGTATT 240  
 TTAAAAATAG GTCTTTAAAT TATATACCCC CCCCATTTGG GTGGAGAACC GGTAAACCAT 300  
 GCCTAGGTGC CTAACCTCn ATAATGGnAC CCCTCCTTAC CATTTGGGCC ATGGGGCCAA 360  
 25 TAAAGCGGGG GGCAATTGGG G 381

## (2) INFORMATION FOR SEQ ID NO: 4452:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4452:

35 TTAATAACTT AATCTATGTT TCCATCCTAC AGGAAACGCG TTATTAATCT TGTGAGTGTT 60  
 40 CTTTCGAACA CTAGCGATTA TTTCTTATGA ATTCAAGCTT ATTTAAACT CTTTATTCAC 120  
 TCGGTTTTGC TTGGTAAAT CTATATTTTA CTTACTTATC TAGTTTTCAA TGTACAATTT 180  
 CTTTTTAGTC AAGCGCTCGC ATAAGCAATA TCACTTTAAC CAAAAATAT TTGAATGTTA 240  
 45 AATAAACATT CAAAACTGAA TACAATATGT CACATn 276

## (2) INFORMATION FOR SEQ ID NO: 4453:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4453:

GGCGAAACCG CGTAGCGTTT TTAAAGTCTG ATGTGAAAGC CCACGGTCAA CCGGGAGGGT 60  
 5 CATTGGAAAC TGGAAACTT GAGTGCAGAA GAGGAAAGTG GAATTCCATG TGTAGCGGTG 120  
 AAATGCGCAG AGATATGGAG GAACACCACT GAGCGAAGCG ACTTTCTGGT CTGTAAGTGA 180  
 CGCTGATGTG CGAAACGTGG GGGATCAAAC AGGATTAGAT ACCCTGGTGA GTCCACGCCG 240  
 10 TAAACGATGA nTGCTAAATG TTAGGGGGTT TCCGCCCTT AGTGGCTGCC AGCTAnACGC 300  
 ATTGAAGCAC TGCCGCCTGG GGAGTGACGA CCGCAAnTTG A 341

## (2) INFORMATION FOR SEQ ID NO: 4454:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 20 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4454:

25 ACnCTCCCCA AAGTCATATC GTCGTTAGTA ACGTCCTTCA TCGGCTTCTA GTGnCCAAGG 60  
 CATCCACCGT GCGCCCTTAA TAACTTAATC TATGTTTCCA CCATTTTAT AAGTCAAACG 120  
 CTCACATACG GCTTCGTTTT CATTATTTTA AATGCTCATT TACATAAGTA AACTCTGCTT 180  
 30 TAAAATAATT TAACTCATTG TCTGCTAAAC GTTTTCTTTT ATAAAAAGAT TTAAACGCGT 240  
 TATTAATCTT GTGAGTGTTT TTTCGAACAC TAGCGATTAT G 281

## (2) INFORMATION FOR SEQ ID NO: 4455:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 40 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4455:

45 ATGTCTTCAC TTATACTTCT AGTCACAGAT TTAAATAATC AAAAGTGCAC ATTATTAAAA 60  
 TATCAATTTT AACTCAATG CGGCTCATCG CATTCAATTC TTGTCTAGCA ACGTCTACT 120  
 50 CTAGCGGAAC GTAAGTTAGC TACCATCCTC GCTAAGAACC TTTCTTGACT TGTGACAATC 180  
 GCTTGCTTCT TTCCTCTCCT TCGGCTCTCG CTACTCATT TAGCTCTACT AAACGCTTG 240  
 CGCTCTTTTC TCGTTTCGTC AGATTCAAAC GTTTTCnGT 279

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4456:

ATTTTGACGT TTTAGGCATA AAAAAAAGAG ACCTTGCGGT CTCAATGCGG CTCATCGCAT 60  
 CCATTTTTTG CCTGGCAACG TTCTACTCTA GCGGAACGTA AGTTGGCTAC CATCGTCGCT 120  
 AAAGACCTTT CTTGACTTGT GACAATCGCT TGCTTCTTTC CTCTCCTTCG GCTCTCGCTT 180  
 ACTCATTTAG CTCTACTAAA CTCGTTGCGC TCTTTTCTCG TnTCGTCAGA TTCAAACGTT 240  
 nTCACCTCGC CAAGCCATT TTCTTGTT TACTT 275

## (2) INFORMATION FOR SEQ ID NO: 4457:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4457:

ATCCGATTCA CAAAGCACAT CATCATATAC AAGTCAGTCA ACAAGCCAAA GTGAATCCAC 60  
 ATCGACATCA ACGTCACTAA GCGATTCAAC AAGTATATCT AAAAGTACGA GTCAATCAGG 120  
 TTCGGTAAGC ACATCAGCGT CATTAAAGTG TTCAGAGAGT GAATCTGATT CACAAAGTAT 180  
 CTCAACAAGT GCAAGTGAGT CAACATCAGA AAGTGCCTCA ACATCACTCA GTGACTCAAC 240  
 AAGTACAAGT AACTCAGGAT CAGCAAGTAC GTCAACATCG CTCAGTAACT CAGCAAGCGC 300  
 AntTGAATCC GATTTGTCGT CAACATCTTT AAGTGGATTC AACATCTGCG TcATGCCAA 360  
 AGnnGTGAAT CCGATTCA AAGCACATCA GCATCCTTAA 400

## (2) INFORMATION FOR SEQ ID NO: 4458:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4458:

AGTCGCTGTC TGAATCTGAA TCACTGTCTG AATCCGAATC GCTATCTGAT TCTGAGTCGC 120  
 TATCTGAACC TGAGTCGCTG TCTGAGCCTG AGTCACTGTC TGAATCCGAA TCCGGATCCG 180  
 5 GGTCTGGGGn TGGTTCCGGT TCTGGGTCTG GGACTTGGTT CTGGATCTGG CGTTGGTTCT 240  
 GGGTCTGGGG TCTGGACTGG TTCTGGGGTC AAACGGCGGC CCTGGAGTGG GGTCTTTCGG 300  
 AATnAACGGC GGAATCACCA TCAAGCAACT TnCAACAACC ATAACGAAAA A 351

10 (2) INFORMATION FOR SEQ ID NO: 4459:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 271 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4459:

ATCCTGCAGT TGATCAGTAT GGTGATATTA ATTTAGTTAA TACGAACGCG TCATCTACAA 60  
 GTGAAATCAT TTACGATTTA ATCTCACATT TTAATGATGA AGCAATTGTT AATAAAGATA 120  
 25 TCGCGAGCGT TTTATATCTT GGTATCGTCG GTGATACTGG GCGATTCCTT TTnACAATA 180  
 CCTCAGAACA TACTATGGAA ATTGCTGGAA AGTTAATTGG GCATGATATT GATCATAATG 240  
 CGCTTTTAAA TAAAATGATG GAGAAGGnCC C 271

30 (2) INFORMATION FOR SEQ ID NO: 4460:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 283 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4460:

ACTGTGGATT AATATTATGC CTGGCAACGT TCTACTCTAG CGGAACGTAA GTTCGACTAC 60  
 CATCGACGCT AAGGAGCTTA ACTTCTGTGT TCGGCATGGG AACAGGTGTG ACCTCCTTGC 120  
 45 TATAGTCACC AGACATATGA ATGTAATTTA TACATTCAAA ACTAGATAGT AAGTAAAAGT 180  
 GATTTTGCTT CGCAnAACAT TTATTTTGAT TAAGTCTTCG ATCGATTAGT ATTCGTCAGC 240  
 GCCACATGTC ACCATGCTTC CACCTCGAAC CTATnAACCT CAG 283

50 (2) INFORMATION FOR SEQ ID NO: 4461:

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 274 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4461:

CTTCTACAAG TCCTGAATAT ACTTATGAAT CTCTTCTTTC GTGTATGCAA ACTGACGTTG	60
TAATTTAAAT AACGTCTCAT CTTTCCATTG CGAATCTTGA TATTGTATAT TTTCAAATC	120
AAAGTCAACT TTATGGTTAT CAATCCACGC TTTATATGGT AATTCTCCAG CAATCGCACC	180
TTTTAAATCA TTATTTTCAA TGACTTTATT CTGTTAAAAT CAACAACAT AACTTTCCnG	240
GATTCAATTG ACCTTTAAAA GCAACATTAC TTCC	274

(2) INFORMATION FOR SEQ ID NO: 4462:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 271 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4462:

GGCTGCTAAA AATCTTGGTA TTCACGTTGC ATCACCAGTA TTTGACGGTG CAAACGATGA	60
CGATGTATGG TCAACAATTG AAGAAGCTGG TATGGCTCGT GATGGTAAAA CTGTACTTTA	120
TGATGGACGT ACAGGTGAAC CATTGATAA CCGTATTTC A GTAGGTGTAA TGTACATGTT	180
GAAACTTGCG CACATGGTTG ATGATAAATT ACATGCGCGT TCAACAGGAC CATATTCCT	240
TGnTACACAA CAACCACTTG GCGGTnAAGC G	271

(2) INFORMATION FOR SEQ ID NO: 4463:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 300 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4463:

GCGGCTCATC GCATTCAATT CTGTCTAGC AACGTTCTAC TCTAGCGGAA CGTAATTAGC	60
TACCATCCTC GCTAAGAACC TTTCTTGACT TGTGACAATC GCTTGCTTCT TTCCTCTCCT	120
TCGGCTCTCG CTTACTCATT TAGCTCTACT AAACGTTG CGCTCTTTTC TCGTTTCGTC	180
AGATTCAAAC GTTTTCACTT CGCCAAGCCA TTTTCTTTG TGTTTACTTT TTAATTGAC	240

55

## (2) INFORMATION FOR SEQ ID NO: 4464:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 361 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4464:

TACCGAATCG AAGCCCCAGT AAACGGCGGC CGTAACTATA ACGGTCCTAA GGTAGCGAAA 60  
 TTCCTTGTCG GGTAAGTTCC GACCCGCACG AAAGGCGTAA CGATTTGGGC ACTGTCTCAA 120  
 CGAGAGACTC GGTGAAATCA TAGTACCTGT GAAGATGCAG GTTACCCGCG GACAGGACGG 180  
 GAAAGACCCC GTGGGAGCTT TTACTGGTTA GCCTGGATAT TGGAAATTCG GGCACACTTG 240  
 GTTACAGGAT AGGTAAGGAG CCTTTTGGAA ACGTTGAGCG CTACTTTAnG TTGGGAGGCG 300  
 CTGGTnGGGA TACTTACCCT AACTGTGTTT GGCTTTTCTn AACCGGCACC ACTTATCCTG 360  
 G 361

## (2) INFORMATION FOR SEQ ID NO: 4465:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 292 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4465:

CTGTATGTAC ACCACCAATC GGTTTAGGTT TAGCAACGTT TGTTCAAAG TATAAATTCA 60  
 ATCAITCCGA AAGAGAAATG GGTAAGGCTT CCTTCACTAT GGGACTATTT GGTATTACTG 120  
 AAGGTGCTAT TCCTTTCGCA GCCCAAGATC CATTGCGCAT TATACCTGCA AACATCATTG 180  
 GTGCAATGAT TGCATCAGTC ATTGCAGCCA TTGGTGGTGT CGGCGATAGA GTCGCACATG 240  
 GnGGTCCCAA TCGTGGCTGT ATTAGGTGGG TTTTGTGTTT TTTTnTTTT TT 292

## (2) INFORMATION FOR SEQ ID NO: 4466:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 308 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

GCAAACAAAA CAGTATTAGT AGATTATGAA AAATATGGTA AGTTTTATAA CTTATCTATT 60  
 AAAGGTACAA TTGACCAAAT CGATAAAACA AATAATACGT ATCGTCAGAC AATTTATGTC 120  
 5 AATCCAAGTG GAGATAACGT TATTGCGCCG GTTTTAACAG GTAATTTAAA ACCAAATACG 180  
 GATAGTAATG CATTAAAGA TCAGCAAAAT ACAAGTATTA AAGTATATAA AAGTAGATAA 240  
 TGCCnCTGAT TTATCTGAAA GTTACTTTGT GGAATCCCGG AAACCTTGAG GGTGGCCCCCT 300  
 10 AATAnTGG 308

## (2) INFORMATION FOR SEQ ID NO: 4467:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 271 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4467:

AAGCAGGCGC TCTCCAGCT GAGCTAAGCC CCCATAATAA TTACAGTATA TCGGAAGAC 60  
 25 AGGATTCGAA CCTGnGACCC CTTGGTCCCA AACCAAGTGC TCTACCAAGC TGAGCTACTT 120  
 CCCGTATAAT TAAngCGCCC GATAGGAGTC GAACCCATAA CCTCTTGATC CGTAGTCAAA 180  
 CGCTCTATCC AATTGAGCTA CGGGCGCATA TGTTTTTATT GAAAATAGTG CCGAGGACCG 240  
 30 GAATCGAACC GGTACGTGAT CACTCACCGC A 271

## (2) INFORMATION FOR SEQ ID NO: 4468:

35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 306 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4468:

TGTGTTAGGT ATTACATCAT CACATTTATC TGCGTCAAAG TCCAGCTGTC GATAAAGTTG 60  
 45 TAAACTGTAA AAACGCAATT TCTGAATTAG AAAATGATAA ACGTAAAGCA GTAAGTGCTG 120  
 AAGAnTATAA AAAAGCTGAC GACATTCAAA ATGAAATCAA ATCATTACAA GATAAATTAG 180  
 AAAATAGTAA TGGTGAACAT ACTGCTGTTG CTACAGTTCA TGATATTTCA GATACTATTC 240  
 50 AACGATTAAC TGGTATTCCA GTTTCTCAA TnGATGATAA CgnTATTGAA CGTTTAAAAA 300  
 ATATTT 306

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## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4469:

GGTTTATTAA CAGCATTCTT ATCAGCATT GTAACTGTTA TTGTTTATAA CTTCTGTGTG 60  
 AAGCGCAATA TTACAATTAA AATGCCGAAA GAAGTACCGC CGAATATTTT ACAAGTATTT 120  
 AAGGACTTAA TTCCATTTTC AGCGGTAATC ATCATTCTTT ATGCATTAGA TTTAGTCATT 180  
 CGCAACAGCT TTAAATCAAA TGTAGCGGAA GGTATTTTAA AATTATTCGA ACCATTATTT 240  
 ACAGCAGCAG ATGGATGGGT TGGTGGTCAC CATTTAACTT TGGGnGCnTT TGCATTAATC 300  
 CTGGGTTTGT AGGGTAATCC ATGGGTCCG 329

## (2) INFORMATION FOR SEQ ID NO: 4470:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4470:

AACTGGGTGA TAAGGTCCTG TTCGAAAGGA AACAGCCCAG ACCACCAGCT AAGGTCCCAA 60  
 AATATATGTT AAGTGGAAAA GGATGTGGCG TTGCCAGAC AACTAGGATG TTGGCTTAGA 120  
 AGCAGCCATC ATTTAAAGAG TGCgTAATAG CTCACTAGTC GAGTGACACT GCGCCGAAAA 180  
 TGTACCGGGG CTAAACATAT TACCGAAGCT GTGGATTGTC CTTGGACAAT GGTAGGAGAG 240  
 CTTCTAAGGA CTTGAAGCTG ATCGTAAGAC TGTGGAGCGn TAGAATGAGA TGCCGTGTGA 300  
 TAGnAAAGAC GGTGAGATCC CTCCACCGTT GACTAAGTTC CAGAGGAAGC TCTCCGTCGG 360  
 GTTATCCGGT CCTAAGnGAG GCCGACAGCT AGGCATGGnT 400

## (2) INFORMATION FOR SEQ ID NO: 4471:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

TCATTTTATAG AAATATTATC TTTTCCACAA ATCATTTGAT ATAAAGTGCG ATCATTTGCC 60  
 GCGAGTGCTG CCATTGACAC TAGCTGTTGC GTATCATTTT TGGCTAGCAC TTCGGGATAC 120  
 5 TTTCTTAGCT GAACAGTTAG ATGACCTAAT TGATCTTTGA AAATATCATT ATCTTGACCC 180  
 ATATATGACC ACCAAGCTGT TTCATCACAA ACCATGACAT ACTTAGCTAG TGCTTCATCT 240  
 TTTTCTATAA GCTGACGTAA TAATTGTCTG CTTGTCCTCC GTTTTnCATG TACCGCGAGG 300  
 10 CGTAAnCTTA AAGGGCCCCAA GGnCG 325

## (2) INFORMATION FOR SEQ ID NO: 4472:

(i) SEQUENCE CHARACTERISTICS:  
 15 (A) LENGTH: 276 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4472:

CCCGTCTTTC GCTACTCACA CCGGCATTCT CACTTCTAAG CGCTCCACAT GTCCTTACGA 60  
 25 TCATGCTTCA ACGCCCTTAG AACGCTCTCC TACCATTGTC CAAAGGACAA TCCACAGCTT 120  
 CGGTAATATG TTTAGCCCGG TACATTTTCG GGGGCAGTGT CACTCGACTA GTGAGCTATT 180  
 ACGCACTCTT TAAATGATGG GCTGCTTCTA AGnCAACATC CTAGTTGGTC TGGGGCAACG 240  
 30 CCACATCCTT TTTCCACTTT AACAnATATT TTGGGA 276

## (2) INFORMATION FOR SEQ ID NO: 4473:

(i) SEQUENCE CHARACTERISTICS:  
 35 (A) LENGTH: 333 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4473:

AATTInCCAA AAAATTCAAA TGGCTCATTT ACCAAAAGGT AAACCTCCGC CTTTAAnTTT 60  
 45 CTTaATGCAT kGTCTAACAA cCGCTTTCTT TAAAgaATA GATTGTCAAG CGCTCGCATA 120  
 AGCAATATCA CTTTAACCAA AAAATATTTG AATGTTAAAT AAACATTCAA AACTGAATAC 180  
 AATATGTCAC GTTATTCCGC ATCTTCTGAA GAAGATGTTT CGAATATATC CTTAGAAAGG 240  
 50 AGGTGATCCA GCCGCACCTT CCGATACGGC TACCTtGTTA CGACTTCACC CCAATnCAT 300  
 TGTCCACCT TCGACGGGCT AGCTCCGAAA AGG 333

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- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 325 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4474:

10 TATAAAATAG CAACGTTATT CCAATTATCT TAATGGTTAT CTTATCCTCA ACTAAATTGG 60  
 AGGAATCACT ATGACAATTA ATAAAGTAAC CGTTCCTGGC GCAGGCACAA TGGGCGCTCA 120  
 15 ACTGGCAGCA CTTTTTGTGA ATGCTGGACT TAAAGTAANA CTATTAGATA TTGTAGTGGA 180  
 CAAAAACGAT CCAATCTCA TTGCGAAAAA ATCTTACGGT TAAATTACAG GTAAGAAACG 240  
 GCCGCTACTA TTCGnCTTAA ATCTAGCGGT CATTACCAT ATGGTATTTT GATGTGCTTG 300  
 20 GTAAATGTGT GCTGTTTGAT ATCGA 325

(2) INFORMATION FOR SEQ ID NO: 4475:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 308 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4475:

30 TAACTGCGGC AACATTTGCT TGTTTTGGTT ATGGTTGGCA CATTGATGTC GGCATTCATA 60  
 CAATACATCT AGTATTATCT GGTATTTTTG ATCGTTATCC AAAGTTAAAT AATGATTATT 120  
 35 GGACATTGGG GTGAGTTTAT CCCATTCTTC TTAGAAACGT ATGGATGAAG CTTATTCGCT 180  
 GACATTTnAC CACCCTGTAA GCTATACTTT AAAAATAATT TTTAATCACA CCGAGTGGCA 240  
 40 TGTTAACGAG CCACAGTTTG ATTTAGTCAA GAAGnAGAGG TATTGTAGAn TCTTATGCGC 300  
 TGATATCC 308

(2) INFORMATION FOR SEQ ID NO: 4476:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 280 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4476:

CCTACCTATC CTGTACAAGC TGTGCCGAAT TnCAATATCA GGCTACAGTA AAGCTCCACG 120  
 GGGTCTTTCC GTTCCTGTGC CGGGTAACCT GCATCTTCAC AGGTACTATG ATTTCAACCGA 180  
 5 GTCTCTCGTT GAGACAGTGC CCAAATCGTT ACGCCTTTTCG TCGGGGTCGG AACTTACnCG 240  
 ACAAGGAATT TCGCTACCTT TAGGACCGTT ATAGTTACGG 280

(2) INFORMATION FOR SEQ ID NO: 4477:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4477:

20 GCTAAGAACC TTTCTTGACT TGTGACAATC GCTTGCTTCT TTCCTCTCCT TCGGCTCTCG 60  
 CTTACTCATT TAGCTCTACT AAACCTCGTTG CGCTCTTTTC TCGTTTCGTC AGATTCAAAC 120  
 25 GTTTTCACTT CGCCAAGCCA TTTTCTTTG TGTTTACTTT TTATTTTGAC GTTTTAGACA 180  
 TAAAAAAGA GACCTCACGG nCTCAACTTG CCTGGCAACG TTCTACTCTA GCGGAACGTA 240  
 ATTGGGCTAC CATCGnCGCT AAAGACCTTT CTTGACTTG 279

(2) INFORMATION FOR SEQ ID NO: 4478:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 base pairs  
 (B) TYPE: nucleic acid  
 35 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4478:

40 GAGGATCCCG GAATGTTGAA CCCATCACTG ATTCTGGTTC ATAATTATCC ATCATCCATA 60  
 ACGTTAAATC TAAAGCGTGT GTACCGATAT CGATTAAATGG TCCTCCACCT TGAGCTTCTT 120  
 45 CGTCTAGAAA GACACCCCAT GTTGGnACTG CTCGACGACG AATGGCATGT GCCTTTCCGA 180  
 AGTAAATGTC TCCTAAGTCG CCACGTTGCG CTGCTTGATG TAAAAATTGA CTATCTGCTC 240  
 \ GGAACGATT TTGATAACCT ATTGTTAATT TT 272

(2) INFORMATION FOR SEQ ID NO: 4479:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 base pairs  
 (B) TYPE: nucleic acid  
 55 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4479:

5 GAAATTGGGA ATCCAATTTT nCTTTGTTGG GGCCCATCCC CAACTTGCAC ATTATTGTAA 60  
 GCTGACTTTT CGTCnCTTAC TGTGTTGGGG CCCTCACCCC AACTCGCATT GCCTGGTAGA 120  
 ATTTCTTTTC GAAATTCTCT GTGTTGGGGC CCCTGACTAG AATTGAAAAA AGCTTGTTAC 180  
 10 AAGCGCATT TCGTTCAGTC AACTACTGCC AATATAACTT CGTAGAGCAT AGAATATTGA 240  
 TTTATGTCCC AGCCTGAGTT AATT 265

## (2) INFORMATION FOR SEQ ID NO: 4480:

## (i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 343 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4480:

20 ACATAGAAAT GCCACTTTTA CAAACAAATG AATATTCGTC TTTTACATC ATTACGCATA 60  
 25 ATAAAAGAAG CTAAGCAACA TGTAAACCGT TGTCACTTAA CTTCTTGTTT TTCCGATGAC 120  
 AGCTTCTATT TAGAGAATGT CATGATTATT TTATATTCAC TTCAATGTTA TCAATATTAG 180  
 30 TGCCATCTAT GACGTCTGCC ATACGATGCT CTGGCAGTTT TTTGGTGGTA ATTCAAACGT 240  
 ATATTCCAC CGTTTTTCATT TAATAACGTT GTCCnGGACC CATGTACCGT AAGATATGTT 300  
 TTCATAGTGG TTCCAATTAA ACCAnTCTTC AGGAACCTCn TAG 343

## (2) INFORMATION FOR SEQ ID NO: 4481:

## (i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 288 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 40 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4481:

45 ACTGCGGCAA TAGCAGCAGC ACCACAAACG GCCTGTGTCC GGACACCTAG GTAATAATGC 60  
 GCATGTTTTT GTCACCATGC CAACAGTTTG TTGACAAAGA GCATCATTAC AATACTGGAA 120  
 50 AATAACGACA CCTACATCGA TGGCTAATAG TTTACTACCT TGACCGATAA TATCGAATAT 180  
 ATTGAGTTTA AGTCCATATA GGATGATTGC AAATCTTAAT AAATATTTAG ATGAAAACGT 240

## (2) INFORMATION FOR SEQ ID NO: 4482:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4482:

GAGGCATCCC CGGGCCTTCC TTCCCAACAG TCGCTTCAAA GTTTGGTGGT AAACCTGnTA 60  
 CATCAAATTA TCGGTGCTAC TGtnAGGTAC GTGTAATCTT CGCTATTTTA TTAGCCGTAT 120  
 CACATCAAGT GGCTTCCCTA CTGGAACCAA TTTGCTATTC GCCTTATTAT CAGGTGCAGG 180  
 ATGGGGATTG GGACAAATCA TTACATTTAA AGCGTTCGAA TTAGTCGGCT CATCTCGTGG 240  
 CCATGCCAGT CACAACAGCA TTCCAATTAT TAGGCGCATC TTTATGGGG 289

## (2) INFORMATION FOR SEQ ID NO: 4483:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4483:

AATCAAAAGT GCACATTATT AAAATATCAA TTTCACACTC AATGCGGCTC ATCGCATTCA 60  
 TTTCTTGTCT AGCAACGTTT TACTCTAGCG GAACGTAAGT TAGCTACCAT CCTCGCTAAG 120  
 AACCTTTCTT GACTTGTGAC AATCGCTTGC TTCTTTCCTC TCCTTCGGCT CTCGCTTACT 180  
 CATTTAGCTC TACTAAACTC GTTGCCTCTT TTTCTCGTTT CGTCAGATTC AAACGTTTnC 240  
 ACTTCGCCAA GncATTTTTTC TTG 264

## (2) INFORMATION FOR SEQ ID NO: 4484:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4484:

CTGTACCACC TATAATCGTT TTAATCGATT GGGGGACGCA TAGGATAGGC GAnGTGGCGA 60

TGAGCTGTGA TGGGGAGAAG ACATTGTGTC TCGAGTCGT TGATTTCACA CTGCCGAGAA 180  
 NAAGCCTCTA GATAGAAAAA GGTGCCCCGTA CCGCAAACCG ACACAGGTAG TCAAGATGAG 240  
 AATTCTAAGG TGAGCGAGCG A 261

(2) INFORMATION FOR SEQ ID NO: 4485:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4485:

ATGCAGCTAT TATTTTTGAC AGATTCCATA TCGTTCAACA TTAAATAGA GAACTTAATA 60  
 AGTATCGTGT ACAAGTTATG AATGAATACC GTAATAAAAA AGGACCTGAT TATACAATTT 120  
 TTAAGAATAA CTGGAAAGTC CTATTGATGG ATACTAGTAA AACCATATTT AGTAAATACA 180  
 GATGGANTAA ATCTTTTAAG GCTTATAAAC GCTCATCTGA CATTGTAGAN GTCATGCTTT 240  
 CAAAAGACGA TATACTACGA C 261

(2) INFORMATION FOR SEQ ID NO: 4486:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4486:

AGCAACATGA TGCACTTCTC GTGTCTCACC AGATTTAGCG ACTAACTTG TAGACATACG 60  
 TAAATCTGCT TTAATAAGTA ATTAATGCAC ATGACTTATT GCGAGTAACA TCGGCATTGC 120  
 AAAGCCATTG CTATCAACTA ATCCACTATC ATCTAACACT AGANTTTGAG CGCCTTGCTT 180  
 TACAGCATTG ACTGCTTCTC GGCCTAATGC TTCTAACGCA TCTTCCAAAT CCCCTTCATA 240  
 TACCGTTGAT AAATAAGTTA 260

(2) INFORMATION FOR SEQ ID NO: 4487:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4487:

5 ATGAGGTGCA TAGGGATAAA ACAGnnAGCA GCAATTGTC GCTATTTGTA AATTGTATCC 60  
 TGGCTTAAGT TGGCCATTTT TCATATGGTC TTCCTTCATT CTCATAAAAG TTGCATCATG 120  
 ATCAGTTTTA GAAAAGCTAT TTCTATCTTT AAGAATCGAT TTTTGTCTT CATATTTATT 180  
 10 TTTTCTTTTCG GAATAATCAT CAAATTTATT TTTGAACCTC TTAATCTTAG TTCTTTTTTA 240  
 CGGGTCTGTT TTCCAATTTG AGTACTATCC TCGTCCCCA ATAGAATGAA TTTAAACCTT 300  
 CCGATTTTCCT TTAAnC 316

## (2) INFORMATION FOR SEQ ID NO: 4488:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 307 base pairs  
 (B) TYPE: nucleic acid  
 20 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4488:

25 CACTTTTACT GCTAAAACGT CAATTGTTGA TGAGTCGTGT TTTATCTCAA GATGTGTTAC 60  
 TCAAAAAGTT ATAGAAGAAG CTAATAAGT TAAACAGAG ATTGATACTG CCAGAAGATA 120  
 30 ACTGTATCTC TCCATCTACT GTAAGTCCGT ATTAGAACTA AAGCGGCTAA TTCATTACGA 180  
 ATTAAACCCT TTAATTGTTT GCCAGACACA TCGTATGGA TGAATTTAAA GCGTnAAAT 240  
 GTACTGGATC ATGAGTTCAT TTTTATAGnT ATGTACnCAT GTGTATAGTA TTTAGAAATA 300  
 35 GACTCAA 307

## (2) INFORMATION FOR SEQ ID NO: 4489:

## (i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 344 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4489:

45 TTGGCAAATG TCATATAACT AGTAACATGA TCATCGACAT CAAATTTAGT ATGATCAAAT 60  
 50 GTTCCCCAAT CATTAAATTG ATTCGGTTGT TTGCTCAATT GATTATATGT TTTTCCTAGC 120  
 ACTTCATGCG GCACCATATC TTTACCTAGT AGCCCCACAA AGATAAGTCT AACAAGTGGC 180  
 55 ACCATAATCG ATAAACTACC GCCACCTGCA CGCTTATGGT AAAACACCCA GCCAGCACTT 240



TAGCAGTATG CCACnCCGGn GACGATATGG TAGCGACGTA AnAA

344

(2) INFORMATION FOR SEQ ID NO: 4490:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 313 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4490:

CCCAACCGGC ACATTGTTGT AAGCTGACTA TATGTCACTT CnTGTGTTGG GGCCCCGTGTC 60

TTCGACTGGC ACTGCTCCCT CAGGAGTCTC GCCATTAATA CTACGTATTA ACATGTAATT 120

TTACTTTTAA ATACTTTAAA AAAATAAGAC ACTTTGGTCC AACTTAAGCC AGGGATACAA 180

TTTACAAATA GCGACAAATT CTCAATTTGT nTTATCCTAT GGACCTATTT CAAAACCCAA 240

CAGGTACTnA GTAACITTTGA ATTCCATTTT TTAACAATGG ATTGCAAAAT GACCTTACGG 300

TTCAITTTGAC CGG 313

(2) INFORMATION FOR SEQ ID NO: 4491:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 291 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4491:

AGGTCTGACT CTAGAGGATC CCCGATGAGT TTAAGAAAAA ATATCAAACA CCTGAATTAT 60

ATTTTAAAGC TTGGCAAGGT TTTTACCACG AGGTTCAAA TGAGCCAGAA CGTGATGAAG 120

TAATGCGTTA TATTCTGACT TTCTTAAATA ACAGCGTCAA TACAATGGGC TTTATTGTTG 180

AAGATGACGA AATTGTAGAA ATTTAATATT CTAAAAAGGT TGGGACATAA ATCCCTAAAA 240

AACAGCAGTA AGATAATTTT CCATTAGAAA ATATCTTACT GCTGTGCnA A 291

(2) INFORMATION FOR SEQ ID NO: 4492:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

GCCGTCTCAG CCTTGSTCTT CGACTGGCAC TGCTCCCTCA GGAGTCTCGC CATTAACTACT 60  
 ACGTATTAAC ATGTAATTTT ACTTTGAAAT ACTTAAAAA ATAAACACT TTGCCCAACT 120  
 5 TACTACTACCA ATAGAACTG CTGTTAGAAT TCCTCAAAT GATATTTTCGC GATATGTTAA 180  
 TGAAATTGTT AAAAAGATAG CTGATAGCGA GATTTCGATGG AATTCAGACA TCATCGTGCG 240  
 10 CGCAACATCC TATCATCTAA AAATGATGTT AAAAATCACC TGCATATTGC ATATACTGCA 300  
 ATCTGGAATT TTCTGGGCCG TGAGAATGAG AAAAATnGAC nTCATGAACA GTGATTGCGA 360  
 ATGGATGTGG GTTAAGCTnC AAGATTCAAA CACCTTGcNT 400

15 (2) INFORMATION FOR SEQ ID NO: 4493:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 265 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4493:

25 TGATCCAGAG ATTTCCGAAT GGGGAAACCC AGCATGAGTT ATGTCATGTT ATCGATATGT 60  
 GAATACATAG CATATCAGAA GGCACACCCG GTAGAACTGA AACATCTTAG TACCCGGAGG 120  
 30 AAGAGAAAGA AAATTCGnTT CCCTTAGTAG CGGCGAGCGA AACGGGAAGA GCCCAAACCA 180  
 ACAAGCTTGC TTGTTGGGGT TGTAGGACAC TCTATACGGA GTTACAAAGG AnGACATTAG 240  
 ACGAATCATC TGGAAAGGTG AATCA 265

35 (2) INFORMATION FOR SEQ ID NO: 4494:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 293 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4494:

45 CATTACTAAA AAAGATAATC AAGGTATGAT TTCACGCGAT GTTTCAGAAT ACATGATTAC 60  
 TAAGGAAGAG ATTTCCCTTGA AAGAGCTTGA TTTTAAATTG AGAAAACAAC TTATTGAAAA 120  
 50 ACATAATCTT TACGGTAACA TGGGTTGAGG AACATCGTT ATTAAATGA AAAACGGTGG 180  
 GAAATATACG TTTGAATTAC ACAAAAACT GCAAnGAGCAT CGTATGGGCA GACGTCATAG 240  
 ATGGGCCCTA TATTGATACC ATTGGAGGTG AATnTAAATA ACCATGCACT CTC 293

55

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4495:

ACTTACAAAG TTCTGTGAAC CAAGTACCAT CAACTGCTGG TATGACGCAA CAAAGTATTG 60  
 ATAACTATAA TGCGAAGAAG CGTGAAGCAG AAACTGAAAT AACTGCAGCT CAACGTGTTA 120  
 TTGACAATGG CGATGCAACT GCACAACAAA TTTCAGATGA AAAACATCGT GTGCGATAAC 180  
 GCATTTAACA GCATTtAAAC CAAGCGAAAC ATGANTTTAA CTGCAGATTA CACATGCCTT 240  
 AGGAGCAAGC AGTGCA 256

## (2) INFORMATION FOR SEQ ID NO: 4496:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4496:

GTCATCAGAA ACCCTTGTC CACAAGGCTT GTATTTTTTA TACTTATTTT TTAAATTAAA 60  
 TTCATCATT TCTAATTAA AACAAATAC TAAACGTTTC ATAATTATCG CCTGTACAAT 120  
 ACGCACAAAA ACATGTCTTG AAACGCCTTT CATTACTCTA AATACCCAA TATACTTTTT 180  
 ATATCGTTCG GATTCTGAGT ATTCAGACG ATTTTCTGCA TAAAAATAAA CGTGTTTCAA 240  
 GGCAATATAT TGCA 254

## (2) INFORMATION FOR SEQ ID NO: 4497:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4497:

AATCGGCTGT CTGATTCTGA ATCGCTATCT GAGTCCGAAT CGnTATCTGA ATCCGAGTCG 60  
 CTATCCGAGT CTGAGTCGCT ATCTGAATCC GAGTCACTGT CGGAGTCGGA ATCACTATCT 120

GAGTCACTGT CGGAATCTGA ATCGCTATCT GAATCCGAAG TCACTGGTCG GGAATCTGAG 240  
TCACTGTnGG AATCTGAATC GCTATCTGA 269

5

(2) INFORMATION FOR SEQ ID NO: 4498:

(i) SEQUENCE CHARACTERISTICS:

10

- (A) LENGTH: 273 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4498:

20

CACCCCGGCA CTATAAAAT GGAGCAGAAG ACGGGATTTCG AACCCGCGAC CCCAACCTTG 60  
GCAAGGTTGT ATTCTACCGC TGAAGTACTT CTGCATATGC GGGTGAAGGG AGTCGAACCC 120  
CCACGCCGTA AGCTTAGnAT ACCTCAAGTC TAGTGCGTCT GCCAATTCCG CCACACCCGC 180  
AAATGGTGAG CCATAGAGGA TTCGAACCTC TGACCCTCTG ATTAAAAGTC AGATGCTCTA 240  
CCAAGTGGC TAAATGGCTC TnAGGTGC CGG 273

25

(2) INFORMATION FOR SEQ ID NO: 4499:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 314 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4499:

40

GTAGTAAAC GCATTTAGTG ATTGAAACAG GCAAGATAGA CGCGGGATAT CACGGCAATT 60  
TAGGGATTAA TATCAAGAAT GACGCTATTG CATCGAATGG TTATATCACA CCAGGTGTTT 120  
TTGAATATTA AAAGGAGAAT CGATTTGAAG TGCnnCATAA GACAATACGG ACTTATCAAA 180  
TCAACGAAGG AGACAACTA GCTCAATTGG TTATCGTGCC TATATGGACA CCTGAACTAA 240  
AGCAAGTGA GGAATTCGAA GTTGTTcAnA CGTGGAGAAA AGGCTCGGAG AGCGGGTGAA 300  
AGCATCTTAG TCGA 314

45

(2) INFORMATION FOR SEQ ID NO: 4500:

(i) SEQUENCE CHARACTERISTICS:

50

- (A) LENGTH: 304 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

55

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4500:

5 ATTGTAAGGC TATCATGTCA AAGATTATAA CAATAAATCT GGTGAGATT TGGTGGCGGG 60  
 GCGATGGAAG CTATCTATTT GACCATCCAT TTGGCAAAGG TTTGGGAGTT ACACAGGTGG 120  
 ACTTAACTTT AATGGCGGTC GTCATATGG TATCGACTTT GGTATGCCTA CAGGAACGAA 180  
 CCATTTATGC TGTAAAAAGG CCGTATAGCT GATAAAGTAT GGnCTGATTA CCGTGGCGGT 240  
 10 AATTCTATAC AAATTAGGAC CCGTGCTAAC GAATGGAnCT GGTATATGCA TTTATCTAnG 300  
 CATT 304

## (2) INFORMATION FOR SEQ ID NO: 4501:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 20 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4501:

25 TTCCTTCATT CTCATAAAAG TTGCATCATG ATCAGATCAG TTTTAGAAAA ACTATTTCTA 60  
 TCTTTAAGAA TCGATTTTIG TTCTTCATAT TTATTTTTC TTTCCGnATA ATCATCAAAT 120  
 TTCTTTTGA ACTTCTTAAT CTCAGTTATT TTTTACGGG TCTGTTTTCT AATTTGAGCA 180  
 30 CAATCTTCGT TCTCAATAAG AATGATTTAA ATCTnCGATT TCTTTATCTA AATGGACTAC 240  
 CAATTAAATC TAT 253

## (2) INFORMATION FOR SEQ ID NO: 4502:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 40 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4502:

45 AGTTCGGTCC CTATCCGTCG TGGGCGTAGG AAATTTTnGA GGAGCTGTCC TTAGTACGAG 60  
 AGGACCGGGA TGGACATACC TCTGGTGAC CAGTTGTCGT GCCAAnGCAT AGCTGGGTAG 120  
 CTATGTGTGG ACGGGATAAG TGCTGAAGAT GCTTAAGCAT GAAGCCCCC CAAGATGAGA 180  
 50 TTTCCCAACT TCGTTTATAA GATCCCTCAA AGATGATGAG GTTAATAGGT TCGAGGTGGA 240  
 AGCATGGTGA CATGTGG 257

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4503:

ATACGTTTAA TACACAAAAA ACTGCAAAGC ATCGATGGCA GACGTCATAG ATGGCACTAA 60  
 TATTGATAAC ATTGAAGTGA ATATANAATA ATCATGACAT TCTCTAAATA GAAGCTGTCA 120  
 TCGGAAAAAC AAGAAGTTAA GTGACAAGnT TTACATGTTG CTTAGCTTCT TTTATTATGC 180  
 GTAATGATGT AAAAAGACGA ATATTCATTT GTTTGTAATA GTGGCATTTC TATGTCTTAA 240  
 AAGTGACGAA ACTTCAAATG TGCCAAGTGT 270

## (2) INFORMATION FOR SEQ ID NO: 4504:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4504:

TACCTTGACC GAAGTTCTTA CCTACATCAC CTAAATTAAT GACATGTCCA CCAGTCATAT 60  
 ACTCTAATCC ATGGTCGCCG ATACCTTCAA CGACAACATC TACACCACTA TTTCTAATAC 120  
 AGAATCTTTC TCCTGCACTA CCGTTAATAA ATGCCTTACC ACTTGTCGCA CCATAGAATG 180  
 AGACGTTACC AGCAATAATT TCATTTTGTC GTTCTTCAAA AGGTGCTTTG ACAATGACCG 240  
 TACCACnGn T 251

## (2) INFORMATION FOR SEQ ID NO: 4505:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4505:

AGAAGTTAAG CTCCTTAGCG TCGATGGTAG TCGAACTTAC GTTCCCGCTA GAGTAGAACG 60  
 TTGCCAGGCA AATGACAAAT CGGAGAATTA GCTCAGCTGG GAGAGCATCT GCCTTACAAG 120

TAGCTCAATT GGTAGAnCAC TGACTTGTA TCACTAGGTT GGGGGGTCAG TCCTCTGGCC 240  
GGCACCATCT TTTGnCCATA 260

(2) INFORMATION FOR SEQ ID NO: 4506:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4506:

TTCTTTAGTA GATACTAAGG CGTTATTAGA CGCATTAGAC AATGGTGTGA TTAAAGGTGC 60  
AGCACTTGAT ACGTATGAAT TTGAACGCAA ACTTTTCCCA AGTGATCAAA GGGGCAAAAC 120  
ACTGAACGAT CCATTGTTAG AATCGTTGAT TGACAGGGAA GATGTCATAT TAACACCACA 180  
TATTGCGTTT TATACTGAAG CTGCAGTTAA AAATCTATTG TCGTGCATTA GGTGCAACAT 240  
TAGGTGTATT GCAGCTTGGG GAACTTnGnT ACGGGTAAAT TTAAAATCGG CTGTGGGTAT 300  
TTTGnTTTT GGG 313

(2) INFORMATION FOR SEQ ID NO: 4507:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4507:

GnCAATACGG CCAATTCCTA AGATTGCTAC TTCTGGGTGG ATTGATAACT GGAGTGAACC 60  
ATTGTCCACC AGCTGnAACC GATATTACTG ATTGTGCATG TAGCACCTTT CATTTTCATCG 120  
GCTGTTAATT TACCATCAGC TGGCTTTAAC AGCTAATTCA TTAATTTTCAT CTGAAATTTG 180  
GGAAATAGA CTTACGGATC AGCATGTTTA ACAACAGGTA CTAATAATCC TCTATCAGTG 240  
TCTGCTGCAA TT 252

(2) INFORMATION FOR SEQ ID NO: 4508:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 268 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4508:

5 CATCGAACCA GATGTACTCG CACTTGTTGA GTCTGATGTT GAATCACTAA CACTATCAGA 60  
 TAATGACGTT GAATCACTCA TACTTGTTGA TGTACTTGTC GAAAGCGACA TACTTTGTGA 120  
 ATCACTAGTA CTTGTACGCA TCGAAGTACT AGTTGAAGCT GATGTACTAC GAGAGTCACT 180  
 10 TGTTGATGTT GATGTACTTG CTGATCCTGA TGCACCTGTA CTTCTTGATG TGCTTTGTGA 240  
 ATCGGATTTC GCTCGTGCnT GGTACTnG 268

## (2) INFORMATION FOR SEQ ID NO: 4509:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 296 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4509:

25 CGAGAGTGGC TTAATTCGGT TACTGCTATC ACgTAAGGGG CGGAAACCCC CTAACACTTA 60  
 GCACTCATCG TTTACGGCGT rGACTACCAG GGTATCTAAT CCTGTTTGAT CCCCACGCTT 120  
 TCGCACATCA GCGTCAGTTA CAGACCAGAA AGTCGCCTTC GCCACTGGTG TTCCTCCATA 180  
 30 TCTCTGCGCA TkTCACCGCT ACACATGGAA TTCCACTTTC CTCTGCTGGC ACTCAAGTTT 240  
 TCCAGTGTCC AATGACCCTC CACGGTTGAG CCGTGCGGCTT nCACATCACA CTTAnA 296

## (2) INFORMATION FOR SEQ ID NO: 4510:

35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 257 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4510:

45 TTACTACTTA CTGAGTGACC TGTACCTGCT TTCGGAGTAA TTGTGATTGA TGAATTTGGT 60  
 TTTATAGTAT TGGCATTGAA CGTCACTTTA CCAGTTTGTC CATCTAACGT TACATAGTCA 120  
 GGCTTATTCG CAATTGTCCA TTGnTTATTT TGACCACGAA CAACATTAAT TGTCTTACTA 180  
 50 TGTGCTGCA CCATTACCCA CTTnTTTCACT GTAAGCAATA TCCATTGCTT GAGTTGGGAT 240  
 TAATTAAATG GTCCTGA 257

## (2) INFORMATION FOR SEQ ID NO: 4511:

55



(A) LENGTH: 250 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4511:

10 AAAATCACAT CAGCCTGCAT TAACGACGTC GTTAATTTAT ATACATCTCC TG TAGTATCT 60  
 AGATAATTCT TTCCAACGCT AAATTCTAAT TCAAGTTCTC GTAAATCCAT CAACTCTATT 120  
 15 TGATGTCCCT CATTGATGAC TTCTAGTTCA TTTTITAAAT CATCCATAGC AATTCTCGTT 180  
 TTAGAACCTA CTGTGGAACC TGACAATAAT ACAATATTCA nGAnGACGCC CCTCCTATTT 240  
 TGATAAATGC 250

20

(2) INFORMATION FOR SEQ ID NO: 4512:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 253 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4512:

30 AGCTGGnTTC GAACCAACGA GTGACGGAGT nAAAGTCCGT TGCCTTACCG CTTGGCTATA 60  
 GCCCAATATA TAGATGGTGG AGGGGGGCAG ATTCGAACTG CCGAACCCGA AGAGCGGATT 120  
 35 TACAGTCCGC CGCGTTTAGC CACTTCGCTA CCCCTCCAGC TTATTCATAT AATTTAATAA 180  
 TCAAAATGGT GGAAGAATGA CGGGTTCGAA ACCGCCGACC CTCTGCTTGT AAGGCAGATG 240  
 CTCTCCCCAG CTG 253

40

(2) INFORMATION FOR SEQ ID NO: 4513:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 252 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4513:

50 GnCGACCCTT AATAACTTAA TCTATGTTTC CACCATTTT ATAAGTCAAA CGTTAACATG 60  
 nAAGTTACGT TCTTTTATAA AAAGATTAA ACGCGTTATT AATCTTGTGC AGTGTTCCTT 120  
 55 CGAACACTAG CGATTATTTT TTATGAATTC AAGCTTATTT AAAACTCTTT ATTCACTCGG 180

GTGGAGACTA GC

252

## (2) INFORMATION FOR SEQ ID NO: 4514:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 244 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4514:

GTCAATTGAAT ATGGAAACTT TAGAATTACA AGGCGCTAAA TTACGATACC ACCAAGTCGG	60
ACAAGGACCC GTGCTCATCT TTATTCCTGG TGCAAACGGT ACCGGAGACA TTTTCTGCC	120
TCTTGCAGAA CAGTAAAAG ACCATTTTAC TGTGTAGCC GTTGATCGTC GTGATTATGG	180
AGAAAGCGAG TTAAGTGAAC CACTCCCTGA TTCCGCTTCA AACCCTGACA GTGATTATCG	240
TGTC	244

## (2) INFORMATION FOR SEQ ID NO: 4515:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 243 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4515:

TATTAGGCAA ATCCGGTACT CGTTAAGGCT GAGCTGTGAT GGGGAGAAGA CATTGTGTCT	60
TGGAGTCGTT GATTTCACAC TGCCGAGAAA AGCCTCTAGA TAGAAAATAG GTGCCCCGTAC	120
CGCAAACCGA CACAGGTAGT CAAGATGAGA ATTCTAAGGT GAGCGAGCGA ACTCTCGTTA	180
AGGAACTCGG CAAAATGACC CCGTAACTTC GGGAGAAGGG GTGCTCTTTA GGGTTAACGC	240
CCA	243

## (2) INFORMATION FOR SEQ ID NO: 4516:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 267 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4516:

GATTGTCCTT TGGACAATGG TAGGAGAGCG TTCTAAGGGC GTTGAAGCAT GATCGTAAGG 120  
 ACATGTGGAG CGCTTAGAAG TGAGAATGCC GGTGTGAGTA GCGAAAGACG GGTGAGAATC 180  
 5 CCGTCCACCG ATTGACTAAG GTTCCAGAG GAAGGCTCGT CCGCTCTGGG TTAGTCGGGT 240  
 CCTTAAACCT GAGGCCGCAA nnGTAGG 267

## (2) INFORMATION FOR SEQ ID NO: 4517:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 319 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4517:

20 TTGAATCTGA CGAAACGAGA AAAGAGCGCA ACGAGTTT TAGAGCTAAA TGAGTAAGCG 60  
 AGAGCCGAAG AGAGGAAAGA AGCAAGCGAT TGTCACAAGT CAAGAAAGGT CTTTAGCGAC 120  
 GATGGTAGCC AACTTACGTT CCGCTAGAGT AGAACGTTGC CAGGCAAAAA ATGGGATGCG 180  
 25 ATGAGCCGCA TTGGAGACCG CAGTCCTnTn TnTTTTTTTA TGGCCTTAAA ACGTCAAAT 240  
 TAAAAAGTTA AACACAAAGA AAATGGGCTT TGGCGAGTGG AAACGTTTTG AATCTGGACG 300  
 GAACGAGAAA GAGCGCAGC 319

## (2) INFORMATION FOR SEQ ID NO: 4518:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 259 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4518:

40 GGTATAATAG ATGACTATGT ACTATTTCCG GTACATCCTT GGCAATATCA GCATATTCTG 60  
 CCGAACGTCT TTGCGAAAGA GATTAGTGAA AAGTTGGTTG TACTATTACC GTTAAAATTT 120  
 45 GGAGATTATC TGTCGTCTTC AAGTATGCGT TCATTAATTG ATATTGGCGC ACCGTATAAC 180  
 CATGTCAaNG TACCATTTC AATGCAGTCA TTAGGCGCAT TAAGGCTAAC GnCTACGGTT 240  
 ACATGAAAAA CGGGGAACA 259

## (2) INFORMATION FOR SEQ ID NO: 4519:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 253 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4519:

	ATAGGGTGTGTT GCTGAATAGG GCGTTTAGTA TTTGGTCGTA CCGnnAACCA GGTGATCTAC	60
10	CCTTGGTCAG GTTGAAGTTC AGGTAACACT GAATGGAGGA CCGAACCGAC TTACGTTGAA	120
	AAGTGAGCGG ATGAACTGAG GGTAGCGGAG AAATTCCAAT CGAACCTGGG AGATAGCTGG	180
	TTCTCTCCGA AATAGCTTTA GGGCTAGCCT CAAGTGATGA TTATTGGAGG TAGAGCACTG	240
15	TTTGGACGAG GGG	253

(2) INFORMATION FOR SEQ ID NO: 4520:

	(i) SEQUENCE CHARACTERISTICS:
20	(A) LENGTH: 245 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4520:

	AACTCGTTGC GCTCTTTTCT CGTTTCGTCA GATTCAAACG TTTTCACTTC GCCAAGCCAT	60
30	TTTTCTTTGT GTTTACTTTT TATTTTGACG TTTTAGACAT AAAAAAAGAG ACCTCACGGT	120
	CTCAACTTGC CTGGCAACGT TCTACTCTAG CCGAACGTAA GTTGGChACC ATCGTCGCTA	180
	AAGACCTTTC TTGACTnGTG ACAATCGCTT GCTTCTGTCC TCTCCTTCGG CTCTCGCTTA	240
35	CTCAT	245

(2) INFORMATION FOR SEQ ID NO: 4521:

	(i) SEQUENCE CHARACTERISTICS:
40	(A) LENGTH: 251 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4521:

	GGGCCTAAGT GGA CTGGAAC CACCGACCTC ACGCTTATCA GGCGTGCGCT CTAACCAGCT	60
50	GAGCTATAGG CCCATTAAATT TGAATGAACA AACATTCAAA ACTGAATACA ATATGTCACG	120
	TTATTCCGCA TCTTCTGAAG AAGATGTTCC GAATATATCC TTAGAAAGGA GGTGATCCAG	180
55	CCGCACCTTC CGATACGGCT ACCTTGTTAC GACTTCACCC CAATCATTTG TnCCCACCTT	240

## (2) INFORMATION FOR SEQ ID NO: 4522:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4522:

nATAGAACCT GAAACCGTGT GCTTACAAGT AGTCAGAGCC CGTTAATGGT TGATGGCGTG 60  
 CCTTTTGTAG AATGAACCGG CGAGTTACGA TTTGATGCAA GGTTAAGCAG TAAATGTGGA 120  
 GCCGTAGCGA AACGATGTCT GAATAGGGCG TTTAGTATTT GGTCGTAGAC CGAAACCTGG 180  
 TGATCTACCC TTGGTCaGT TGAAGTTCAG GTAACACTGA ATGGAGGACC GAACCGACTT 240  
 ACGTTTGAA 249

## (2) INFORMATION FOR SEQ ID NO: 4523:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4523:

TCCCTATCCG TCGTGGGCGT AGGAAATTG AGAGGAGCTG TCCTTAGTAC GAGAGGACCG 60  
 GGATGGACAT ACCTCTGGTG TACCAATTGT CGTGCCAAG CATAGCTGGG TAGCTATGTG 120  
 TGGACGGGAT AAGTGCTGAA GATCTnAAGC ATGAAGCCCC CCTCAAGATG AGATTTCCCA 180  
 CTTCGGTTAT AAGATCCCTC AAAGATGATG AGGTTAATAG GTTCGAGGTG GAAGCATGGT 240  
 GACAGTGG 248

## (2) INFORMATION FOR SEQ ID NO: 4524:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4524:

AACGTTAAGA TCCCTATTAA ATTATCTTAG GAATCATCAT GGGCATTAT GATGTCTTAA 60

AAATTAGTAA TCTGAATCTG CTTCTAAACC TTGTCATAAT TTGanCGGCT GTGGCTCGnA 180  
 CCAATACGGG TCGGACCTGC TThAACCATT TTATTGGAAA TCTTCTAAAT TACGGACGGC 240  
 5 ACCCGGATGC TTTTACTTCT ATATCAGCAC CTACTGTATC TTTCATTAAT TTAACGGCTT 300  
 CTGCAGTCGG ACCGGCAACT GCAAAA 326

## (2) INFORMATION FOR SEQ ID NO: 4525:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 301 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4525:

AAGAGCACCC TTCTCCGAGT TACGGGGTCA TTTGCCGGTT CCTTAACGAG AGTCGCTCGT 60  
 CACCTTAGAT TCTCATCTTG ACTACCTTGT CGGTTTGCGG TAnGGCACCT ATTTTCTATC 120  
 TAGAGGTTTT CTCGGCATGT GAAATCAACG ACTCGAGACA CAATGTCTTC TCCCATCACA 180  
 25 GTCAGCCTTA ACGAGTACCG GATTTGCCTA ATACTCAGCC TACTGCTTAG nGGCATCCAT 240  
 CGCAGTThGC TATCCACTGG TCCCCCTCGA TTAAACGATT ATAGGTGGTA CAGATATCAA 300  
 C 301

## (2) INFORMATION FOR SEQ ID NO: 4526:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4526:

TGATATTATG AGCTGTGTTT TTAGCTTTAG AACCGAAGTC CCCTGCTTTT TTACCAAGAT 60  
 TTTCAGTAAC TTGThCCATC CATTTTTTCT TTTTCGTACC ACCATGGAAT TTTGGCAAAA 120  
 45 CACCCATCCG CTGTAACTTC AGAGTGTGTCAT TGGCATTAT TACACTATCT CCAACTCCTA 180  
 GTGGAACAAC CACATCTCGT CCTTGGGGTG CATGGAATGT nCCGTCAGCC CTGTGAATTA 240  
 T 241

## (2) INFORMATION FOR SEQ ID NO: 4527:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4527:

CGATCACACT CTTCCGTCGT CATCGCCATT GGCTTTTCAC ACAATACATG GACACCATGG	60
10 TGTCAATGCT TCTATAGAAA GATCAGCATG GAATTTATTA GGTGTACAAA TGACCACCGC	120
ATCAACAAGT TTAACAGCT CGCTAGGTGT CTCAACTGCA TGAGGTATAT TGAAAGCGCT	180
TGCACCAT nCAATCATCT GGCCTGTTA TTGAATATCT TGTGACTGGC AACTTAATGA	240
15 GnACTGTGTC TTTTGGAGTT TCCAGnCAAT GCCGGAATT ATGGACGGGT CTTGGTGGCA	300
ATACCACCCA ACACCT	316

20

(2) INFORMATION FOR SEQ ID NO: 4528:

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(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 251 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4528:

30 GTCCCAAGGG TTGGGCTGTT CGCCATTAA AGCGGTACCG ACGACTGGGT TCAGAACGTC	60
GTGAGACAGT TCGGTCCCTA TCCGTCGTGG GCGTAGAAAT TTGAGAGGAG CTGTCCTTAG	120
TACGAGGAGG AnCGGGATGG ACATACCTCT GGTGnACCAG TTGTCGTGCC AACGGCATAG	180
35 CTGGGTAGCT ATGTGTGGAC GGGATAAGTG CTGAAAGCAT CTAAGCATGA AGCCCCCCTC	240
AAGATGAGAT T	251

40

(2) INFORMATION FOR SEQ ID NO: 4529:

45

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 318 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4529:

50 AGTACGTGAC GTTCACTACT CTCCTATGG CCGTATGTGT CCAATTGAAA CACCTGAGGG	60
ACCAAACATT GGATTGATTA ACTCATTATC AAGTTATGCA CGTGTAATG AATTCGGCTT	120
TATTGAAACA CCATATCGTA AAGTTGATTT AGGATACACA TGCTATCACT GATCAAATGA	180

55

ATGGTCGTTT AGGTGATGAG TGTATGCGTT CGGGnACnAT CAGTATGCAA GAAAAGGTTT 300  
 GTGACGCGAC AGTGTChA 318

5 (2) INFORMATION FOR SEQ ID NO: 4530:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 240 base pairs  
 (B) TYPE: nucleic acid  
 10 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4530:

TAGCTGTGTG ATAAATTGCA AGTGCGGCAC CACATAAGCC GAACATCATC GTAATAAAAC 60  
 GGCCTGACAT ACAGCGTGAC ACACCTGAAT AATACTTCGT CACATCTGGA TCACCAAGTT 120  
 20 GAGCAAAGAn GATGTTCTnC GTACCTTGAA CTAAGTGCCC TTTGACTTCT AAAGTACCAC 180  
 CAAGTGCCGT CTGCCAAAAC GGTAAGTAAA AAATATGGTG TAAACCGAGT GGACCTAACA 240

(2) INFORMATION FOR SEQ ID NO: 4531:

- 25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 254 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4531:

CGGCTCTTCT GGGACGTAA CCCTAAAGTG CACCCCTTCT CCCGAATTAC GGGGTCATTT 60  
 35 TGCCGAGTTC CTTAACGAGA TTCGACTCGn TCACCTTAGA ATTCTCATCT TGA CTACCTG 120  
 TGATCGGTTT GCGGTTAGGG GCACCTATTT TCTATCTAGA GGCTTTTCTC GGCAGTGTGA 180  
 40 AATCAACGAC TCGAAGACAC AATGTCTTCT CCCCATCACA GCnCAGCCTT AACGAGTACC 240  
 GGATTTGCCT AATA 254

(2) INFORMATION FOR SEQ ID NO: 4532:

- 45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 238 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4532:

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TGAATAAACC GAATGTGGCT AAAGTCGTTA ACGCAAATA TGACGTCATC TATAACGGAC 120  
 ATACTTTTGC AACATCTTTA CCAGCGnAAT TTGTAGTAAA AGATGTGCAA CCAGCGAnAC 180  
 5 CAACTGTGAC TGAAACAGCG GCAGGAGCGA TTACAATTGC ACCTGGAGCA AACCAAAC 238

(2) INFORMATION FOR SEQ ID NO: 4533:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4533:

GGTCATTAAT AAAATATCTA AAGCCATTAC TGCATAAAAA TCTCATCAAG CCAATACCTA 60  
 20 CATTGTACTA CTGGnCACTT TAGACAGGnC AAGGGTGTAG CTACCGATAA TTCAGGAGCA 120  
 TTAACGCAAC CGACATTTGA CTGTATTAAA TGATAGAGGT TCTGGAAAAC GCCCCAGGTG 180  
 GTGGAGTTCA AGAAATAATT CACAGGGCTG ACGGAACATT CCTGCACCCC AAGGACGAGA 240  
 25 TGTGGTTGTT CCACTAGGAG TTGGAA 266

(2) INFORMATION FOR SEQ ID NO: 4534:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4534:

TACTCAGAGG ATACCCCGAC GTAATGCATT CAATTCAATT TTTAAACGTA TTATTTTCATT 60  
 40 GAGCAGAAAG AAAATTATGG CACCAAACCTT TAATATTTTT TTCAATGTCA TTCTTTTGAn 120  
 GGGAGTGGGA CAGAAATGAT ATTTTCGCAA AATTTATTTTC GTCGTCCCAC CCCAACTTGG 180  
 CATTGTCTGT AGAAATTGGG AATCCAATTT CTCTTTGTnG GGGCCCATCC CCAACTTGCA 240  
 45 CATTATTGTA AGCTGACTTT TCGT 264

(2) INFORMATION FOR SEQ ID NO: 4535:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4535:

5 GCGAATGGAT AACAGTTGAT ATTCCTGTAC CACCTGATAA ATCGTTTTAA TCGATGGGGG 60  
 GACGCATAGG nATAGGCGAC TGCCGATTGG ATTGCACTCT AAGCAGTAAG GCTGAGTATT 120  
 AGGCAAATCC GGTACTCGTT AAGGCTGAGC TGTGATGGGG AGAAGACATT GTGTCTTCGA 180  
 GTCGTTGATT TCACACTGCC GAGAAAAGCC TCTAGATAGA AAATAGGTGC CCCGTACnGC 240  
 10 AAACCGACAC 250

## (2) INFORMATION FOR SEQ ID NO: 4536:

## (i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 235 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4536:

20 AATGACGGGT TCGAACCGCC GACCCTCTGC TTGTAAGGCA GATGCTCTCC CAGCTGAGCT 60  
 25 AATTCTCCGA TTTAAACTG CCTGGCAACG TTCTACTCTA GCGGAAnTAA TTCGAACtAC 120  
 CATCGACGCT AAGGAGCTTA ACTTCTGTGT TCGGCATGGG AACAGGTGTG ACCTCCTTGC 180  
 TATAGTCACC AGACATATGA ATGTAATTTA TACATTCAAA ACTAnATAGT AAGTA 235

## (2) INFORMATION FOR SEQ ID NO: 4537:

## (i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 234 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4537:

40 TGCATCTTCA CAGGTACTAT GATTTCACCG AGTCTCTCGT TGAGACAGTG CCCAAATCGT 60  
 TACGCCTTTC GTGCGGGTCG GAACTTACCC GACAAGGAAT TTCGCTACCT TAGGACCGTT 120  
 45 ATAGTTACGG CCGCCGTTTA CTGGGGCTTC GATTCTGAGC TTCGCAGAAG CTAACCACTC 180  
 CTCTTAACCT TCCAGCACCG GGCAGGCGTC AGCCCTATAC ATCACCTTAC GGTT 234

## (2) INFORMATION FOR SEQ ID NO: 4538:

## (i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 242 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4538:

5 ACCCTCTGCT TGnAGGCAG ATGCTCTCCC AGCTGAGCTA ATTCTCCGAT TTAAAAGTGC 60  
 CTGGCAACGT TCTACTCTAG CGGAACGTAA GTnGACTACC ATCGACGCTA AGGAGCTTAA 120  
 CTTCTGTGTT CGGCATGGGA ACAGGTGTGA CCTCCTTGCT ATAGTCACCA GACATATGAA 180  
 10 TGTAATTTAT ACATTCAAAA CTAGATAGTA AGTAAAAGTG ATTTTGCTTC GCAAACCATT 240  
 TA 242

## (2) INFORMATION FOR SEQ ID NO: 4539:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 234 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 20 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4539:

25 TCATTAACAC CATCACCATA AATAAACCT TCCATATCTG TTCCTGTGCC AATAAGCCA 60  
 TATTGCGTTT GgnCTGTCGT GCCAGTGCAA GATTTCAC GATAATTTCT AGGCGTCACT 120  
 GCTGGCGAAC CATCTAATGG ATAATCATAA TCCATCGTGC GTCCAAGAAG TACTTGnTTT 180  
 30 ATTTAAAGTT TGTATTGTGG AATCCTGTGC ACATGTTCTC ACTCCTCTGT ACCT 234

## (2) INFORMATION FOR SEQ ID NO: 4540:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 242 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 35 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4540:

ACACAAAGAA AAATGGCTTG GCGAAGTGAA AAcnGTTGAA TCTGACGAAA CGAGAAAAGA 60  
 45 GCGCAACGAG TTTAGTAGAG CTAAATGAGT AAGCGAGACC GAAGAGAGGA AAGAAGCnAG 120  
 CGATTGTCAC AAGTCAAGAA AGGTTCTTAG CGAGGATGGT AGCTAACTTA CGTTCCGCTA 180  
 GAGTAGAACG TTGCTAGACA AGAAATGAAT GCGATGAGCC GCATTGAGTG TGAAATTGAT 240  
 50 AT 242

## (2) INFORMATION FOR SEQ ID NO: 4541:

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(A) LENGTH: 240 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4541:

10 GCCCTTAATA ACTTAATCTA TGTTTCCACC ATTTTATATA GTCAAACGCT CACATACGGC 60  
 TTCGTTTTCA TTATTTTAAA TGCTCATTTA CATAAGTAAA CTCTGCTTTA AAATAATTTA 120  
 ACTCATTGTC TGCTAAACGT TTTCTTTTAT AAAAAGATTT AAACGCGTTA TTAATCTTGT 180  
 15 GnAGTGTCTCT TTCGAACATA GCGGATTATn TCTTATGAAT TCAAGCTTAT TTAAAACTCT 240

(2) INFORMATION FOR SEQ ID NO: 4542:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 242 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4542:

AAGCTAGCAA TGATGTCAAG CAATGGCAAC ATGTGCTCAn TTAGCTAATA TGCAAGCACA 60  
 30 TGGTGAATAT GACGAGGTTG CAACTTCAAC GCGGAGGnTG ATGAATGCCT TACGTTTGCG 120  
 TGAGACAGTA GCTATGGGCC GCGGTATTAC AGGTGGTAAT GGCATACTGA GCTGACGATT 180  
 ATGATATTGT CACGTTTTCT TCTCTGTATG CAGAAGCGAT TTACACGTAC GAGGTACACA 240  
 35 TG 242

(2) INFORMATION FOR SEQ ID NO: 4543:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 239 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4543:

TGGTGAGCCA TAGAGGATTC GAACCTCTGA CCCTCTGATT AAAAGTCAGA TGCTCTACCA 60  
 50 ACTGAGCTAA TGGCTCTTCC ATGGTGCCGG CCAGAGGACT TGAACCCCCA ACCTACTGAT 120  
 TACAAGTCAG TTGCTCTACC AATTGAGCTA GGCCGGCAAT ATGTAAGATT AAATGGTGGA 180  
 55 GANTGACGGG TTCGAACCGC CGACCCTCTG CTTGTAAGGC AGATGCTCTn CCAGCTGAG 239

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 239 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4544:

ATAGAGGATT CGAACCTCTG ACCCTCTGAT TAAAAGTCAG ATGCTCTACC AACTGAGCTA 60  
 ATGGCTCTTC CATGGTGCCG GCCAGAGGAC TTGAACCCCC AACCTACTGA TTACAAGTCA 120  
 GTTGCTCTAC CAATTGAGCT AGGCCGGCAA TATGTAAGAA TAAATGGTGG AGAATGACGG 180  
 GTTCGAACCG nCGACCCTCT GCTTGTAAGG CAGATGCTCT nCCAGCTGAG CTAAATTCT 239

(2) INFORMATION FOR SEQ ID NO: 4545:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 233 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4545:

AATTCATGCT TTCAAAAGAC GATATACTAC GACACTCCTA CGAACTTGTC CAAGGATTAC 60  
 GAAAAGACCT AAGGTTATGT AATTGGCCTA AATTTATTAA TCGTTTAAAT TCAGTTAGTA 120  
 AAAAGTCTGT GAGTAAGGGT GTATGGAAAG TGGTTAATA TTATAGAAAA CATCAAAGGA 180  
 TGTTAAGAAA TACnATTTAT TACCCAGCAT TTAATAATGG TGCTATAGAA GGA 233

(2) INFORMATION FOR SEQ ID NO: 4546:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 247 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4546:

ACTTTGTTGT CTTCCATCAA CTTGAGACTT CATAACGTTT TGCATCTTCG CCACCTTCAC 60  
 CACTATTACT CTTTCCACCT AATTGGTTCA TGGCTTGTC TAnTTTTTCA TGTGCTTCCG 120  
 CTGAAATCGA TCCATAACTC ATCGCCCCTG TATTAAAGCG TTTGACAATG TCACTTACCG 180  
 GTTCAACTTG GncGATGTCA ATCGGTGTAC ATGCTTTAAA TTCAAGTAAA TGTCTAATGT 240

## (2) INFORMATION FOR SEQ ID NO: 4547:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4547:

GAGGAAATTA CTGAAAACAA TCATCATATT TCTCATTCTG GTTTAGGAAC TGAAAATGGT 60  
 CACGGTAATT ATGGCGTGAT TGAAGAAATC GAAGAAAATA GCCACGTGGA TATTAAGAGT 120  
 GAATTAGGTT ACGAAGGTGG CCAAATAGC GGTAATCCAG TGCATTTGAG GAAGACACAG 180  
 AAGAAGTTTA AACCGAAATA TGnAACCAAG GTGGGCATTA TCGTTGGTTA TCGATTTTCG 240  
 ATAGTGTACC TCAAATTTCA TGGGTCCAAA TTAATGGTTA ACCCATCCAT TCGAnGnAGG 300

## (2) INFORMATION FOR SEQ ID NO: 4548:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4548:

TTGCTATAGT CACCAGACAT ATGAATGTAA ATTATACATT CAAAACTAGA TAGTAAGTCA 60  
 AAGTGATTTT GCTTCGCAAA CATTTATTTT GATTAAAGTCT TCGATCGATT AGTATTCGTC 120  
 AGCTCCACAT GTCACCATGC TTCCACCTCG AACCTATTAA CCTCATCATC TTTGAGGGGA 180  
 TCTTGATAAA CCGnAAGTTG GGGAAATCTC ATCTTTACGG GGGGGCTTCA TGCTTAGGAT 240  
 GGCTTTnCAG CACTTTATGC CCGGTnCCAC ACATTAGGCT TACCCAGCCT ATGCCCCTTT 300  
 GGCACG 306

## (2) INFORMATION FOR SEQ ID NO: 4549:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4549:

CTTCTACTTT TGTACCATCA ATAAGATTTT GCTTTAAACA TTGACTATGA AACTGGATAA 120  
 ATAAAGATTTC AATTAAACGCA TCAGTATTAG GATTCACCTCT AATACGATTA ATAGTTTTAT 180  
 5 AAGAAGGTGn TTGATTTTGA GCTAACCACA TCATTGGAAT ACTGTCATGn AG 232

(2) INFORMATION FOR SEQ ID NO: 4550:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4550:

CTGGGTTTCAG AACGTCGTAT GnAGTTCGGA TCCCTATCCG TCGTGGGCGT AGGAAATTTG 60  
 20 AGAGGAGCTG TCCTTAGTAC GAGAGGACCG GGATGGACAT ACCTCTGGTG TACCAGTTGT 120  
 CGTGCCAAng CATAAGCTGG GTAGCTATGT GTGGACGGGA TAAGTGCTGA AACATTCTTA 180  
 AGCATGAAGC CCCCCTCAAG ATGAGATTTT CCAACTTCGG TTATAAGATC CCTCAAAGAT 240  
 25 GATGAAGTTA ATAAGTTC 258

(2) INFORMATION FOR SEQ ID NO: 4551:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4551:

TTACAGGCAT GCGAGTTGGG GTGAGGGCCC ACACAGAAGC TGACGAAAAG TCATGACAAT 60  
 40 AATGTGCAAG TTGGGGATGG GCCCACAAG AGAAATTGGA TTCCCAATTT TACAGACAAT 120  
 GCAAGTTGGG TGGGACGACG AAATAAATTT GCGAAAATAT CATTTCTGTn CCCTCCCTCA 180  
 AAAGATGACA TTGAAAAAAT ATTAAAGTTG GTGCCATATT TTCTTCTGCT CATGAATATA 240  
 45 CGTTAAAATT GATTGATCAT CGCGAATTGA TATTATTCTC ATTATAAAAA TACTTATTAC 300  
 ACTTACCGTA TGATAGTTTG nTATATACTC TGATAAAGTC AAACCTAATA GCGTTTCTAG 360  
 50 CTGTGnGTGT TTCATAATTA TATACATTAT CAGGCTTTAA 400

(2) INFORMATION FOR SEQ ID NO: 4552:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4552:

	ATAGGAAACT GCCAATTGGA CGGTTGCCGC ATTCAAACCC AGCAGGATTA CGGCGAATTG	60
10	CACGTGAAnC ATTTCTACAG CTTGATCTTG ACCTATGATT TTA CTCTTA AACGATTAGA	120
	AATATTTTTT AAACGTTCAA TATCGTTATC ATCCATTGG AGAACTGGG AATACCATTG	180
	AATCGTTGnA ATAGTATCTG GAAATATCAT GGAAGTAG CAACAGCAGT GTGTTGCACC	240
15	ATTnACTGAT TTTGCTAATT TATCTTGGTG AATGGATTG GATTGTCATT TTGGAATGTG	300
	CGTGCAGCTT TT	312

20

(2) INFORMATION FOR SEQ ID NO: 4553:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 254 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4553:

30	AGCAGCGATC AAAATAATC CGCAATACGC TGGCAAATA CCAATACCAA ACCATAGAAC	60
	AACAAATGGT GCCCATGCTA TCGGAGATAT CGGCCTAATC AATTGAAATA GCGGTTGAT	120
	AGCGTTGTAT AGCCAACGAT TCCTTCCAAG CAAGAAGCCC AATGGAATAG CAACCAACAA	180
35	TGCGACAACA AAGnCCGCTA CAAATCTCCA TGAACATAATT GCTAAATGTG GnGAATTCT	240
	CCAGTAACAA TGGA	254

40

(2) INFORMATION FOR SEQ ID NO: 4554:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 251 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4554:

50	GGTCTGAATC GCTATCTGAG TCTGAATCGC TATCTGAGTC TGAATCACTG TCTGAGTCCn	60
	AGTCACTGTC TGAATCTGAC TCACTATCTG ATTCTGAGTC GCTATCTGAT TCTGAGTCGC	120
	TGTCTGGAAT CTGAATCACT GTCTGGAATC CGAATCGCTA TCTGGATCTG AGTCGCTATC	180

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CTGGGGCTTG G

251

(2) INFORMATION FOR SEQ ID NO: 4555:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 251 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4555:

TACACAAAGA GATAAATTAC TTATGCAAAG GCGGAGGAAT CACATGTCTA TTACTGAAAA 60  
 ACAACGTCAG CAACAAGCTG AATTACATAA AAAATTATGG TCGATTGCCA ATGATTTAAG 120  
 AGGGAACATG GATGCGAGTG AATTCGGTAA TTACATTTTA GGCTTGATTT CTATCGCTTC 180  
 CTATCTGAAA AAGCCChACC AGAATATGCA GTGCCCTGTC AAGnGAAGAC ATCACGTTCC 240  
 AGAAGCATGG C 251

(2) INFORMATION FOR SEQ ID NO: 4556:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 243 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4556:

AGCTACCCCG GGGATAACAG GCTTATCTCC CCAAGAnTT CGCATCGACG GGGAGGTTTG 60  
 GCACCTCGAT GTCGGCTCAT CGCATCCTGG GGCTGTAGTC GGTCCCAAGG GTTGGGCTGT 120  
 TCGCCCATTA AAGCGGTACG GAGGCTGGGT TCCGAACGTC GTGAGnCCGT TCGGTCCCTA 180  
 TCCGTCGTGG GCGTAGGAAT TTGAGAGGAG CTGTCCTTAG TACGAGAGGA CCGGGTGGAC 240  
 ATA 243

(2) INFORMATION FOR SEQ ID NO: 4557:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 235 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4557:

TCATTATTTT AAATGCTCAT TTACATAAGT AAACCTGCT TTAAAATAAT TTAACCTATT 120  
 GTCTGCTAAA CGTTTTCTTT TATAAAAAGA TTAAACGCG TTATTAATCT TGTGAGTGTT 180  
 5 CTTTCGAACA CTAGnCGATT ATTTCTTATG AATTCAAGCT TATTTAAAAC TCTTG 235

## (2) INFORMATION FOR SEQ ID NO: 4558:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4558:

CCGTTAAGCA CTAAATCCGC TTAATAACGG CTTTCTATCG CGCGCAACAT CTCGTTTGAC 60  
 20 TGCTTTTTCT TTCAAAGCTT GACGTTATCA TATTTTTTCT TACCTCGTGC ACACCAAGTA 120  
 ATACTTTACA ATGTCCATGC TTCAAATAAA GCTTTAACGG ACAATCGAAT AACCAAnCTC 180  
 ACGTGTTTGA TCACCCAATT TAATGATTTT ACGCTTGTGC AATAATnATT TTCGAGACGA 240  
 25 GAGGATCGGA TTAAACGAT CCCCTCCTCG TATGG 275

## (2) INFORMATION FOR SEQ ID NO: 4559:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4559:

TTATATGGAT GTATCGCCGA AGCAAGTTGT TTCAGCAGCG ACAnATGTAT TCCGATGACT 60  
 40 CAAACCGTGC ATTGATGGGT GCGAACATGC AACGTCAAGC AGTGCCTTTG GATGAATCCA 120  
 GAAGCACCAT TTGTTGGTAC AGGTATGGAA CACGTTGCAG CACGTGTATT CTGnGTGCGG 180  
 CTATTACAGC TAAAGCACAG AGGTCGTGTT GAACATGTTG GAATCTAATG AAAT 234

## (2) INFORMATION FOR SEQ ID NO: 4560:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

TTATTTTGAC GTTTTAGACA TAAAAAAGA GACCTCACGG TCTCAACTTG CCTGGCAACG 60  
 TTCTACTCTA GCGGAANTAA nTGGCTACCA TCGTCGCTAA AGACCTTTCT TGACTTGTGA 120  
 5 CAATCGCTTG CTTCTTTCCT CTCCTTCGGC TCTCGCTTAC TCATTTAGCT CTACTAAACT 180  
 CGTTGCGCTC TTTTCTCGTT TCGTCAGATT CAAACGTTTT CACTTCGCCA AG 232

## (2) INFORMATION FOR SEQ ID NO: 4561:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4561:

20 TCAAAGGACG CATACCATTA CGGGTCTGCT ACTTGTAAGC ACACGGTTTC AGGTTCTATT 60  
 TCACTCCCCT TCCGGGGTGC TTTTnACCTT TCCCTCACGG TACTGGTTCA CTATCGGTCA 120  
 CTAGAGAGTA TTTAGCCTTA GGAGATGGTC CTCCAGATT CCGACGGAAT TTCACGTGCT 180  
 25 CCGTCGTACT CAGGATCCAn TCAAGAGAGA CAACATTTTC GACTACAGGA TTATTACCTT 240  
 CTTTGATTCA TCTTGTC 257

## (2) INFORMATION FOR SEQ ID NO: 4562:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4562:

40 TACCTAATAA GTTGTGAATT TGAACAGCGG CTGCTTTACA nTGGAAGTGC TGATTCAGTT 60  
 GCCACAATTA CCATACCAAT TTTCTTTTGT TCTTCGTCTG TnATAATGTC CTTAGCAGCG 120  
 TTAGCTCCGA TTGAACGAT GTCTTGGTTT ACAGGACTAA CAGCCATTTT AGTTTGACCA 180  
 45 ATTCCAATTA AAAATTTGTT TGGGTCTACT TGGCGTGGCT TCCTGCTGAA TTTAGCCATG 240

## (2) INFORMATION FOR SEQ ID NO: 4563:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4563:

CAAAGCTTAC TTACAGCTCC CCAAAGCATA TCGTCGTTAG TAACGTCCTT CATCGGCTTC 60  
 5 TAGTGCCAAG GCATCCACCG TCGGCCCTTA ATAACTTAAT CTATGTTTCC ACCATTTTAA 120  
 TAAGTCAAAC GCTCACATAC GGCTTCGTTT TCATTATTTT AnATGCTCAT TTACATAAGT 180  
 10 nGACTCTGCT TTAATAAAT TTAATCATT GTCTGCTAAA CGTTT 225

## (2) INFORMATION FOR SEQ ID NO: 4564:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 233 base pairs  
 15 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4564:

TGTTAATTGG nGAATTTGGA TACTGGTTAT ATTcAGCTGC ACCGCAAGCA ACTTCTATTG 60  
 ATGGCCTAAC TGCCTTTTAA CCTCAAGCAA TGGGTATGGT AATTGTTGCA GTCATTTATG 120  
 25 GCTTTATGAA TATGAAAGCA GAGGAATCCC ATTCCCGTAA TAAAATTACG GTGGTTACAA 180  
 AATTATTTCA GGTTTCTTTC TTTTGcATTG GGGTGCTTTA ACCATATCTT nTT 233

## (2) INFORMATION FOR SEQ ID NO: 4565:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 225 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 35 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4565:

AGCTCAGATA GCGCTCAGAC TCAGACAGCG ACTCAGATTC AGATAGCGAT TCAGACTCAG 60  
 ACAGCGACTC AGACTCAGAC AGCGACTCAG ACTCAGATAG CGACTCAGAT TCAGATAGCG 120  
 ATTCAGACTC AGACAGCGAC TCAGATTCAG ATnGCGATTC GGAnTCAGAC AGCGATTCAG 180  
 45 ATTCAGACAG CGACTCAGAC TCGGATAGCG ATTCAGATTC AGATA 225

## (2) INFORMATION FOR SEQ ID NO: 4566:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 237 base pairs  
 50 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4566:

CCAACTGGAG CTAATGGCTC TTCCATGGTG CCGGCCAGAG GACTTGAACC CCCAACCTAC 60  
 5 TGATTACAAG TCAGTTGCTC TACCAATTGA GCTAGGCCGG CAATATGTAA GAATAAATGG 120  
 TGGAGANTGA CGGGTTTCGAA CCGCCGAnCC TCTGCTTGTG AAGGCAGATG CTCTCCCAGC 180  
 10 TGAGCTAATT CTCCGATTTA AACTGGCCT GGGCAACGTT CTACTCTAGC GGGAACT 237

## (2) INFORMATION FOR SEQ ID NO: 4567:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4567:

GTTGGAGATA GTGTAATAAT GCCAATGAGC CACTCTGAAG TTACAGCGGA TGGGTGTTTT 60  
 GCCAAAATTC CATGGTGGTA CGAAAAAGAA AAAATGGATG GAAACAAGTT ACTGAAAATC 120  
 25 TTGGTAAAAA AGCAGGGGAC TTCGGTTCTA AAGCTAAAC ACAGCTCATA ATATCAAAAA 180  
 GGTGCAGAGG AAATGGTTGA nnGGCAGCGG ATAAATCAAG ATGGTGCACT TGGTTAGCGT 240  
 30 TAAATCGCGA TGTGTGGGTT AnTACACATC CGGGAAGTAG TAATAAGTAT GTCAGTTTAA 300

## (2) INFORMATION FOR SEQ ID NO: 4568:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4568:

ATCCCGTGGA GGTTCAGTC CTCTCGGCCG CATCAAAATT CTTAATTTAA ATAAGCGGGT 60  
 GTAGTTTAAAT GGCAAAACCT CAGCCTTCCA AGCTGATGTT GTGGGTTTCA TTCCCATCAC 120  
 45 CCGCTCCATA GATAATTTTA ATGAACATTG AAAACTGAAT GACAATATGT CAACGTTAAT 180  
 TCCAAAAACG TAACTATAAG TTACAAACAT TnATTTTAGT ATTTGATGGA GCCTnAATCC 240  
 50 AAACATTCCA 250

## (2) INFORMATION FOR SEQ ID NO: 4569:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4569:

GATCCCCTAG CTTTACGTTT AACTTTATAT GGGTATAACT CGAATATAAT TTGGCGCTCT 60  
10 ATGTCATGGG ACAACGAGTA GACATTTAAT AACGGATCAG GTTCTGGTGA CGGTATCGAT 120  
AAACCAGTTG TTCCTGAACA ACCTGGTGAG CCTGGTGAAA TTGAACCAAT TCCAGAGGnT 180  
TCAGATTCTG ACCCAGGTTT AGATTCTGGG CAGCGnTTCT AATTCAGATA GCGGT 235

15

(2) INFORMATION FOR SEQ ID NO: 4570:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 223 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
20 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4570:

AATCTATTTT TTCTATTGTT AAATCGCTAT CTCCATCTTC TTTTATCTCT GGTATTATTT 60  
TTTCTTCAAC TAAGTCACGA TATAATGTTT TTGAATTTTC GTTCAATTTC GATTCGTGAT 120  
30 TTTGAATACT TTTCTTCCAC ACAAATGTAT ACCTATTGGC ATTAGCnTCT ACTTTTGTAC 180  
CANCAATAAG ATTTTGCTTT AAACATTGAC TATGAACTG GGA 223

35

(2) INFORMATION FOR SEQ ID NO: 4571:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 267 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
40 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4571:

CATGATATTT TGAACCGCAT GGTAAAGTT GCAAAGACGG TCTTGCTGTC ACTTATAGAT 60  
45 GGATCCGCGC TGCATTAGCT AGTTCGTAAG GTAACGGCTT ACCAAGGCAA CGATGCATAG 120  
CCGACCTTAG AGGGTGATCG GCCACACTGG nACTAAGACA CGGTCCAGAC TCCTACGGGA 180  
GGCAGCAGTA GGGAAATTTT CGCAATGGGC GAAAGCTGTA CGGCGCAACG TCGTGTGnAG 240  
50 TGCTGCAGGT TCTTCGGATC GTAAAAT 267

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(2) INFORMATION FOR SEQ ID NO: 4572:

(A) LENGTH: 221 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4572:

10 AATnCAACTT TTACTTACTA TCTAGTTTGT AATGTATAAA TTACATTCAT ATGTCTGGTG 60  
 ACTATAGCAA GgnGGTCACA CCTGTTCCCA TGCCGAACAC AGAAGTTAAG CTCCTTAGCG 120  
 TCGATGGTAG TCGAACTTAC GTTCCGCTAG AGTAGAACGT TGCCAGGCAT AATATTAATC 180  
 15 CACAGTAGCT CAGTGGTAGA GCTATCGGCT GTTAACCGAT C 221

## (2) INFORMATION FOR SEQ ID NO: 4573:

## (i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 230 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4573:

GCAGAAATGC CAGCCGCATT GAGTGAACAC AGAGTTACAG GGTATTCTGT AGCCGAACCA 60  
 30 TTCGGTGCA n TGGGGGAAAA GTTAGGCAAA GGTAAGACTT TGAAACATGG TGATGACGTT 120  
 ATACCTGATG CGTATTGCTG TGTGCTAGTA CTnAGAGGGG AATTGCTTGA TCAACACAAG 180  
 GATGTAGCGC AAGATTGTGA CAAGTTATA AAAAGTCTGG CTTTAAAATG 230

35

## (2) INFORMATION FOR SEQ ID NO: 4574:

## (i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 230 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4574:

TCACATATCG ATAACATGAC ATAATCATG CTGGGTTTCC CCATTCCGAA ATCTCTGGAT 60  
 CAAAGCTTAC TTACAGCTCC CCAAAGCATA TCGTCGTTAG TAACGTCCTT CATCGGCTTC 120  
 50 TAGTGCCAAG GCATCCACCG TGCGCCCTTA ATAACCTAAT CnATGTTTCC ACCATTTTTTA 180  
 TAAGTCAAAC GCTCACATAC GGCTTCGTTT TCATTAnTTT AAATGGCTCA 230

## (2) INFORMATION FOR SEQ ID NO: 4575:

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(A) LENGTH: 309 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4575:

10 CTTACAATAG TGTGCAAGTT GGGGTGGAGC CCCGACACAG AGAAATTAGC TCCTCAATTT 60  
 CTACAGACAA TGCAAGTTGG CGGGGCCCCA ACACAGAAGC TGGCGAAAAG TCAGCTTACA 120  
 ATAGTGTGCA AGTTGGGGTG GGACGACGAA ATAAATTTTG CGAAAATATC ATTTCTGTCC 180  
 15 CACTCCCAAA AAGACCGCAG TAGGATAATT CCATTTGGAA ATACCTTACT GCCnGTTTTT 240  
 AAAGTAATAG CnAATATTTT GGAATTAnGT TTCCTAGTTA ACCATACCAA CTAATGGCCT 300  
 CCTTAAATT 309

20

(2) INFORMATION FOR SEQ ID NO: 4576:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 240 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4576:

30

TGATTCTAGG AATTCAAGCT TATTTAAAAC TCTTTATTCA CTCGGTTTTG CTTGGGTAAA 60  
 ATCTATATTT TACTTACTTA TCTAGTTTTC AATGTACAAA TAATGGTGGG CCTAAGTGGA 120  
 35 CTCGAACCAC CGACCTCAG CTTATCAGGC GTGCGCTCTA ACCAGCTGAG CTATAGGCC 180  
 ATTTTTTTGA ATGTTAAATA AACATCnAAA CTGGRATACC ATATGTCACG GTAATCCGCA 240

35

(2) INFORMATION FOR SEQ ID NO: 4577:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 233 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4577:

50 CTTCGTGTTA AAATTTGATG CACAATGGTC ATCATTTTTA TCTTTCCAAT AAGTACTGTC 60  
 TGGGTAAAAA TnTATTAATT GGGTGGTTTC TGAAATGCAA TCTTTTAAAC GACTTCAGGG 120  
 TAATCTTTTA ACACATGCAT CGCAACGATT GAACCTnAAC TTGAACCTAA TATATAGACA 180

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## (2) INFORMATION FOR SEQ ID NO: 4578:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4578:

TAGGCATACC AAAGTCGATA CCATAGTGAC GACCGCCATT AAAGTTAAGT CCACCTGTGT	60
AACTCCCAAA CCTTTGCCAA ATTGGATGGT CAAATAGATA GCTTCCATCG CCTCGGCCAC	120
CAAAATCTTC AAACCACGAT TTACTTTGnC TACTAATTTT TTTTGTAGCA ATGAGTACGC	180
GCCTTAGCAA TTTTnGTAG CGTAGTCCGC TCCAAAATAA TATTAACTG ACATACTTAT	240
TACnAGTTCC CTGGATGTGT ACATAATCCA CACATCGCGA TTTATCGCTA ACAGAGCACA	300
CTTGATTACG CGCGCTCAAC ATTC	324

## (2) INFORMATION FOR SEQ ID NO: 4579:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4579:

AATGTAAAA CTGATTTCTA TTAATTATTT GATAGAAATC ACTTTTTTGT ATTTTATAAT	60
GTACAGCTCG TTGCATTCAT ATAGCTTGAA GTCACGTTTA AAACCATATC TATCATTATG	120
GTATGCATAT CGTTTAAAC CTATTCTTTT GTTnTAGGA CATATAAATT CATCATTAAAT	180
TCGTCATATT TCCAATTTTG AGTGnAAAA ATGTCACTTT TAAACTTTC	229

## (2) INFORMATION FOR SEQ ID NO: 4580:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4580:

CGGGGACTCn AACCCGTGTT GACCGCCGTG GAAAGGGCGG TGTCTTAACC GCTTGnACCA	60
---	----

CTCTACCACT GAGCTACTGT GGATTAATAT TATGCCTGGC AACGTTCTAC TCTAGCGGAA 180

CGTAAGTTTCG ACTACCATCG ACGCTAAGGA GCTTAACTTC TGTGTTCCGC ATGGGAACA 239

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(2) INFORMATION FOR SEQ ID NO: 4581:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 233 base pairs

(B) TYPE: nucleic acid

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(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4581:

15

CCGnACGAAT TTACACGTGT TCCGTCGTAC TCAGGATCCA CTCAAGAGAG ACAACATTTT 60

CGACTACAGG ATTATTACCT TCTTTGATTTC ATCTTTCCAG ATGATTCGTC TAATGTCGTC 120

20

CTTTGTAACT CCGTATAGAG TGTCTACAA CCCCAACAAG CAAGCTTGTT GTnTTGGGCT 180

CTTCCCCTTT CGCTCGCCGC TACTAAGGGA ATCGAATTTT CTTTCTCTTC CTC 233

(2) INFORMATION FOR SEQ ID NO: 4582:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 218 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

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(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4582:

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TTAGTAAAAA GTCTGTGAGT AAGGGTGTAT GGAAAGTGGT TAAATATTAT AGAAAACATC 60

AAAGGATGTT AAGAAATACA ATTTATTACC CAGCATTTAA TAATGGTGCT ATAGAAGGAA 120

TTAATAATAA GATAAAATTA ATCAAGTGAA TTTCTTTTGG TTACAGAAAT TTCAnCanCT 180

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TTAAAGCACG TATAATGATG GATTTTCAGC TTGTACAA 218

(2) INFORMATION FOR SEQ ID NO: 4583:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 251 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4583:

TAATAAACAT GCCATACGTA ATAAGTGGCG TTGTATTAAA ATCATCTATA ATAGCCATAT 60

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ATTTTGGAAT CATTGTTAAA AATGGAATTA AAGTTCTAGT GATCTGTTGG GTTTGGAAA 180  
 TAGGTCATAG GGThAAAACh TTTTGGAGAA TTTGTCGCTA TTTGTTAAAT TGTATCCCGG 240  
 5 CTTGAAGTTG G 251

(2) INFORMATION FOR SEQ ID NO: 4584:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4584:

TTTAGGACCG TTATAGTTAC GGCCGCCGTT TACTGGGGCT TCGATTTCGTA GCTTCGCAGA 60  
 20 nTAACCCACT CCTCTTAACC TTCCAGCACC GGGGCAGGCG TCACCCCTAT ACATCACCTT 120  
 ACGGTTAGCA GAGACTGTGT TTTTGATAAA CAGTCGCTnG GCCTATTCAA TGGGGGCTCT 180  
 TCTGGGGGTT AAACCTAAAG AGCAACCCTT CTCCCGAAGT TACGGGGTC 229

(2) INFORMATION FOR SEQ ID NO: 4585:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4585:

TTATAAAAAG ATTTAAACGC GTTATTAATC TTGTGAGTGT TCTTTCGAAC ATAGCGATT 60  
 TTTCTTATGA ATTCAAGCTT ATTTAAAACT CTTTATTCAC TCGGTTTTGC TTGGTAAAT 120  
 40 CTATATTTAC TTACTTATCT AGTTTTCAT GTACAATTnG TTTTtagTCA AGCGCTCGCA 180  
 TACTGCTnTA TTTTCAAAAA ATCAAATGCT CATTTACA 218

(2) INFORMATION FOR SEQ ID NO: 4586:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4586:

GGAATTCCAC TTTCCTCTTC TGCACTCAAG TTTTCCAGTT TCCAATGACC CTCCACGGTT 120  
 GAnCCGGGGC TTTTCACATC AGACTTAAAA AACCgcCTAC GCGCGCTTGT ACGCCCAATA 180  
 5 ATTCCGGATA ACgCTTGCCA CCTACGTATT TACCGCGGC TGCTGGCAGC TATTnAGCCG 240  
 T 241

(2) INFORMATION FOR SEQ ID NO: 4587:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4587:

CAGCCACCTG TTGCCACCAG CTACACTTGC ATTGTTTGCT ACGACACGCC CAAACAATGC 60  
 TGAAGTGAAT AAGAAATCAA TCATTGCTC TTCTGTAAA TCATGTGTTT TTTCTAATTT 120  
 AAAAAGTGCA CCGGAATGG TACCCGAGGA ACCAGCTGTT GCGTTGCAC AAATAATACC 180  
 25 CATCGCAGCA TTGACTTCAT TGTTCGAAGG CACChTTGAC TGCGGCAATC ATTCATATCC 240  
 GACnAAGCAG ATG 253

(2) INFORMATION FOR SEQ ID NO: 4588:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4588:

ATGAACGGGT GGTAGCGAGT GGACGAAAAA CATCAATGAA AAGCTAGCTG TAGTTGCAAG 60  
 AGAAACTGGC TTACGATGGC ATTGGATCAA CACATGCGGC ATTGAGAAAT CCACGCATGG 120  
 CTGAGACGTT TACGATTGCG CGAAAAATGA ATCCTGAAGG CATTTTAGCA ATGTTGGTGC 180  
 45 GGACGTACCA GTAGAAAAGG CTTTGGAAGC AGTTGAAT 218

(2) INFORMATION FOR SEQ ID NO: 4589:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4589:

GCCATGGCTC CACAGGTAGG ACTCGAACCT ACGACCGATC GGTAAACAGC CGATAGCTCT 60  
 5 ACCACTGAGC TACTGTGGAT TAATATTATG CCTGGCAACG TTCTACTCTA nCGGAACGTA 120  
 AGTTCGACTA CCATCGACGC TAAGGAGCTT AACTTCTGTG TTCGGCATGG GAACAGGTGT 180  
 GACCTCCTTG CTATAGTCAC CAGACATATG nATGTA 216

## (2) INFORMATION FOR SEQ ID NO: 4590:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4590:

AGATTTAAAT AATCAAAAGT GCACATTATT AAAATATCAA TTTCACACTC AATGCGGCTC 60  
 ATCnCATTCa TTTCTTGTCT AGCAACGTTT TACTCTAGCG GAACGTAAGT TAGCTACCAT 120  
 25 CCTCGGCTAA GAACCTTTCT TGAATTGTGA CAATCGGCTT GCTTCTTTCC TCTCCTTCGG 180  
 CTCTCGCTAC TCAATTTAGC TCTACTAAAC TCGGTTGCGG CTCTTTTCTn GTTT 234

## (2) INFORMATION FOR SEQ ID NO: 4591:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4591:

AATTGACTGA CTTCGTTTTA CCGCGTGTIT AATATTGTTA TACATATATT CTAATTGCAC 60  
 ATTTAAACTT CGTAAATGCC AATGTGnGTG GGACAGAAAT GATATTTTCG CAAAATTTAT 120  
 45 TTCGTCGTCC CACCCCAACT TgncACATTA TTGTAACCTG ACTTTCCGCC AGCTTCTATG 180  
 TTGGGGCCCC GCCAACTTGC ACATTATTGT AAGCTG 216

## (2) INFORMATION FOR SEQ ID NO: 4592:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4592:

ATTCGGATA ACGCTTGCCA CCTACGTATT ACCGCGGCTG CTGGCACGTh TTAGCCGTGG 60  
 5 CTTTCTGATT AGGTACCGTC AAGATGTGCA CAGTTACTTA CACATATGTT CTTCCCTAAT 120  
 AACAGAGTTT TACGATCCGA AGACCTTCAT CACTCACGCG GCGnTGCTCC GTCAGGCTTT 180  
 10 CGCCATTGCG GAAGATTCCC TACTGCTGCC TCCCCG 216

## (2) INFORMATION FOR SEQ ID NO: 4593:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 base pairs  
 15 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4593:

TTGGACTAGA ACCAATGAAG GACGTTACTA ACGACGATAT GCTTAAAGGA GCTGTAAGTA 60  
 AGCTTTGATC CAGAGATTTT CGAATGGGGA AACCAGCAT GAGTTATGTC ATGTTATCGA 120  
 25 TATGTGAATA CATAGCATAT CAGAnGGCAC ACCCGGAGAA CTGAAACATC TTAGTACCCn 180  
 GTGGAAGAGA AAGAAAATTC GATTCCCTTA GTAGCGGCGA GCAGAACG 228

## (2) INFORMATION FOR SEQ ID NO: 4594:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 35 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4594:

CAATCGTTGA AGGAAATGTA CCAGCAGCAA TCAAAGACAA AGAAATTATT TCTGTAGACA 60  
 TTTCATCATT AGAAGCTGGA ACGCAATATC GTGGTGCTTT TGAAGAAAAT ATTCAAAAAT 120  
 45 TAATCGAAGG TGTAAATCT TCACAAAATG CCGTACTATT CTTTGATGAA ATCCATCAAA 180  
 TTATCGGTTT AGGTGCCACA GnaAGTGGAT TCCAGGTTAG CCAAAGGGGT TAATCTGGAT 240  
 TAATTTTTTT Tn 252

## (2) INFORMATION FOR SEQ ID NO: 4595:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs  
 (B) TYPE: nucleic acid  
 55 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4595:

5 ACTCTCTAGT GACCGATAGT GAACCACTAC CGTGAGGAGA AGGTGAAAAG CACCCCGGAA 60  
 GGAGnTGAAA TAGAACCTGA AACCGTGTGC TTACAAGTAG TCAGAGCCCG TTAATGGGTG 120  
 10 ATGGCGTGCC TTTTGTAGAA TGAACCGGCG AGTTACGATT TGATGCAAGG TTAAGCAGTA 180  
 AATGTGGAGC CGTAGCAGAA GCACGGTTCT GGAATAGGGG CGTTTTAGTT ATTTTGGGTC 240  
 GTTACCCGGG AGnAAAG 258

## (2) INFORMATION FOR SEQ ID NO: 4596:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 229 base pairs  
 (B) TYPE: nucleic acid  
 20 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4596:

25 CCTACCGCTG CAGCCGCTGG ATCTGCTGGA GTTGCACTAG GATCTGCCGG TGCCGCACGT 60  
 CTACTTCTCT TTTTCGGTCT ATTAGATGCT GGTTCAGCAA TTGCAACTAG CTCTGGTTTA 120  
 30 TTTGAAGAAT GACGAACATC TTCTTGAATT TCCTTTAAAG TAGATGTCCT CCTGAACCAT 180  
 TnCATTTGTTT AGTTGGGTAC ATTAATGcng TATTATCGAC ACTACATCA 229

## (2) INFORMATION FOR SEQ ID NO: 4597:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 246 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 40 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4597:

45 GCTCACCTTA GAATTCTCAT CTGCACTCA CCTGGTGGTC GGTTTGGCGG GTAGGGTCAC 60  
 CTATTTTCTA TCTAGCAGGC TTTTCTCGGC AGTGTGAAAT CAACGACTCG AAGnCACAAAT 120  
 GGTCTTCTCC CCATCACAGC TCAGCCTTAA CGAGTACCGG ATTTGCCTAA TACTCAGCCT 180  
 50 TACTGCTTAG ACGTGCAATC CAATCGCAGC CTTCGCCTAT CCTACTGnGG TCCCCCATC 240  
 GATTAA 246

## (2) INFORMATION FOR SEQ ID NO: 4598:

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(A) LENGTH: 223 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4598:

10 AAGAAAATAA AGAATGCTAC AATTACGATT GCAATCAAAC CAAAGAACCA TAATGATGTG 60  
 TACCAAGTGC TGCACCTTTA GTAATGACAA CGTTTAAACT TAGCAACATA ACTACTAGAA 120  
 CAATTAGCCC TGCAACGTCA AATTTATGTG TATTGGTAAT TTCTGATTTC GTTTCAGGCG 180  
 15 TCCCTTTGAT GAGTAGCATT GAAAGTACGG nAACGATGnG TTG 223

(2) INFORMATION FOR SEQ ID NO: 4599:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 219 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4599:

nTnTCACTGT TTGACCCGGT ACCGTGTCAG ATAATCCGCG ACGCAATGCA ATCGTTCGTG 60  
 30 CAATGTTTTG GCCTTGTAAT CCTTCTGGAA AAGCCGTACC AACAATGACA TCTTCAATCA 120  
 TATTCITATT GAATTTTCCG TCAATACGTT TCAATACGCC TTGTAATACT TTGGCTGCGA 180  
 CATCATCAGG TCTTTCGTGG AATAATGCGC CTGCTTTGC 219

35

(2) INFORMATION FOR SEQ ID NO: 4600:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 208 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4600:

AAGGTTAAGA GGAGTGGTTA GCTTCTGCGA ATACCGAATC GAAkCCCCAG TAAACGGCGG 60  
 CCGTAACTAT AACGGTCCTA AGGTAGCGAA ATTCCTTGTC GGGTAAGTTC CGACCCGCAC 120  
 50 GAAAGGCGTA ACGATTGGG CACTGTCTCA ACGAGAGACT CGGTGAAAAT CATAGTACCT 180  
 GTGAAGATGC AGGTTACCCG CGGACAGG 208

(2) INFORMATION FOR SEQ ID NO: 4601:

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(A) LENGTH: 286 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4601:

10 AGTGCCAGTG ATTAAGTGCA TTTTTCATA GATCAGGGAA GACTACCAAG CTTATGTTGA 60  
 AGGACATCTT TTGGCGTTAC CGGTTGGGCA GGTATGTTGT ATTACCGTTC ACAACAGCAT 120  
 CACTTGAACA ACATTTGTTA ACGGATTATT TGGCAATTCG TTATTGTCGA ACATGCGnAG 180  
 15 TTGGTGAGAT TTAATCATCG CTAAAGATGT GAAATAGATC GAAAATGGTT TAAGCAAACG 240  
 TTGCTCAGGT GTTACTACGT GATATGCCTA GCGAGTATAC TACAAC 286

(2) INFORMATION FOR SEQ ID NO: 4602:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 264 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4602:

30 ATATGGCTAT GGTATTCACA TATCGATnAA CATGGACATA ACTCATGCTG GGTTTCCCCA 60  
 TTCGGGAAAT CTCTGGGATC AAAGCTTACT TACAGCTCCC CAAAGCATAT CGTCGTTAGT 120  
 AACGTCCTTC ATGGCTTCTA GTGCCAGGCA TCCACCGTGC GGCCTTAATA ACTTAATCTA 180  
 35 TGGTTCCACC CATTTTATA GGTCAAACGG TAACATGAGG TAGGGTCTTT TATAAAAAGG 240  
 nTTAAACGGG GTATTAATCT TGTG 264

(2) INFORMATION FOR SEQ ID NO: 4603:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 246 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4603:

50 GAAACGTTAG CACAAGCCAT GAACCAATTA GGTGGAAGA GTAATAGTGG TGAAGGTGGC 60  
 GAAGATGCAA AACCGTTATG AAGTACAAGT TGATGGAAGC AACAACTAA GTGCGATTAA 120  
 55 ACAAGTTGCT TCTGGGCGTT TTGGTGTAnC TAGTGATTAT TTACAACATG CCAAAGAATT 180

TATCCn

246

## (2) INFORMATION FOR SEQ ID NO: 4604:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 248 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4604:

ATTAAC TAAC ATGGGCATCT ACGATGGAAA CAGACGTGGT ATCCTCGCTA TTATCCAGCT 60  
 AnCGCCATGC TGGCTCGTTT TTCAAATCAA GCCATTTTAA ATTTTGAAA GGTGTATGGA 120  
 CCAAGCCCTA TGACATTGCA TTCACCGATT GAACACGATG TTATCGCCAT GTCTCATGGA 180  
 GAAAATCAAG AGCATCATTC AGCAGTATCG CGATGCTACA TTACGCGCGA TTAAAGCAGn 240  
 TTTGATGG 248

## (2) INFORMATION FOR SEQ ID NO: 4605:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 246 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4605:

CAAGTTTTCC AGTTTCCAAT GACCCTCCAC GGTGAGCCG GGACTTnTCA CATCAGACTT 60  
 AAAAAACCGC CTACGCGCGC TTTACGCCCA ATAATTCCGG ATAACGCTTG CCACCTACGT 120  
 ATTACCGCGG CTGCTGGCAC GTATTAGCCG TGGCTTTCTG ATTAGGTACC GTCAAGATGT 180  
 GCACAGTTAC TTAACACATG ATGTTCTTCC CCTAAATGAA CAGAGTTTTG TTTGTTTTn 240  
 TGGGTT 246

## (2) INFORMATION FOR SEQ ID NO: 4606:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 212 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4606:

TGTATCTGCA GTTAAATCAT GTnTCGCTTG GTTTAATGCT GTTAATGCGT TATCGACACG 120  
 ATGTTTTTCA TCTGAAATTT GTTGTGCAGT TGCATCGCCA TTGTCAATAA CACGTTGAGC 180  
 5 TGCAGTTATT TCAGTTTCTG CTTACAGCTn CT 212

(2) INFORMATION FOR SEQ ID NO: 4607:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4607:

TAGTCAAGAT GAGAATTCTA AGGTGAGCGA GCGAACTCTC GTTAAGGAAC TCGGCAAAAT 60  
 20 GACCCCGTAA CTTCTGGGAGA GGGGTGCTCT TTAGGGTTAA CGCCGAGAAG AGCCGCATGA 120  
 ATAGGCCCAA GCGACTGTTT ATCAAAAACA CAGGTCTCTG CTAAACCGTA AGGAnTGTAT 180  
 AGGGGCTGAC GCCTGCCCCG TGCTGGAAGG TTAAGAGGAG TGGTTAGCTT CTGCGAGTAC 240  
 25 GGAATCGAAG CCCAGTAAA CGGCGG 266

(2) INFORMATION FOR SEQ ID NO: 4608:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4608:

TTCACTACGT AAATACGCAC GTGAAAAGG TGTTAnATTA AAGCAGTTTC TGGATCTGGT 60  
 40 AAAAATGGTC GTATTACAAA AGAAGATGTA GATGCATACT TAAATGGTGG TGCACCAACA 120  
 GCTTCAAATG AATCAGCTGC TTCACTGACA AGTGAAGAAG TTGCTGAAAC TCCTGCAGCA 180  
 CCTGCAnCAG TGAACATTAG AAGGCGACTT CCCAG 215

(2) INFORMATION FOR SEQ ID NO: 4609:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

GGGTTTCATAC ATGTCAATAG TAACCGTCTT AACTTGTTGT CGATTTTTTA AATCGAATCG 60  
 CTCGAAATAG GCACGCAAGA ATCTTGTAGT TCTATTTTCT AAAATATCTA TAACATCATG 120  
 GTATCATTAT CTATAAAAAT GAAACTCATT GATCCAGTTA CATTTTTAAC GCTTTTAAAT 180  
 TCATCCATAG CGATGTGGTT CCTGCCAACC ATTAAAGGGG TTAATTCTnGA ATnGATTAGC 240  
 C 241

## (2) INFORMATION FOR SEQ ID NO: 4610:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4610:

ATTCATTTCT TGTCTAGCAA CGTTCTACTC TAGCGGAACG TAAGTTAGCT ACCATCCTCG 60  
 CTAAGAACCT TTCTTGACTT GTGACAATCG CTTGCTTCTT TCCTCTCCTT CGGCTCTCGC 120  
 TTACTCATTT AGCTCTACTA AACTCGTTGC GCTCTTTTCT CGTTTCGTCA GATTCAAACG 180  
 TTTCArTTcG CCAAGCCATT TTTCTTTGGT GnTTA 215

## (2) INFORMATION FOR SEQ ID NO: 4611:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4611:

GTGCCATCTT TCTTCATCAA TTCATTAATA ATTGCTGGGA CGCCACCAGC TTCATGCACA 60  
 TCATGCATTG AATACGATGA ACTAGGTGCT ATTTTGTATA AATATGGCGT GCGTTTGGCA 120  
 ATAGCATTAA TGCGCTCTAA GTCATAATCA ATACCAGCTT CATTGGCAAT GGCTAACGTA 180  
 TGCAGTACCG TGTTTGTGTA ACCACGGCAC ATCTTCGCCA ATTTCTTCTT TAAACAAGTT 240  
 TAAATTATCT TGTGATTCAG GTAAATCCAT CTTGTTAGCT ACTACGATTT GAGGTCTATC 300  
 TTCTAAACGT TGCTCGTACG GCGGCTAATT CTGGATTAAT GACTTTATAA TCTTCAATAG 360  
 GGTCTCTACC TTCAGAACCG CTCCATATCC ATCCTGTGGA 400

## (2) INFORMATION FOR SEQ ID NO: 4612:

(A) LENGTH: 258 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4612:

10 AATACTATTA AGAAGTCCTG AAAAATTCAC ATTAGCAGTT GGATTGTTCA ACTTTATTAA 60  
 TGATAAGTAT GCAAATAATT TCACAGTGTT TGCAGCAGGG GCAATTATGA TTGCAGTACC 120  
 TATAGCAATC GTATTCTTGT TCTTGCAACG CTATTTAGTA TCAGGTTTAA CAACAGGTGC 180  
 15 CGACCAAAGG GTTAGTTTGA ATTTAGGAGT GGGGCCAGAT TGGTTAAGGA CCnCCTAATG 240  
 ACCGTTAAGG TTnAAAGG 258

(2) INFORMATION FOR SEQ ID NO: 4613:

20

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 210 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4613:

30 GACTTCGTTT CAGTGTA AAA TTTTCTAAT GTAACAGATA TGCTATTATT CATTGGAATG 60  
 ATTAGTGCTT CATCTTTTTT ACCCCAATAT TTTATAAGTG CAATTCGTAT GTGCACGTGC 120  
 TTTGCCACTT TTAATCAACG CTTAACCTCC TAAATTCTCA ATCCAAGTAT GTGCTGCACC 180  
 35 AGCTTTTTTC TACAGCTTTT ACAATATnn 210

(2) INFORMATION FOR SEQ ID NO: 4614:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 235 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

40

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4614:

TAGCGTATTA ATCGGCGGAT CGGCTGAGCG TATCTGAGTC TGAATCGCTG TCTGAGTCTG 60  
 50 AGTCGTATCC GAGTCTGAGT CGCTGTCTGA nTCTGAATCA CTGTCTGAAT CCGnATCGCT 120  
 ATCTGAATCT GAATCGCTAT CCGAGTCTGA GTCGCTGTCT GAATCTGAAT CGCTGTCTGA 180  
 GTCCGAATCG CTATCTGAAT CTGAGTCGCT GTCTGAGTCT GAATCGCTAT CTGAA 235

55

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4615:

ATGTGCGTGG TTTATTTTAA TAGGTTAGTA ATATATTAGG TCATGTTATG TTTAAATTTA 60  
 TAATGAATAA ATAATTTAGA AATATGCTTC CGATTGTTTCG ATGCTTTAAT TCAGTTAGAA 120  
 GCATCATAGA ATGCATGATT ACTGTTGTAA AGATACGTAA TGTTTTGTAT TGA CTGTATG 180  
 TCnTTGGATA GAGTTACAAA CTTATTTTG 209

## (2) INFORMATION FOR SEQ ID NO: 4616:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4616:

ATGCGCAAGA TATGGAGAAC ACCATCGCGA AGCGACTTTC TGGTCTGTAA CTGACGCTGA 60  
 TGTGCGAaAC nTGGGGATCA AACAGGATTA GATACCCTGG TAGTCCACGC CGTAAACGAT 120  
 GAGTGCTAAG TGTTAGGGGG TTTCCGCCCC TTAGTGCTGC AGCTAACGCA TTAAGCACTC 180  
 CGCCTGGGGA GTACGACCGC AAGTTGGAAA CTCAAAGGAA TT 222

## (2) INFORMATION FOR SEQ ID NO: 4617:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4617:

CAGTTTGCAA CACCCCAATT CTTGCCAGTC AGCATGATTC TGTTCAATTC TGCGATTTCT 60  
 TTGTCGATAT TTTCAAATCT TGTGGACTT GATCTAAATC AATTGGTGCT TCTTCTTCGA 120  
 ATGTATCAAC ATATCGCGGT ATGTTTAAAGT TGTAATCGTT ATCGGnGATC TCTTGTAATG 180  
 TCGCGCTGTG GCTATATTTA TCAATCGTGG CTTTACGCTT ATATGGGGCT ATAATACGTT 240

## (2) INFORMATION FOR SEQ ID NO: 4618:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4618:

TCTAATTGAT AGTGAATATA ATTAGAGTTn GAGGCTGGGA CATAAATCCC TAAATTTCan 60  
 CAGTAAGATA ATTTTCAATT AGAAAATATC TTACTGCTGT TCTCTATTTA TACAATACTT 120  
 CATTGGAATG GCTTCGCTTT CCTAGGGTGC CGTCTCAGCC TCGGTCTTCG ACTGGGCACT 180  
 GCTCCCTCAG GGGTCTCGCC ATTTAATACT ACGTAT 216

## (2) INFORMATION FOR SEQ ID NO: 4619:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4619:

ATGTATCGCG CCGAGCAACA CAAGATAAGC ATTGTAGATG TGGATGCCTT AACTGGGCAA 60  
 GCGATTnGTC GTCCTAAAAC AGGTACATAT GCGTATCTG ACCTAGTCGG TTTAGATATT 120  
 GCAGTGTCTG TAATTAAAGG CATGCAACAA GTACCTGAAG AAACACCCnT ATTTTCATGA 180  
 TGGTCAAAAT TTGTAAATAC GTTGTTTTGA CAATGGGCGC ACCTCGGACC GTAAAACG 238

## (2) INFORMATION FOR SEQ ID NO: 4620:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4620:

AACCATTGAA GCACCCCAATT ACGTTTTGGC TGACACGnAC GTATATCGCC TGCCCAAGCA 60  
 GATGCAGCCT TATTAACACC TGAACCACTT CGAACGCCAC TACCTTTAAG TGACTTCAAC 120  
 CATTTTTCCT GGATCTTTAG CTGTATGCAT TGCCCTGGAT GCGACCCTTG nCATCAATTG 180

TTGACCAGC

249

## (2) INFORMATION FOR SEQ ID NO: 4621:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 267 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4621:

TGGACCTGTA AAAGGAGACT CGATTGTAGA AAAAGAAGAA ATTCCATTCA AGAAAGAACG 60  
 TAAATTTAAT CCTGATTTAG CACCAGGGAC AGAAAAAGTA ACAAGAGAAG GACAAAAAGG 120  
 TGAGAAGACA ATAACGACGC CAACACTAAA AAATCCATTA ACTGGAGAAA TTATTAGTAA 180  
 AGGTGAATCG AAGAGAAATC ACAAAGTCCG TTnTGGnTTA CAGGTACGGC AGAACGATAC 240  
 ACAGTCTCGG GCGATTGTCTG AGTCCAC 267

## (2) INFORMATION FOR SEQ ID NO: 4622:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 231 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4622:

CAAAAGGTAG TTAAATTAG GAGTGGGGAA ATTGATAAGA CCACTAATGA CGATAAAGAT 60  
 TAAAAGGAnG ACGTTATGAT GACGATTAAA GTTGGATCAT TGGGTGTGGT GGTATTCCAA 120  
 TGGCAAGCAC ATGCCAAGTT TACAAAAAGT TGAAATGTTG AAATGAnCGC ATTTTGTGAC 180  
 GTAGACATTT CGAAGCAGCG AGTGCGGCAG AAGCATACGG ACTGACAATG C 231

## (2) INFORMATION FOR SEQ ID NO: 4623:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 301 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4623:

CGAAACCGGC CCGACCCGGA CChACCCGAG GAAAGGTACC CnAAAGnTGA AGCCCCGGGAA 60



CCCAACACCC ACCCGGACAC CAGAAGTGCC GGAGTGAGCC AGAAACTCCA ACACCGCCAA 180  
 CACCAGAGGT ACCAGCTGAA CCTGGTAAAC CAGTACCACC TGCCAAAGAA GAACCTAAAA 240  
 5 AGCCTTCTAA ACCAGTGGAA CAAGGTAAAG TAGTAACACC TGTTATTGAA ATCAATGAAA 300  
 A 301

10 (2) INFORMATION FOR SEQ ID NO: 4624:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 222 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4624:

20 CGAGGTGCTG CAGAAGGTGT CATTCGTCGT TATTTAATTG AAGAAAAGAA CTACTTAGAA 60  
 GCTGTGATTG GTTTGCCAGC GAATATTTTC TATGGGACAA GTATTCCAAC ATGTATTTTA 120  
 25 GTATTTAAAA AATGTCGCCA ACAAGACGAC AACGTACTAT TTATCGATGC ATCCAATGGT 180  
 TTTGAAAAAG GGGnAAATCA TAATCATtnG GCGATGCCCA AG 222

(2) INFORMATION FOR SEQ ID NO: 4625:

- 30 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 301 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4625:

TGGAAAGTGA ATCAAAGAGG TAATATCCGT AGTCGAAATG TTGTCTCTCT TGAGTGGATC 60  
 40 CTGAGTACGA CGGAGCACGT GAAATTCGGT CGGAATCTGG GAGGACCATC TCCTAAGGCT 120  
 AAATACTCTC TAGTGACCGA TAGTGAACCC AGTACCGTGA GGGAAAGGTG AAAAGCACCC 180  
 45 CCGGAAGGGG AAGTGAAATT AGGAACCCCTG AAAACCCGTG TGCTTTACCA AAGTTAnGTT 240  
 CAAGAGGCCC CGTTTAAATT GGGGTnnAAT TGGCGGTGCC CTTTTTTGGT AGGAATTGAA 300  
 A 301

50 (2) INFORMATION FOR SEQ ID NO: 4626:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 223 base pairs
  - (B) TYPE: nucleic acid
  - 55 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4626:

5 GAATGAAGGA AGACCATATG AAAAATGGCC AACTTAAGCC AGGATACAAT TTACAAATAG 60  
 CGACAAATTC TCAATTTGTT TTATCCTATG ACCTATTTCA AAACCCAACA GATACTAGAA 120  
 10 CATTAAATCCC ATTTTtanCA ATGATTCAAA ATACCTTCGG TTATTTACCA GAGTATATTG 180  
 TAGCTGATGC AGGTTATGGT AGTGAGCAAA ACTATATGGC nat 223

## (2) INFORMATION FOR SEQ ID NO: 4627:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 221 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4627:

20 TTGTTGGGGC CCCGCCnCGC nCATTGCCTG TAGAATTTCT TTTCGAAATT CTCTGTGTTG 60  
 25 GGGCCCCTGA CTAGAATTGA AAAAAGCTTA TTACAAGCGC ATTTTCGTTC AGTCAATTAC 120  
 TGCCAATATA ACTTCGTAGA TCATAGAACA TTGATTTATT TCCCAGCCTA TTCTTTTCAT 180  
 30 AAAAAAAGA CGGATTAATT ATCCGCTTTT TCCTTATATC T 221

## (2) INFORMATION FOR SEQ ID NO: 4628:

35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 208 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4628:

40 ATATATTCGT ATTTATAGTA AAATTAAATA AAGAGnATTA TATAACACGA GGTGTAGTAA 60  
 45 GTATGAAATT TGAGnAAATA TATAGATCAC ACTTTATTGG AAGCCTGAGT CAACACGTAC 120  
 GCAAATCGAT CAAATCATCG ATGAAGCGAA GCATACCAAT TTAAATCTG TATGTGTGAA 180  
 TCCACCACAT GTTAAATATG CAGCAGAG 208

## (2) INFORMATION FOR SEQ ID NO: 4629:

55 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 305 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4629:

5 ACAATAATGC ATCATAATGC GCAACAACAA TCAATACTGC GAAAACAGAA GCACAACAAG 60  
 TGATTAATAA TGAGCGTGCA CACCACAACA AGTTTCTGAC GCACTAACTA AAGTTCGTGC 120  
 ACACAACTAA GATTGATCAG CTAAAGCTTA CTTCAAAATA AAGAGATATA GCCATTAGTA 180  
 10 ACGTTAAAT AACTTACAAG nTCTGTGACC AGTACCTCAC TGTGGTATGA CGCACAAGTA 240  
 TTGATACTnT ATCGAGAGCG TGAGnGAACT GAATACTGCG CTCACGGTAT TACATGCGTG 300  
 CACTG 305

## 15 (2) INFORMATION FOR SEQ ID NO: 4630:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 213 base pairs  
 (B) TYPE: nucleic acid  
 20 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4630:

TCGACTACCA TCGACGCTAA GGAGCTTAAC TTCTGTGTTT GGCATGGGAA CAGTGTGACT 60  
 CCTTGCTATA GTCACCAGAC ATATGAATGT AATTATACAT TCCAACTAG ATAGTAAGTA 120  
 30 AAAGTGATTT GCTTCGCCAA ACATTTATTT TGATTAAGTC TTCGATCGAT TAGTATTCGT 180  
 CAGCTCCACA TGTCACCATG CTTCCAnCTn GAA 213

## (2) INFORMATION FOR SEQ ID NO: 4631:

## 35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 213 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 40 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4631:

45 GAnGTGAAAT AGAACCTGAA ACCGTGTGCT TACAAGTAGT CAGAGCCCGT TAATGGGTGA 60  
 TGGCGTGCCT TTTGTAGAAT GAACCGGCCA GTTACGATTT GATGCAAGGT TAAGCAGTAA 120  
 ATGTGGAGCC GTAGCAAAAA CnAAGTTCTG AATAGGGCGT TTAGTATTTG GTCGTAGCCG 180  
 50 GAAACCAGGT GATCTACCCT TGGTCAAGTT GAA 213

## (2) INFORMATION FOR SEQ ID NO: 4632:

55

- (A) LENGTH: 205 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4632:

70 GCTTTTAAAT CAAATGATAG CGGAAGGGnA TTTTAAAT ATTCTGAACCA TTATTTACAG 60  
 CAGCAGATGG ATGGATTGGT GTCACAATTA TCTTTGGTGC CTTTGCAATTA TTCTGGTTTG 120  
 TAGGTATTCA TGGTCCGTCA ATTGTAGAGC CAGCAATTGC AGCCATTACA TATGCGAATA 180  
 15 TCGAAGCGAA CTTCAAGTTG CTTCA 205

## (2) INFORMATION FOR SEQ ID NO: 4633:

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 204 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4633:

AGTTATATTG ACAGTAGTTG ATGGGGCCCC AACATAGAGA AATTGGAACA CCAATTTCTA 60  
 30 CAGACAATGC AAGTTGGGGT GGGCTCTAAC ATAAAGAAnt ACTTTTTCTn TAGAAATTAG 120  
 TATTTCTTAT ACATGGGTTT TACTCAGTAT TTCCTATTCT TAAGTGCACA TTAGCAGCGG 180  
 CTAATGTGTT AAGAACTACT ACAT 204

35

## (2) INFORMATION FOR SEQ ID NO: 4634:

## (i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 226 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4634:

GCCGATGGAT TAGAGTATAT GACGTGGTGG CATGTCATTA ATTTAGGTGA TGTAGGTAAG 60  
 AACGTTnGGG CAAGGTATGA GTGGTGGTAT TGC GTTACGT TAGCCCGTCT GATGTAGAAG 120  
 50 CTTTTGTTGA AAATAATCAA CTAGATACGC TTTCGTTTAC AAAGATTAAA CACCAAGAAG 180  
 AAAAAGCATT CATTAGCAA ATGCTGGAAG AnCCATGTGT CACACA 226

55

## (2) INFORMATION FOR SEQ ID NO: 4635:

(A) LENGTH: 208 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4635:

10 CATATAGTTT TGCTCACTAC CATAACCTGC ATCAGCTACA ATATACTCTG GTAAATAACC 60  
 GAAGAGTTGT TGAATCATTG TTAAAAATGG GATTAATGTT CTAGTATCTG TTGGGTTTGT 120  
 AAATAGGTCA TAGGATAnAA CnGTACGGAG AATTGTGCGC TATTTGTAAA TTGTATCCTG 180  
 15 GCTTAAGTTG GCCATTTTTC ATATGGTC 208

(2) INFORMATION FOR SEQ ID NO: 4636:

20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 228 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4636:

TTTTCTTTG TGTTTATTTT TATTTTGAAC GTTTTAGGAC ATAAAAAAAA GTAGACCTTG 60  
 30 CGGTCTCAAT GCGGCTCATC GCATCCATTT TTTGCCTGGC AACGTTCTAC TCTAGCGGAA 120  
 CGTAAGTTGG CTACCATCGA CGCTAAGAAC CTTTCTTGAC TTGTGACAAT CGCTTGCTTC 180  
 TTTCCGCTTC TTCTGCTCGn GCTTACTCAT TGAGCnCTAC TAAACTCG 228

35

(2) INFORMATION FOR SEQ ID NO: 4637:

40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 212 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4637:

CATGGTTCAA AAGTGAAAGA CGGTCTTGCT GTCACCTATA GATGGATCCG CGCTGCATTA 60  
 GCTAGTTGGT AAGGTAACGG CTTACCAAGG CAACGATGCA TAGCCGnCCT GAGAGGGTGA 120  
 50 TCGGCCACAC TGGAGCTGAG ACACGGTCCA GACTGCTACG GGAGGCAGCA GTAGGGnATC 180  
 TTCCGCAATT GGCGAAAGCT GTACGGGCAA CG 212

55

(2) INFORMATION FOR SEQ ID NO: 4638:

(A) LENGTH: 256 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4638:

10 ATnTnATTAA ATAGAGAACA GCAGTAAGAT ATTTTCTAAT TGAAAATTAT CTTACTGCTG 60  
 TTTTITAGGG ATTTATGTCC CAGCCATTTT TGTATTCATA TTAAATTTTC GATAATTTTT 120  
 CAGGAAGCAT TTTAATTTTA CTAATGAAGC CATATTTTTA GATTAACCAA AATTAATATT 180  
 15 TACATTTTCCT AACCATTTTT ATGTAAACATT TACAGTTCCA AAAATGGGGG TAATAATCCA 240  
 GGTTAGGATA AAGAGG 256

(2) INFORMATION FOR SEQ ID NO: 4639:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 209 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4639:

30 AnAGnAACCA CTACATAATA AATCATTAGT GGCTCTTTAT CATTTCTGTC CCACTCCCCCT 60  
 GAGAAGTTTA AAATTTTATA TGTTGGCTTG TTATGTTAAG GGAATTAACA TGGTTGTCTT 120  
 GTTTATATTA TGTGATTCCA ACATTACTAG TCCTGGTAAA TCTAATCCG TAAAATGCTA 180  
 35 AATCTAACCA TCTATTAAAT TTAAAACC 209

(2) INFORMATION FOR SEQ ID NO: 4640:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 224 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4640:

nGnAAAGGTG AAAAGCACCC CGGAAGGGAG GTGAAATAGA ACCTGAAACC GTGTGCTTAC 60  
 50 AAGTAGTCAG AGCCCGTTAA TGGGTGATGG CGTGCCTTTT GTAGAATGAA CCGGCGAGTT 120  
 ACGATTTGAT GCAAGTTAAG CAGTAAATGT GGAGCCGTAG CAGAAGCATG GTCTGAATAG 180  
 55 GTGCGTTTAG TATTTGGTCG TAGCCCGCAG AACCAGGGTG ATCT 224

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4641:

CACTCACnCA GATTTTTTAAG TCCTGTGCGT CTGCCAGTTC CGCCACCCCG GCACTATAAA 60  
 AATGGAGCAG AAGACGGGAT TCGAACCCGC GACCCCAACC TTGGCAAGGT TTTATTCTAC 120  
 CGCTGAACTA CTTCTGCATA TCGGGGTGAA GGGAGTCGAA CCCCCACGCC GTAAGCTAnG 180  
 ATCCTAAGTC TAGTGCCTCT GCCAA 205

## (2) INFORMATION FOR SEQ ID NO: 4642:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4642:

AGCTGACATG ATCAGTCAGC TTACAACAAT GTGCCGGTTG GGGTGGCTGG ACACGGCACC 60  
 CTGAGGGAAG GGCACCCGTC ATCAAAAATT CTATTTATAG AATTTTACAG TAATGTGACA 120  
 GACGGGCAAA GCGAACCATT CAATACGAAG TATTGTATAA ATAGAGAACA GCAGTAAGAT 180  
 ATTTTCTAAT TGAAAATTAT CTTACTGCTG TnTTTTTAGG GATTATGTn CCCAG 235

## (2) INFORMATION FOR SEQ ID NO: 4643:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4643:

AGnAAGGTGG GGATGACGTC AAATCATCAT GCCCCTTATG ATTTGGCTAC ACACGTGCTA 60  
 CAATGGACAA TACAAAGGCA GCGAAACCGC TAGTCAAGCA AATCCCATAA ATTGTTCTCA 120  
 GTTCGATTGT AGTCTGCGAC TCGACTACAT GAAGCTGGAA TCGCTATAAT CTAGATCAGC 180  
 ATGCTACGTG ATAGTTCCGG GTCTnTACAC ACGCCCGTCA CACCACGGAG GGTTTTACAC 240

## (2) INFORMATION FOR SEQ ID NO: 4644:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4644:

CAGCAGGCCA CCAAAATTGT GGTCGAGAT GTTCATATAA AACTTTATAT AATTCATCAG 60  
 TTCCTAACAT TTACACCCTC CATTTTAGAG GGAGTGGGAC AGAAATGATA TTATCGTAAA 120  
 ATTTATTTTCG TCGTCCCACC CCAACTTGCA TGTCTGTAGA AATGGGGATC CAATTCnCTT 180  
 GTTGGGGGCC CGCGGGCAAG GThACTAGAA TGAAAAAGC CTGTTACAAG CGATTTTCGG 240  
 TTCAGTCCAC TACTGGCAAT ATAACCTTGTA GAGCTAGGAC ATTGG 285

## (2) INFORMATION FOR SEQ ID NO: 4645:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4645:

GCTATTACTC TGCTATCAAT GTACCTAAAG CTACCGATGA TTTCCGAGAC ATAGACCGTG 60  
 CGCTTGThTG GGGGTTCAAC TGGAACTTG GTCCATTCCA ATTATGGGAT GCAATGGGGn 120  
 TACGAACGTG TTAAACAGT ATGGAAGACG AACTTGGAGA CTTACCACAA TGGGTTAGTG 180  
 ATTTAGATGG TGGCTTTTGA TAAACA 206

## (2) INFORMATION FOR SEQ ID NO: 4646:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4646:

ACAGTTACCG ATACAACTGA AGATGATAAC GATGCAGATG GTGGCGACGT TGACGTCACA 60  
 CTTACGGATC ATGATGATTT CACACTTGAT AACGGATACT TCGAGATGAT ACATCAGACA 120



CnGACAGTGA TTCAGATTCA GACAGCGACT CAGATTcGnA TA

222

## (2) INFORMATION FOR SEQ ID NO: 4647:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 200 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4647:

GTACTATTCG TGTGTGACAA TGTTCTTCCA GCATTGCTT AATGAATGCT TTTTCTTCGT 60  
 TTAATCTTTG TAAACGAAAG CGTATCTAGT TGATTATTTT CAACAAAAGC nTCTACATCA 120  
 GncGGGATAA CGTAAGCAAT ACCACCACTC ATACCTTGAC CGAAGTTCTT ACCTACATCA 180  
 CCGAAATTAA TGACAGTCCA 200

## (2) INFORMATION FOR SEQ ID NO: 4648:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 201 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4648:

CCACCATTAA TTTAATACCT ATTTGGGGGC TTAGCTCAGC TGGGAGAGCG CCTGCTTTGC 60  
 ACGCAGGAnG TCAGCGGTTT GATCCCGCTA GTCTCCACCA TTATTGTAC ATTGAAAAC 120  
 AGATAAGTAA GTAAATATA GATTTTACCA AGCAAAACCG AGTGAATAnA GAGTTTTAAA 180  
 TAAGCTTGGA ATTCATTAAG A 201

## (2) INFORMATION FOR SEQ ID NO: 4649:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 218 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4649:

AGTAAATACA GATGGAATAA ATCTTTTAAG GCTTATAAAC GCTCATCTGn CATTGTAGCA 60  
 ATTCATGCTT TCAAAAGACG ATATACTACG ACACTCCTAC GAACTTGTCC AAGGATTACG 120

AAAGTCTGTG AGTAAGGGTG TATGGAAAGT GGTnAAAT

218

## (2) INFORMATION FOR SEQ ID NO: 4650:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 202 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4650:

GTGGCGGTGC GACTGTCAGA AGCACGTAA ATTAATGAAA GATACAGTAG GTGCTGATGT 60  
 AGAAGTAAAA GCCATCAGGT GGCCTACGTA ATTTAGAAGA TTTCAATAAA ATGGTTGAAG 120  
 CAAGTGCGAC ACGTATTGGT GCGAGCGCAG GTGTTCAAAT TATGCAAGGT TTAGAAGCAG 180  
 ATTChGATTa CTAATATnTA TG 202

## (2) INFORMATION FOR SEQ ID NO: 4651:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 209 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4651:

AGCGGCGGAC GGGTGAGTAA CACGTGGATA ACCTACCTAT AAAACTGGnA TAACTTCnGG 60  
 AAACCGGAGC TAATACCGGA TAATATTTTA AACCGCATGG TTCAAAGTA AAAGACGGTC 120  
 TTGCTGTCAC TTATAGATGG ATCCGCGCTG CATTAGCTAG TTGGTAAGGT AACGGCTTAC 180  
 CAAGGCAACG ATGCATAGCC GACCTGAGA 209

## (2) INFORMATION FOR SEQ ID NO: 4652:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 202 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4652:

TGAAGATGCA GGTACCCGC GACAGGACGG AAAGACCCCG TGGAGCTTTA CTGTAGCCTG 60  
 ATATTGAAAT TCGGCACAGC TTGTACAGn TAGGTAGGAG CCTTTGAAAC GTGGAGCGCT 120

CCACTTATCG TGGTTGGAGA CA

202

## (2) INFORMATION FOR SEQ ID NO: 4653:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 205 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4653:

CCGTGCGACC CCTTTGGTCC CAAACCAAGT GCTCTACCAA GCTGAGCTAC GTTCCCGGTA 60  
 TAATTAACGC GCCCGATAGG AGTCGAACCC ATAACCTCTT GATCCGTAGT CAAACGCTCT 120  
 ATCCAATTGA GCTACGGGCG CATATGTTTT TATTGAAAAT GGTGCCGAGG ACCGGAATCG 180  
 AACCGGTACG TGATCACTCA AcnGn 205

## (2) INFORMATION FOR SEQ ID NO: 4654:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 264 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4654:

AGACGAAACG TTGTTGTTGC GAAGATAAAT CGCACAGCGA TTGAGCCTAT CTGCTGCACC 60  
 ATTAAGTGGT GAAGTAACAC CATTATCAGA AGTGCCTGAT CAAGTGTTC ACGAAAAAAT 120  
 GATGGTGACG GTATCGCTAT CAAACCTTCA CAAGGTGAAG TTCGTGCACC ATTCAACGGT 180  
 AAAGTACCAA TGATTTCCCA ACCAAACATG CCATTGGTCC TGTATCAGAT AGTGGTTAGn 240  
 CTATTAATCC ACACGGGTTA GAnG 264

## (2) INFORMATION FOR SEQ ID NO: 4655:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 211 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4655:

GACGATTACA TATCATCGCT AATAACTTAG CATTAAAACC GCTTGATGCG CCACCACAAG 60

AACACAACGA ACTGGGnACA TGCTTCGGTT AAATCCATCA ATTTCAACGC TTGTnACGCG 180  
 AAATCAGTTT GCTCTTGGCT GCAGTAAATC G 211

5 (2) INFORMATION FOR SEQ ID NO: 4656:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 212 base pairs  
 (B) TYPE: nucleic acid  
 10 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4656:

TTTACATTTA TCGGTTTAGT CAGATTCAAA CGTTTTCACT TCGCCAAGCC ATCTTTCTTT 60  
 GTGTTTGCTT TTATTTTGAC GTTTTAGACA TAAAAAAGA GACCTTGCGG TCTCAATGCG 120  
 20 GCTCATCGCA TCCACTTTTT GCCTGGCAAC GTTCTACTCT AGCGGAACGT AAGTTCGACT 180  
 ACCATCGACG CTAAGGnGCT TAACTGnTGG GT 212

(2) INFORMATION FOR SEQ ID NO: 4657:

- 25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 200 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4657:

35 TGGGTTCGAA nTCCACTTAG GACCCACCAT TAACTTAATA CCTATTGGG GGCTTAGCTC 60  
 AGCTGGGnAG AGCGCCTGCT TTGCACGCAG AGGTCAGCGG TTCGATCCCG CTATCTCCAC 120  
 CATTATTTGT ACATTGAAAA CTAGATAAGT AAGTAAAATA TAGATTTTAC CAAGCAAAAC 180  
 40 CGAGTGAATA AAGAGTTTTA 200

(2) INFORMATION FOR SEQ ID NO: 4658:

- 45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 185 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4658:

TACAGTATAT CGGGAAGACA GGATTGGAAC CTGCGACCCC TTGGTCCCAA ACCAAGTGCT 60

55

CTCTTGATCC GTAGTCAAAC GCTCTATCCA ATTGAGCTAC GGGCGCATAT GTTTTTATTG 180

AAAAA 185

5 (2) INFORMATION FOR SEQ ID NO: 4659:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 208 base pairs  
 (B) TYPE: nucleic acid  
 10 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4659:

AAGTGTTAGG GGGTTTCCGC CCCTTAGTGC TGCCAGCTAA CGCATTAAAGC ACTCCGCCTG 60

GGGAGTACGA CCGCAAGTGT ATAACTCAAA GGAATTGACG GGGACCCnCA CAAGGTTGGA 120

20 GCATGTGGTT TAATTCGAAn CAACGCGCAG TAACCTTACC AAATCTTGAC ATCCTTTGAC 180

AACTCTAGAG ATAGAGCCTT CCCCTTCG 208

(2) INFORMATION FOR SEQ ID NO: 4660:

- 25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 365 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4660:

35 ACGTCGCGAG AACGCAATTA GCTGAAAAAG ATTACAACAT TAGAACAAGA TTTAAAGTCA 60

CATTTAGTGA ACATCAAAGG CCGAATAACA TCATAAATTA CGATTAGATA TAACAAAAGA 120

GCTTGGGACA TAAGTCCTAA AGTCTTAGGC AAGTAAAAAA GTGATTCTA TTATTTATTT 180

40 GATAGAAATC ACTTTTTGAT ATGTATTTnt ATGTACAGCT CGTTGAGCnc TATTTTCCTT 240

ATATTAGTGC CATAATACAA ACCTAGCTCT TGTTTAACTT TATTATTCCG AACTGACATC 300

45 GGTGAACCCA ATAGCCTCAT AAGCAAACAG CTTACATCAT TTTCTGAnT GGTTTTCGTT 360

CTGTC 365

(2) INFORMATION FOR SEQ ID NO: 4661:

- 50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 209 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 55 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4661:

AAAGTATTTTC TTTATGTTGG GGGGCACCCC ACTTTGnCAT TGTCTGTAGA AATTGGGAAT 60  
 CCAATTCTCC TnATGTTGGG GCCCCGAGT TCAACTACTG CCAATATAGT GTTGTAGTGT 120  
 CTAAGACATA AAAGTTCATC TCACTCACAA TTACTTTATA GCCTATCCAT CATCTTTTCT 180  
 ACATGAAATT TTTCCAAGTG ATATATTTT 209

## (2) INFORMATION FOR SEQ ID NO: 4662:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4662:

TTATGGCACT TAAAACCAGC GATGACGATT GCAGTATCAC ATGGTATCTT CAACATAACA 60  
 AATACTTTGA TTCAATTACC ATTTGTAGCA GGTTTAGCAT GGATTGTTAC AAAGCTTGTC 120  
 CCAGGTAAAG ATATTGCTGA TGACTATAAA CCTCAGCACT TAAACCAAGG TCTGTTATCA 180  
 CGCACCTGGT GTTTGCATAC CAGGAACTCC AAAAGGATTA CCAAATGTnG GGGCAGAnTG 240  
 GCCTAA 246

## (2) INFORMATION FOR SEQ ID NO: 4663:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 226 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4663:

AATGGTGTAT TATGAGTAGT AATAATTAGC AAAGAGGTAA ATTAAGTGAT GTCGCGTCAT 60  
 TTAAGGAAGC GATTACAAT CGAGAATCAC AAAGTACAAC TGGTATCGGC GAAGGTATnG 120  
 CCATTCCACA TGCCAAAGTG GCCGCAGTTA AGTCACCAGC TATTGCGTTT GGTAAATCTA 180  
 AAGCAGGCGT AGATTATCAA AGnTTTTTGGT ATGCAACCAG CACACT 226

## (2) INFORMATION FOR SEQ ID NO: 4664:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4664:

5 TTCCGTCTCG GCACCATTTT AGCGCCGTAG CTCAATTGGA TAGAGCGTTT GACTACGGAT 60  
 CAAGAGGTAT GGGTTCGACT CCTATCGGGC GCGCATTTTT AAATTAATTG AATAACGGGA 120  
 GTAGCTCAGC TTGGTAGAGC ACTTGTTTTG GGACAAGGGC GCAGGTTTCA ATCCTGTCTC 180  
 10 CCGATTACTT CTAAATCCAT TTATGGGGCT ACTCACTGGG nACGCCTCTT nCAC 234

(2) INFORMATION FOR SEQ ID NO: 4665:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4665:

GTACATCTAA AATCATCCAT GAAGGTTTGT TACCTGAATT ACGBAATGAT TCAACAACCTT 60  
 25 CTAAACGTTT AATTnACCAG TAAGTCTTTG CCAAGTAGCT GATTCCAACCT CATCGCGTAC 120  
 AATTTAAGTC TTCGTCAAGA TCAATCCTCT TCAAGTAAAT CTTTAATAAC CTTCTGCACC 180  
 CATTTTTGCA CGAATT 196

(2) INFORMATION FOR SEQ ID NO: 4666:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 226 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4666:

CCGCCGAACA ACTACTTTGT TTGTTGATTC TCTCCACCTG TTTCAGTAGT TCAGATTCTT 60  
 TAGATTGTGG TTTTITAGTT GGTGCCATGC TTAAACCTTT TCATTGATTT CAATAACAGG 120  
 45 TGTTACTACT TACCTGTTCC ACGGTTTAGA AGGCTTTTAG GTTCTTCTTG GCAGTGGTAN 180  
 GGTTTACCAG TTCAGCGGTA CCGCGGTGTT GGnCGTGTG GATTTT 226

(2) INFORMATION FOR SEQ ID NO: 4667:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4667:

5 GTTCTGAATA GGGCGTTTAG TATTTGGTCG TAGCCGAnAA CCGGTGATCT ACCCTTGGTC 60  
 AGGTTGAAGT TCAGGTAACA CTGGAATGGG AGGACCGAAC CGACTTACGT TGAAAAGTGA 120  
 10 GCGGATGAAC TGAGGGTAGC GGAGAAATTC CAATCGAACC TGGAGATAGC TGGTTCTCTC 180  
 CGAAATA 187

## (2) INFORMATION FOR SEQ ID NO: 4668:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 182 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4668:

CTAAGTGGAG TTGTCACAAC ATCTTTAAAC GTTCCAGGTA AATAGTCTTT TGCCATTTCT 60  
 25 GAAAATGCTT TTGCCAACGT TTTATAAATA TCCAGTCTG AACGCGATTC CCATAACGGA 120  
 TCAATGGCAG GATTGAAAGG ATGTACATAT GGATGCATAT CCGTTGATGA TAAATCATGn 180  
 30 TT 182

## (2) INFORMATION FOR SEQ ID NO: 4669:

35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 182 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4669:

AGTTACGTTA AAAGATGAAA ACGACAAAGT TTTAAAAACA GTTACAACAG ATGAnAATGG 60  
 TAAATATCAA TTCACTGATT TAAACAATGG AACTTATAAA GTTGAATTCG AGACACCATC 120  
 45 AGGTTATACA CCAACTTCAG TAACTTCTGG GAAATGATAC TGCAAAAAGA TTCTAATGGT 180  
 TT 182

## (2) INFORMATION FOR SEQ ID NO: 4670:

50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 185 base pairs  
 (B) TYPE: nucleic acid  
 55 (C) STRANDEDNESS: double



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4670:

5 GGGGCAAAGT CATnCATAG ATTAATGGTT CTCCGATACC TAGGAAACCA ACTGGCAATG 60  
 CACCTTTTAA AGTATTACGT AATGTTGTGT TGCCTTTACA TCTTACCCAA AGTGCTAATG 120  
 CGGCACCTAC TTGTCCAGCA CCAGCCATCG CTGCAATTGG CAATAAGTAA GTAGCACCTG 180  
 10 ATTGG 185

## (2) INFORMATION FOR SEQ ID NO: 4671:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 200 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4671:

20 CTGACGAACG AGAAAAGAGC GCAACGATTT AGTAGAGTAA ATGAGTTAAG CGAGACCGAA 60  
 25 GAAGAGGAAA GAAGCAAGCG ATTGTCACAA GTCAAGAAAG GTTCTTAGCG TTCGATGGTA 120  
 GCCAACTTAC GTTCCGCTAG AGTAGAACGT TGCCAGGCAA AAAAATGGAT GCGATGACCG 180  
 30 CATTGAGACC GCAAGGnTnT 200

## (2) INFORMATION FOR SEQ ID NO: 4672:

35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 261 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4672:

40 CCCGGGGTAC AGTTATTCCC CAGAGTCAAC GCGGGGGTTG GACTCGATGT CGGTCATCGC 60  
 45 ATCCTGGGCT GTAGTCGGTC CCAAGGGTTG GGCTGTTGCG CATTAAAGCG nACGnTGCTG 120  
 GGTTGAGACG CGTGAGCAGT CGGTCCCTAT CCGTCGTGGG CGTAGGAAAT TTGAGAGGGC 180  
 TGTCTTAGT ACAGAGAGGCC GGGATGGCAT ACCTTGGTGT ACCATTGTGCG TGCCACGCAT 240  
 50 AGTGGGTAGT ATGTGTGGAC G 261

## (2) INFORMATION FOR SEQ ID NO: 4673:

55 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 184 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4673:

10

ATAGGGCGTT TAGTATTTGG TCGTAnCCAG AAACCAGGTG ATCTACCCTT GGTCAGGTTG 60  
AAGTTCAGGT AACACTGGAT GGAGGACCGA ACCGACTTAC GTTGAAAAGT GAGCGGATGA 120  
ACTGAGGGTA GCGGAGAAAT TCCAATCAAA CCTGGAGATA GCTGGTTCTC TCCGAAATAG 180  
CGTT 184

15

(2) INFORMATION FOR SEQ ID NO: 4674:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 203 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4674:

30

CCCAGTCAAA CTGCCCCGCT GACACTGTCT CCCACCACGA TAAGGTCGTG GGTTGAGAAA 60  
GCCAACACAG CTAGGGTAGT ATCCCACCAG CGTnCTCCAC GTAAGCTAGC GCTCACGTTT 120  
CAAAGGCTCC TACCTATCCT GTGACAAGnT GTGCCGAATT TCAATATCAG GCTACAGTGA 180  
AAGCTCCACG GGGTTCTTTC CGT 203

35

(2) INFORMATION FOR SEQ ID NO: 4675:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 229 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4675:

45

nnGTTTGTAA ATAATATGGT GGAGACTAGC GGGATCGAAC CGCTGACCTC CTGCGTGCAA 60  
AGCAGGCGCT CTCCCAGCTG AGCTAAGCCC CCATAATAAT TACAGTATAT CGGGAAGACA 120  
GGATTGGAAC CTGCGACCCC TTGGGTCCCA AACCAAGTGC TCTACCCAGC TGGAGCTTAC 180  
TTTCCCGGTA TTATTTAACG CGGCCCGATA GGGAGTCGGA ACCCATTA 229

50

(2) INFORMATION FOR SEQ ID NO: 4676:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 178 base pairs

55

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4676:

TCTAAAAATC GCGCACTTAA ACCGCTTATG ACAATCATT A TTACCTCAAT ATGCTTGTCA 60  
TCACTTGCCT TTATCGTCGT TCATTGGCTA TATAGTTAAT ATGAAAAGAC GCTCAAACAC 120  
TTACAAATTT AGTGTGCnGA GCGTCTTATT TTTATACTTT AAAAGTCGTA TTGGTTGT 178

(2) INFORMATION FOR SEQ ID NO: 4677:

15

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 286 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4677:

GCAAGTAAGC ATAATGTGGA GCCGTAGCGA AACAGTCTGA ATAGGGCGTT TAGTATTTGG 60  
TCGTAGACCG GAAACCAGGT GATCTACCCT TGGTCAGGTT GAAGTTCAGG TAACACTGAA 120  
TGGAAGGACC GAACCGACTT ACGTTGAAAA ATGAGCGGAT GAACTGAAGG TAACCGGAGA 180  
AAATCCCAAT CGAACCTTGG GAGATAAGCT TGGGnTCTCC TCCCGAAAAT AAGCCTTTTA 240  
GGGGCTTAAG CCTCCAAAGT GGATGATTTA ATTTGGAAGG TAAAn 286

(2) INFORMATION FOR SEQ ID NO: 4678:

35

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 229 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4678:

CACACGGCTT ATGGTAACAA AAAATTCCTT TGGAGCATT A TGGAGCGGAA GATAGGTTTA 60  
CACCTATACC TCGTTCCGGA AGGAnTGTTT TAAAAGTGAA CTACTCCCGC AATATTAAAT 120  
ATGGAGCGGA GATAGGATTT ACACCTATAC CTCATTCCAG AGGATGTATT CTAAGAGTGA 180  
AATACTCCCC ATATATTAAA TATGGAGCGG AGATAGGATT GACCATAcn 229

(2) INFORMATION FOR SEQ ID NO: 4679:

55

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 173 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4679:

ATGACTGCTT TTTATTATAC TTTACATTTT TCGTTTCGTC AGATTCAAAC GTTTTCACTT 60  
CGCCAAGCCA TCTTTCCTTG TGTTTGCTTT TATTTTGACG TTTTAGACAT AAAAAAGAG 120  
ACCTTGCGGT CTCAATGnGG CTCATCGCAT CCACTTTTTG CCTGGCAACG TTC 173

(2) INFORMATION FOR SEQ ID NO: 4680:

15

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 183 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4680:

AAAAGTAACA AGAGAAGGAC AAAAAGGTGA GAAGACAATA ACGACGCCAA CAAAAATCCA 60  
TTAACTGGAG AAATTATTAG TAAAGGTGAA TCGAAAGAAG AAATCACAAA AGATCCCATT 120  
AATGnATTAA CAGAATACGG ACCAGAAACG ATAACACCAG GTCATCGAGA CGAGTTTGAT 180  
CCC 183

30

(2) INFORMATION FOR SEQ ID NO: 4681:

35

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 203 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4681:

CGGTGCTTTC ACTTTCCTAC AGACTGGTTA CTATCGGTCA GAGAGAGATT TAGCnTTAGG 60  
AGATGGTCCT CCCAGATTCC GACGAATTTC ACGTGTTCG TCGTACTCAG GATCCACTCA 120  
AGAGAGACAA CATTTTCGAC TACAGGATTA nTACCTTCTT TGATTCATCT TTCCAGATGA 180  
TTCGTCTAAT GTCGTCCTTT GTA 203

50

(2) INFORMATION FOR SEQ ID NO: 4682:

55

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 187 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4682:

GGGTCACACC TGTTCCCATG CCGAACACAG AAGTTAAGCT CCTTAGCGTG CGATGGTAGT 60  
 5 CGAACTTACG TTCCGCTAGA GTAGAACGTT GCCAGGCCAAA AAGTGGGATG CGATGGAGCC 120  
 GCATTGGAGA CCGCAAGCCT CTGTTCTTTG ATGTCTAAAA CGTnCAAAAT AAAAGCGAAC 180  
 10 ACAAAGA 187

## (2) INFORMATION FOR SEQ ID NO: 4683:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4683:

GGCTACACTG GTCATGATGC TGCTAAACTA CGTGATTATn ATGAAACACA TCATGCTTTG 60  
 TCTGGATATG AAATGATTGA CGCAGCAAAG GTGCCATTGC AACAAATGAA GTCAATGCTG 120  
 25 CGATGGGTAT ATTTGTGCAA CGCCAACAAC TGGTTCCTCC GGTACCATCC CGGTGCAGTT 180  
 TTAAATT 187

## (2) INFORMATION FOR SEQ ID NO: 4684:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4684:

AGTGCCAAGG CATCCACCGT GCGCCCTTAA TAACTTAATC TATGTTTCCA TCCTACAGGA 60  
 AACCGTTATT AATCTTGTGA GTGTTCTTTC GAACACTAGC GATTATnTCT TATGAATTCA 120  
 45 AGCTTATTTA AAACTCTTTA TTCACTCGGT TTTGTAAAT CTATATTT 168

## (2) INFORMATION FOR SEQ ID NO: 4685:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4685:

ACGGGAAGTA GCTCAGCTTG GTAGAGCACT TGGTTTGGGA CCAAGGGGTC GCAGGTTCGA 60  
 ATCCTGTCTT CCCGATTACT TCTTAAATTC CATTTTATGG GGGCTTAGCT CAGCTGGGAG 120  
 AGCGCCTGCT TTnCACGCAG GAGGTCAGCG GTTCGATCCC GCTAGTCT 168

## (2) INFORMATION FOR SEQ ID NO: 4686:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4686:

ATGATTCAAG CTTATTTAAA ACTCTTTATT CACTCGGTTT TGCTTGGTAA AATCTATATT 60  
 TTACTTACTT ATCTAGTTTT CAATGTACAA TTTCTTTTTA GTCAAGCGCT CGCATACTGC 120  
 nTTATTTTCA AAAAATCAAA TGCTCATTTA CAAAAGTAAA CTCCGCTTTT AATT 174

## (2) INFORMATION FOR SEQ ID NO: 4687:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4687:

TGTTGTTGAA TATGAAGAAG ATACAAACCC AGGTGGTGGT CAGGTTACTA CTGAGTCTAA 60  
 CTTAGTTGAA TTTGACGAAG AGTCTACAAA AnGTATTGTA ACTGGCGCAG TGAGCGATCA 120  
 TACCACAGTT GAAGGTACGA AAGAATATAC AACTGAAGTA ATCTGA 166

## (2) INFORMATION FOR SEQ ID NO: 4688:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4688:

AGAACCTTAC CAAATCTTGA CATCCTTTGA CAACTCTAGA GATAGAGCCT TCCCCTTCGG 60

GCAACGAGCG CAACCCTTAA GCTATTGCCA TCATTAAGTT GGGCATCTAA TTGACTGCCG 180

GTGACAAAC 189

5

(2) INFORMATION FOR SEQ ID NO: 4689:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 227 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4689:

TAACCACTCC TCTTAACCTT CCAGCACCGG GCAGGCGTCA CCCCTATACA TCACCTTACG 60

GTTTAGCAGA GACCTGTGTT TTTTGATAAC AGTCGCTTnG GGCTATTCAC TGCGGCTCTT 120

20

CTGGGCGTTA ACCCTAAGAn ACCCTTCTCC CGAAGTACGG GGGCATTTTG CGAGTCCTAA 180

CGAGGTCGTC GTCACCTAGA TTCTCATCTT GATACTGTGT GGTGCG 227

25

(2) INFORMATION FOR SEQ ID NO: 4690:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 174 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4690:

35

AGATAATGCA CCATCAACTA ATGGATATTT ATGTCCAGTT GGGGGCCAGA AATCATAAAC 60

GTCTTCAGTG TAAGCAACAG CATCTTCATT TnGCAGCCAA AATGCTTGGA TTATGTGCAA 120

TAACCATCGC AACTGCGCCA CACCTTGTGT TGGCTCGCCG CCTGAAGTGG GGTG 174

40

(2) INFORMATION FOR SEQ ID NO: 4691:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 363 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

45

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4691:

TTTTTTTTTA AAAAAAGGGA AGGGAAAAAn AAAAGGGAAA AAAATTTAAC CCAAGGGTTT 60

TTAAAGGGGG CCAATTTTTT CCCAAAAAAA AAACCCTTTG GGTAAATTT TTTTAAAAAA 120

55

GTTAAATTTT TTTAAAAAGG GTTCCCTTTT AAATTTTGGG AAAAACCCCC TTTTTTTTTT 240  
 TTAAGGGAAT TTAAAAAATT TAAGGCCCTC CCCTAAATTA AAATTAAAGG TGGGAAAAAA 300  
 5 AAAATTAATT AAAAACCCTA TTTTTTTTTT TTAATTTTIT AACCCAAAGG GGGTAATTG 360  
 GCC 363

(2) INFORMATION FOR SEQ ID NO: 4692:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 210 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4692:

20 TAGTGTCAAT TTTATTGATA TTTGCAATTA AACTGAAATT TAATTTTTCG GATGTATTTT 60  
 HTTTACTTAA AGTAAATAG AACACGATTT TGATGTCTGG GAATAGTGGA AATGATAAAA 120  
 ACTACTAATG ATTGATTAAG TAGTGGTTCT TAACATTAGC CTCAGCTAAT TGTACTTAA 180  
 25 AAATAGGAAT ACATGAGTAA AACTCANTGG 210

(2) INFORMATION FOR SEQ ID NO: 4693:

- (i) SEQUENCE CHARACTERISTICS:
- 30 (A) LENGTH: 209 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4693:

ATAGTAGTAA AGTATTTTCT TCCAAACATT TATTTTGATT AAGTCTTCAT CATTAGTATT 60  
 40 CTCAGCTCCA CATGCACCAT CTTCCACCTC AACCTATTAA CCTCATCATC TTTAGGATCT 120  
 TATAACCAAT TGGAAATCTC ATCTTGAGGn NGCTTCATCT TAGATGCTTT CACACTTATC 180  
 CCTCCACACA TAGCTACCCA GCTATCCGT 209

(2) INFORMATION FOR SEQ ID NO: 4694:

- (i) SEQUENCE CHARACTERISTICS:
- 50 (A) LENGTH: 222 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear



GCACATTAAC CnAAGCACCA GGCCATATAG CAATTGTTGA TACAGTATTT AAATATTTAG 60  
 CATGTGACGG AATAGTTACA TATGTATTCA CTAAGGCCAT AATGACAAAT CCATTAAAAA 120  
 5 GTTGGATGCT TATTCGACCC TGCTAGATGA TCTGATGAAC GGAACGCATA TTAAATAAGT 180  
 ACGTGGTTAT GGATCAGTAA GATACTCTAC CAGTTACCAG nG 222

## (2) INFORMATION FOR SEQ ID NO: 4695:

- 10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 159 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4695:

20 TCGTTTCTCAA TAGAATGATT TAAATCTTCG ATTTCTTTAT CTAAATGACT ACCAATTAAA 60  
 TCTATTTCTT CTATTGTAA ATCGCTATCT CCATCTTCTT TTATCTCTGG TATTATnTTT 120  
 TCTTCAACTA AGTCACGATA TAATGTTTTT GAATTTTCG 159

## 25 (2) INFORMATION FOR SEQ ID NO: 4696:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 161 base pairs  
 (B) TYPE: nucleic acid  
 30 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4696:

AATATGGTAG TTTTAACTT ATCTATTAAG GTACAATTGA CCAAATCGAT AAAACAAATA 60  
 ATACGTATCG TCAGACAATT TATGTCAATC CAAGTGGAGA TAACGTTATT GCGCCGGTTT 120  
 40 TAACAGGTAA TTTAAAACCA AATACGGATA GTAnTGCATT A 161

## (2) INFORMATION FOR SEQ ID NO: 4697:

- 45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 170 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4697:

CCAAACTCAA TATGGCTTTA TTGGCACAGG GAACAGATAT GGAAGGTTTT ATTTATGGnT 60

ATATGGGATC AACACACAAA GCCGGACGCA GTGAATATTA CGCAAAATGA

170

(2) INFORMATION FOR SEQ ID NO: 4698:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 161 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4698:

CCACGGCTAA CTACTGCCAG CAGCCGCGTA ATACGTAGTG GCAAGCGTTA TCCGGAATTA 60  
 TTGGGCGTAA ACGCGCGTAG GngTTTTTTTA AGTCTGATGT GAAACCCACG GTCAACCGGA 120  
 GGGTCATTGG AAAGTGGAAA CTTGAGTCAG AAGAGGAAGT G 161

(2) INFORMATION FOR SEQ ID NO: 4699:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 248 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4699:

TAAATCTTCA TCAATATGAT CTAACCAATA TTGATAAAAC CTTGATGTGT TTCGTGTCAA 60  
 TGACATACCA TATCGACTAG GTACCTTTTTT AGAATGTTGA TTAATCACAA CAAATATCAT 120  
 GGGCAAGGTC ATCTTGCAAA ATGGATTCCA TTCAAGTGGG AGGGnCGATG ATGGACGTGC 180  
 TGCATGCACT GATGACCCTT TTTGCCCATC CTGGCAAATC CCACCATGAA ATGACTGACG 240  
 CGGACGCh 248

(2) INFORMATION FOR SEQ ID NO: 4700:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 175 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4700:

CCCGACGAAG CGAACGTTTG GCACTGTCTC AACGAGAGAC TCGGTGAAAT CATAGTACCT 60  
 GTGAAGATGC AGGTTACCCG CGACAGGACG GAAAGACCCC GTGGAGCTTT ACTGTAGCCT 120

## (2) INFORMATION FOR SEQ ID NO: 4701:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4701:

TACAGGGTAG TGAGATTTTCG AAACAATATG GAGAAGCAGG ACTTCCTGGA AAATACAATT 60  
 AATGTTTATA CGAATGGTCA TGCTGGTCAA AGTTCTTGCA GGCATATGCA CCGAAAGCTT 120  
 AATGATTCAT CATACTGGAG ATGCGAATGA CTATGTTGGG TAAAGGATTT ATCTGGT 177

## (2) INFORMATION FOR SEQ ID NO: 4702:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4702:

CGATTGGATT GCACGTCTAA GCAGTAAGGC TGAGTATTAG GCAAATCCGG TACTCGTTAA 60  
 GGCTGAGCTG TGATGGGGAG AAGACATTGT GTCTTCGAGT CGTTGATTTC ACACTGCCGA 120  
 GAAAAGnCTC TAGATAGAAA ATAGGTGCCC GTACCG 156

## (2) INFORMATION FOR SEQ ID NO: 4703:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4703:

CTTGAAAAAG ATGGTTATTTC TGTTGAAGTA ATTGACTTAC GTACTGTTCA ACCAATCGAT 60  
 GTTGACACAA TTGTAGCTTC AGTTGAAAAA ACTGGTCGTG CAGTnGTCAG CAAGACGCAC 120  
 AACGTCAAGC TGGTGTGGT GCAGCAGTTG TAGCTGAATT AAGTGA 166

## (2) INFORMATION FOR SEQ ID NO: 4704:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4704:

GCGGTGTCTT AACCGCTTGA CCAAGGAGCC ATGGCTCCAC AGGTAGGnCT CGAACCTACG 60  
 ACCGATCGGT TAACAGCCGA TAGCTCTACC ACTGAGCTAC TGTGGATTAA TATTATGCCT 120  
 GGCAACGTTT TACTCTAGCG GAACGTAAAGT TCG 153

(2) INFORMATION FOR SEQ ID NO: 4705:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 163 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4705:

AGGTAGAGCA CTGTTTGGAC GAGGGGCCCC TCTCGGGTTA CCGAATTCAA ACAAACTCCG 60  
 AATGCCAATT AATTAACTT GGGAAGTCAG ACACATGGGT GATAAGGTCC GTATTCGAAA 120  
 nGGAAACAGC CCAGACCACC AGCTAAGGTC CCAAAATATA TGT 163

30

(2) INFORMATION FOR SEQ ID NO: 4706:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 203 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4706:

40

TAAGGTTGGG ATTGTTTGTG GGCTCGTTGC CACCCATTGT ACGGCACTCA TCAnTTCAAG 60  
 CCACCAGCTA CAGTATATCT CCTTGACCAG CCATAATTG ATTGGCTGCA GTCGCGATGG 120  
 TTTGTAATCC TGATGAGCAG TAGCGATTCA TGTTTGACn GTACCCGTCA GATATCCGCA 180  
 GCAATGCAAT GTGTGCAAG TTT 203

45

(2) INFORMATION FOR SEQ ID NO: 4707:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 153 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4707:

CGGGTGAGAA TCCGTCCACC GATTGACTAA GGTTCACAGA GGAGGCTCGT CCGCTCTGGG 60  
 5 TTAGTCGGGT CCTAAGCTGA GGCGCAGnGT AGGCGATGGA ATAACAGGTT GATATTCCTG 120  
 TACCACCTAT AATCGTTTTA ATCGATGGGG GGC 153

(2) INFORMATION FOR SEQ ID NO: 4708:

10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 150 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4708:

20 nCTATAATGA ATAAATAATT TAGAAATATG CTTCGGATTG TTCGATGCTT TAATTCAGTT 60  
 AGAAGCATCA TAGAATGCAT GATTACTGTT GTAAAGATAC GTAATGTTTT GTATTGACTG 120  
 TATGTCTTTG GATAGAGTTA CAAACTTATT 150

25 (2) INFORMATION FOR SEQ ID NO: 4709:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 156 base pairs  
 (B) TYPE: nucleic acid  
 30 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4709:

35 AAAATTCGGG TTCTCAAATC ATCGGAACAT AACAAAACAA CCTAAGCAAC ATGTAGGCCG 60  
 TTGTCACCTTA ACTTCTTGTT TTTCCGATGA CAGCTTCTAT TnAGAGAATG TCATGATTAT 120  
 40 TTTATATTCA CTTCAATGTT ATCAGTATTA GTGCCA 156

(2) INFORMATION FOR SEQ ID NO: 4710:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 149 base pairs  
 45 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4710:

GTTGATATTC CTGTACCACC TATAATCGTT TAATCGATGG GGGGGACGCA TAGGATAGGC 60

55

TCGTTAAGGC TGAGCTGTGA TGGGGAGAA

149

## (2) INFORMATION FOR SEQ ID NO: 4711:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 160 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4711:

TTGACTTCAA TACCATGGGC CAGGTACnCT TTAAATGTTG TTGTCTCAGT TAATATTAAT 60

TGGCTTTTCT TTTGCATAAT TGACAATGGC TTCTGCCAAT GGGTGTTTCAG AATCTTTTTC 120

AGCAGTAGCA AGTAGTTGGT AGCGTTTGAT TGGTCACCAG 160

## (2) INFORMATION FOR SEQ ID NO: 4712:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 151 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4712:

ATAGTGAACC AGTACCGTGA GGACnAGGTG AAAAGCACCC CGGAACGACG TGAAATAGAA 60

CCTGAAACCG TGTGCTTACA AGTAGTCAGA GCCCCTTAAT GGGTGATGGC GTGCCTTTTG 120

TAGAAATGAAC CGGCGAGTTA CGATTTGATG C 151

## (2) INFORMATION FOR SEQ ID NO: 4713:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 145 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4713:

ACCAGTTGAT CTACCCTTGG TCAGGTTGAA GTTCAGGTAA CACTGAATGG AGGACCGAAC 60

CGACTTACGT TGGAAAAGTG AGCGGGATGA ACTGnGGGTA GCGGAGAAAT TCCAATCGAA 120

CCTGGGAGAT AGCTGGTTCT CTCCG 145

## (2) INFORMATION FOR SEQ ID NO: 4714:

(A) LENGTH: 151 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4714:

10 TGTnACGCAG AGATCGCGGG TTCGATTCCC GTCGAGACCG CCATTTAATT TTATAATTAA 60  
 TAGCGATGTA CCTATAATAA TGGAGGAATA CCCAAGTCCG GCTGAAGGGA TCGGTCTTGA 120  
 AAACCGACAG GCCTTAACGG GCCGCGGGG T 151

15 (2) INFORMATION FOR SEQ ID NO: 4715:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 151 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4715:

25 TCGTATTGAA TGGCTTCGTT TCCTAGGGTG CCGTCTCAGC CTCGGTCTTC GACTGGCACT 60  
 GCTCCCTCAG GAGTCTCGCC ATTAATACTA CGTATTAACG TGTAATTTTA CTTTGnAATA 120  
 30 CTTTAAAAAA ATAAGACACT TTGCCAACTT G 151

(2) INFORMATION FOR SEQ ID NO: 4716:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 152 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4716:

40 GCTGTCATCG GAAAAACAAG AAGTTAAGTG ACAAGGGTTT ACATGTTGCT TAGCTTCTTT 60  
 45 TATTATGCGT AATGATGTAA AAAGACGAAT ATTCAATTGT TTGTAAAAGT GGCATTTCTA 120  
 TGTCTTAAAA GTGACGAAAC TTCACnCTGT GC 152

(2) INFORMATION FOR SEQ ID NO: 4717:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 144 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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55

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4717:

GGATACTAGT AAAACCATAT TTAGTAAATA CAGATGGANT AAATCTTTTA AGGCTTATAA 60  
 5 ACGCTCATCT GACATTGTAG AATTCATGCT TTCAAAGAC GATATACTAC GACTCCTA 120  
 CGAACTTGTC CAAGGATTAC GAAA 144

## (2) INFORMATION FOR SEQ ID NO: 4718:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4718:

ATCATAAGGG GCATGATGAT TTACGTCATC CCCACCTTCC TCCGGTTTGT CACCGCAGTC 60  
 20 AACTTAGAGT GCCCAACTnA ATGATGGCAA CTAAGCTTAA GGGTTGCGCT CGTTGCGGGA 120  
 CTTAACCCAA CATCTCACGA CACGA 145

## (2) INFORMATION FOR SEQ ID NO: 4719:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4719:

AAATACCTTT CCACGATCTT CAGCTGGGCG CCTCTGCACT CGCAAACGCA CTTGATGCAT 60  
 35 CAACAACACC ACCAAATAGT CCCTGCAATA ACCTCACAGT ACAAACGTGTA ATGGTGTCGT 120  
 40 ACACnATGCC ATTTAAAAAT AGCATACCGG CAAAGC 156

## (2) INFORMATION FOR SEQ ID NO: 4720:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4720:

TTAAATCGAG TCTCTTTTAC AGGTCCATAT TTTGTTACGT ATCGACCGGT GGCTAACTAC 60



TAACTCGGAT CAAATTCGTC TCGATGACCT GG

152

(2) INFORMATION FOR SEQ ID NO: 4721:

5

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 146 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4721:

15

CACTAGTTCA AGTTCAGTG GCGACGATTG GTATTTTACA AGAATTTTAT CAACAAGGAT 60

TTAATTAGCT TAAACGCGC AATCCCTGTG TTACTAGGGC GGATAACATT GGTACCACGG 120

TTACAGCTAT CTTAGCTAGT TTAGCC 146

20

(2) INFORMATION FOR SEQ ID NO: 4722:

25

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 156 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4722:

CCACACCAAT ATTTGCGCT AAGTAAATCG CATTAAACGT TTGTCTTCCG CCATTTGAGC 60

CACACTGCTC CAGCTCATAG CGCTATATCG CAGGGAATAA TCATTCCGCC ACCACAACCC 120

35

TAACATTACC CAGCCATACA GCCATACCAG GGCCAC 156

(2) INFORMATION FOR SEQ ID NO: 4723:

40

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 161 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4723:

ACGGTCTTGC TGTCATTAT AGATGGATCC GCGCTGCATT AGCTAGTTGG TAAGGTAACn 60

50

GCTTACCAAG GCAACGATGG CATGAGCCGA CCTGGAGAGG GTGGATCGGG CCACACTGGG 120

AACTGAGACA CGGTCCAGAC TCCTACGGGG AGGCAGCAGT A 161

(2) INFORMATION FOR SEQ ID NO: 4724:

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(A) LENGTH: 165 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4724:

10 CAGAAAGCTC ACGGGGCTTT CGTCTGTGCG GGGTAACCTG CATCTTCACA GGTACTATGA 60  
 TTTCACCGAG TCTCTCGTTG AGACAGTGCC CAAATCGTTA CGnCTTTCGT GCGGGTCGGA 120  
 ACTTACCCGA CAAGTAATTT CGCTACCTTA GGACCGTTAT AGTTA 165

15 (2) INFORMATION FOR SEQ ID NO: 4725:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 149 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4725:

25 GGACGTTATA AGTGCTGAAA CATCTAAGCA TGAAGCCCCC CTCAAGATGA nATTTCCCAA 60  
 CTTCGGTTAT AAGATCCCTC AAAGATGATT AGGTTAATAG GTTCGAGGTG GAAGCATGGT 120  
 30 GCATGTGGA GCTGGACGAA TACTAATCG 149

(2) INFORMATION FOR SEQ ID NO: 4726:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 275 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4726:

40 TTGAATTTTT GAAAAAATA TGCCGAAATA AAAGATGCCA AGATATCCGC CGGGTAAAAA 60  
 45 ATTAAGTTTC CGAAAAACCA GGTGTTGGTA CCCATTGCAT CTGGGGTGGC AAAAGCATT 120  
 GCAGATAAAA TTGTCATCAG TGGTTACGAT GGTGGTACAG GGCTTCACCC AAACGAGTAT 180  
 CAGCATGCCG GTGTTCTTGG GAGATGGTTA GCAGAACACA TCAACATAAA CTAATGCTAA 240  
 50 GAnCGGTAAA GTAGACAnCG GTAGTATACT GAAAT 275

(2) INFORMATION FOR SEQ ID NO: 4727:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 149 base pairs

55

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4727:

ATCAATGAAC AACACATACA GATGGTACTG CGACGCCTAG AGTAACAAAA TAAGTTTTGT 60  
10 AACTCTATCC AAAGACATAC AGTCAATACA AAACATTACG TATCTTTACA ACAGTAATCA 120  
TGCATTCTAT GATGCTTCTA ACTGAATnA 149

(2) INFORMATION FOR SEQ ID NO: 4728:

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(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 158 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4728:

GCACGTTATT CCATTATCTT AATGGTTATC TTATCCTCAA CTAAATTGGA GGAATCACTA 60  
25 TGACAATTAA TAAAGAACCG TTCTTGCGC AGCACAATGG GCGCTCACTG GCAGACTTTT 120  
GTGATGCTGA CTTAAAGTAA ACTATTAGAT ATTGnGTG 158

30

(2) INFORMATION FOR SEQ ID NO: 4729:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 138 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4729:

40

TCATTGACAT CGCTGGAATA GGTGTAAATC CTGCGATTCTG ATCTGGACCA TATTTTTTTA 60  
TTGTATACAG TAATTGTGCT GCGATTATCT CTGTAACGTC TTTCCAATTT GAnCGCACGT 120  
45 GCCCTCCCAT ACCTCGGG 138

(2) INFORMATION FOR SEQ ID NO: 4730:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 187 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

50

55

TAAAGACTAT ACCATTCTAT CCAATAATAA TTGGATTTCG ATTGTCTGA ATTCGTAACC 60  
 GAGAGGCCCC TCGTCCAAAC AGTGCTCTAn CTCCAATAAT CATCACTTGA GGCTAGCCCT 120  
 AAAGTATTTC GGAGAGAACC AGCTATTTCC AGTTCGATTG GAATTTCTCC GCTACCCTCA 180  
 GTTCATC 187

(2) INFORMATION FOR SEQ ID NO: 4731:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 137 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4731:

CGCATCCTGG GGCTGTAGTC GGTCCCAAGG GTTGGGCTGT TCGCCATTAA AGCGGTACGA 60  
 AGCTGGGTTT AGAACGTCGT GAGACAGTTC GGTTCCTAT CCGTCGTGGG CGTAGGAAAT 120  
 TTnAGAGGAG CTGTCCT 137

(2) INFORMATION FOR SEQ ID NO: 4732:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 137 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4732:

TCGTTCTCAA TAGAATGATT TAAATCTTCG ATTTCTTTAT CTAAATGACT ACCAATTAAA 60  
 TCTATTTCTT CTATTGTTAA ATCGCTATCT CCATCTTCTT TTATCTCTGG TATTATnTTT 120  
 TCTTCAACTA AGTCACG 137

(2) INFORMATION FOR SEQ ID NO: 4733:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 137 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4733:

TCGTTCTCAA TAGAATGATT TAAATCTTCG ATTTCTTTAT CTAAATGACT ACCAATTAAA 60

TCTTCAACTA AGTCACG

137

(2) INFORMATION FOR SEQ ID NO: 4734:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 153 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4734:

AAAACATAAA TACAAAAATA TAGCTATTAC TATAAAAAAC AGCAGTAAGC ATATTTCCAA 60  
 ATTGCAAATT ATCCTACTGC TGTTCTTTTT GGGCAGTGGG AACAGCAAAT GATATTTTCG 120  
 ACAAATTTA TTTCGTCGTC CCACCCCAAC TTG 153

(2) INFORMATION FOR SEQ ID NO: 4735:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 142 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4735:

TAGAAATTAC GGACCCAATT TCTCTATGTT GGGGCCCATC CCCAATTGC ACATnATTGC 60  
 AAGCTGACTT TTCGTCACCT GCTTTGTTGG GGCCCCGCCA ATAAGCGTTG TAGTGCCTAG 120  
 TACTTTGATT GATGTCCAAG TT 142

(2) INFORMATION FOR SEQ ID NO: 4736:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 137 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4736:

ATGTTATTCA AAGTAAATTG CTTTGCCTGA TTTTGCAGAC TGATAAATCG CTTCAAGAAT 60  
 TTTTGTAACCT ACCATTGCTT GTTCCGGTTT CACAACTGGT TCAGTATCAT TTACAACnGC 120  
 ATCAATCCAA GCTTTTG 137

(2) INFORMATION FOR SEQ ID NO: 4737:

(A) LENGTH: 144 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4737:

10 GGTCTTTTAG TATTTGGTCG TACACCGCAA ACCAGGTGCA TCTACCCTTG GTCAGGTTGA 60  
 AGTTCAGGTA AACTGAAAT GGAGGACCGA ACCGACTTAC GTTGAAAANT GAGCGGATGA 120  
 ACTGAGGGTA GCGGAGAAAT TCCA 144

15

(2) INFORMATION FOR SEQ ID NO: 4738:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 157 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4738:

25

GGGTAGCTAT GTGTGGACGG GATAAGTGCT GAAACATCTA AGCATGAACC CCCCTCAAGA 60  
 TGAGATTTCC CACTTCGGTT ATAAGATCCT CAAAGATGAT GAGGTTAATA GGTGAGGTG 120  
 30 GAACATGGTG ACATGThATC TGCTTTTCTA ATCATAC 157

(2) INFORMATION FOR SEQ ID NO: 4739:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 145 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4739:

40

GCTTTATGTC TAAAACGTCA AAATAAAAAG CAAACACAAA GAAAATGGC TTGGCGAAGT 60  
 45 GAAAACGGTT GAATCTGACG AAACGAGAAA AGAACGCAAC GAGTTTAGTA GAGCTAnATG 120  
 AGTAAGTGAG AGCCGAAGAG AGGGA 145

(2) INFORMATION FOR SEQ ID NO: 4740:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 234 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50

55

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4740:

5 TAGTAGCACC ACCCTTAGAC CTTCTTGATT TGACATCGTT GTTCTTCCTT CCTTCGGTCT 60  
 CGTTACTCAT TTAGCTCTAC TAAACTCGTT GCGTCTTTTC TCGTTTCGTC AGATCAAACG 120  
 TTTCACTTCG CCAAGCCATT TTTCTTGTGT TTATTTTATT TGACGTTTAG ACATAAAAAA 180  
 10 GAGACCCACG TTCAACTTGC CnGCACGTTT TACTCTGCGG AnTAGTGGCT ACCA 234

## (2) INFORMATION FOR SEQ ID NO: 4741:

## (i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 135 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4741:

20 GCAAGTCTTT TTAAAGGTAA CACTATCATT TATGCAATAC GGCGCATTAC CAGAGTTGCA 60  
 TGGTCAAAAT ATATTGTTGT CATTGAAGA TGGACGTGTA CAAAAATGCG TGTTACGTGA 120  
 25 TCATGATACT GTCAn 135

## (2) INFORMATION FOR SEQ ID NO: 4742:

## (i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 145 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4742:

35 ACCCTGGTAC AGTTGAATTC AGGTAACACT GAATGGAGGA CCGAACCGAC TTACGTTGAA 60  
 40 AAGTGAGCGG ATGAACTGAG GGTAGCGGAG AAATTCCAAT CGAACCTGGA GAnAGCTGGT 120  
 TCTCTCCGAA ATAGCTTTAG GGCTA 145

## (2) INFORMATION FOR SEQ ID NO: 4743:

## (i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 151 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 50 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4743:

55

TGATTATCAT GGGTGC GGGT ATTAACCATT GGTTTAACTC AGATACGATT TATnGTGCAA 120  
TCTTAAACTT AGTTATGGTA TGTGGCGTCA A 151

(2) INFORMATION FOR SEQ ID NO: 4744:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4744:

TAAAGCTAAA AACACAGCTC ATAATATCAA AAAAGGTGCA GAAGAAATGG TTGAAGCGGC 60  
AGGCGATAAA ATCAAGATG GTGCATCTTG GTTAGCGCAT AAAATCGGCG ATGTGTGGGA 120  
TTATGTACAA CA 132

(2) INFORMATION FOR SEQ ID NO: 4745:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4745:

CGTGCGCTCT AACCAGCTGA GCTATAGGCC CATTAAATTTG AATGAACAAA CATTCAAAAC 60  
TGAATACAAT ATGTCACGTT ATTCCGCATC TTCTGAAGAA GATGTTCCGn ATATATCCTT 120  
AGAAAGGAGG TG 132

(2) INFORMATION FOR SEQ ID NO: 4746:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4746:

GTGATCCGAC TCAGATAGCG ATCCGACTCA GATAGCGACT CAGATTCAGA CAGCGATTCA 60  
GATTCAGACA GCGATTCAGA TTCAGATAGC GATTCAGATT CCGACAGTGA CTCAGATTCC 120  
GACAnTGACT CCGATTCA 138



- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 185 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4747:

10 CATTATTGTA AACTGAACTT TTCGTCACCT GCTGGTGnTT GGGGACCCCA CCAACTTGGC 60  
 ACATTATTGG TAAGCTGACT TTTGTCACCT TACTGTGTG GGGCCCCGCC AACTTGCATT 120  
 15 GTCGTAGAA ATTGGGAATC CAATTTCTCT ATGTTGGGCG CCACACCCCA ACTCGACATT 180  
 GCCTG 185

(2) INFORMATION FOR SEQ ID NO: 4748:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 173 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4748:

ACCGAATCCC TTCAGACCGG TACTTGGGTA TTCCTCCAAA ATTATATGGA CCTTGACAGT 60  
 30 ACTCGAACCT GACGTACCGA AACGGTTATG AAGACCGTTA nCTCTAACCA ACTGAGCTAA 120  
 AGGATCCTAA ATATAATTTT ACAACTAATA AATAGTGGAC GGTGGAGGGA TCG 173

(2) INFORMATION FOR SEQ ID NO: 4749:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 212 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4749:

45 ACACAAGGAT AAGGCATTGT TGGATGTGGG ATGCTTTAAC TGGGCAAGCG ATTGGTCGTC 60  
 CTAACACAGG TACATATGCC GGCTATCTGA CCTAGTCGGT TTAGATATTG CAGTGTCTGT 120  
 AATTAAAGGG CATGCAACCA AGTAnCTGAG GAAACAACCT ATTTTCATGG TGTCAAAAAT 180  
 50 TgntAAATAC GGTGTTTGAC AATTGCGCAC CT 212

(2) INFORMATION FOR SEQ ID NO: 4750:

- (A) LENGTH: 140 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4750:

10 AATCTCAGGT TTTACCAAGC AAAACCGATG AATAAAGAGT TTTAAATAAG CTTGAATTCA 60  
 TAAGAAATAA TCGCTAGTGT TCGAAAGACn GCAGCAAGAT TAATAACGCG TTTAAATCTT 120  
 TTTATAAAAAG AAAACGTTTA 140

15

(2) INFORMATION FOR SEQ ID NO: 4751:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 184 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4751:

25

ATTCGTCAGC TCCACATGTC ACCATGCTTC CACCTCGAAC CTATTAACCT CATCATCTTT 60  
 GAGGGATCTT ATAACCGAAG TTGGGAAATC TCATCTTGAG GGGGGTTCAT GCTAGATGCT 120  
 30 TCAGACTATC CCGTCCACAC ATGTAACCAG nATGCGTGGA CGCATGGAAC AGGGATGTCA 180  
 TCCG 184

35

(2) INFORMATION FOR SEQ ID NO: 4752:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 133 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4752:

45 GGGATCTTCC GCAATGGGCG AAAGTGTACG GAGCAACGCC GCGTGAGTGA TGAAGGTCTT 60  
 CGATCGTAAA ACTCTGTTAT TAGGGAAGAA CATATGTGTA AGTAACTGTG CACATCTTnA 120  
 CGGTACCTAA TCA 133

50

(2) INFORMATION FOR SEQ ID NO: 4753:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 162 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

55

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4753:

5 GTATGCTGTG TGGCTTGTCa TGTTCCGGTT TGGTGGCGGA CCTGATTATT CCTGCGnTAT 60  
 ACGCTATGGC TGGAGCACTG TGGCCAAATG GCGGAAGACA AACGTTTAAT GCGATCTACT 120  
 TGGCGCAAAA TATTGGTGTG GCTGTCCGGT CTGCAATGGG CG 162

## (2) INFORMATION FOR SEQ ID NO: 4754:

10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 134 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4754:

20 AATTCGATTc CCTTAGTAGC GCGGACGAAA ACGGGAAnGA GCCCAAACCA ACAAGCTTGC 60  
 TTTGGGGGTT TGTAGGACAC TCTATACGGG GTTAACAAAG GACGACATTA GACGAATCAT 120  
 25 CTTGGGAAAG ATGA 134

## (2) INFORMATION FOR SEQ ID NO: 4755:

30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 139 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4755:

35 AGAGTGCgTA ATAGCTCACT AGTCGAGTGA CACTGCGCCG AAAATGTACC GGGGCTAAAC 60  
 ATATTACCGC AAGCTGTGGA TTGTCCTTTG GACATGGCTA GGAGAGCGTT CTAAGGGCGT 120  
 40 TGAAGCATGn ATCGTAAGG 139

## (2) INFORMATION FOR SEQ ID NO: 4756:

45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 163 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4756:

55

CGTGAAATGC GCAGAGATAT GGAGGAACAC CAGTGGCCGA AAGCCA~~CTTT~~ CTGGTCTGTA 120  
 ACTGGACGCT GGATGTGCCA AACCTGGGGG ATCAAACAGG TTA 163

5

(2) INFORMATION FOR SEQ ID NO: 4757:

10

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 160 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4757:

20

CATGAACTA GATAAGTAGT AAATATAGAT TTTACCAAGC AAAACCGAGT GAATAAAGAG 60  
 TTTTAAATAA GCTTGAATTC ATAAGAAATA ATCGCTAGTG TTCGAAAGAC ATCACAGAT 120  
 TAATACCGCG TTTAATCTTT TATAAAGGAC CGTAACTTCA 160

(2) INFORMATION FOR SEQ ID NO: 4758:

25

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 177 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4758:

35

TACATGGGTT TATTGTTGAA GATGACGAAA TTGTAGAAAT TTAATATTCT AAAAAGGTTG 60  
 GGGACATAAA TCCCCCTAAA AAAACCAGCA GTAAGATAAT TTTCAATTAG AAAATATCTT 120  
 ACTGCTGTTC TCTATTTATA CCAATTACT TTCGTAATTG TTAAAATTTT AAAAGGA 177

(2) INFORMATION FOR SEQ ID NO: 4759:

40

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 127 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4759:

50

CGGTGTGTAC AAGACCCGGG AACGTATTCA CCGTAGCATG CTGATCTACG ATTACTAGCG 60  
 ATTCCAGCTT CATGTAGTCG AGTTACAGAC TACAATCCGA ACTGAGAACA AChTTATGGG 120  
 ATTTGCT 127

55

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4760:

GGGCCCCCTCG TCGGGTTACC GAATTCAGAC AAATCCGnA ATGCCAATTA ATTAACTTG 60  
 GGAGTCAGAA CATGGGTGAT AAGTCCGTGT TCGAAAGGAA ACAGCCCAGA CCACCAGCTA 120  
 AGTCCCAAAT ATATGTTAAT GAAAG 145

## (2) INFORMATION FOR SEQ ID NO: 4761:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4761:

TAAACAAGGC GCGTTGGGCC TATTCCTGCG GGCTCTTCTG GCGGTTAACC CTAAAGAGCA 60  
 CCCCTTCTCC CGAAGTTACG GGGTCATTTT GCCGAGTTCC TTAACGAGAT TGCTCGCTCA 120  
 CCTTAGAATT CCATCTGACT ACGGTCGTTG CGTACGGCAC TATTTCTTCA AGCTTCCGCA 180  
 TTAACACACC AAAACAGCTC CCACCACCAC TANATCGAnC AACACTAG 228

## (2) INFORMATION FOR SEQ ID NO: 4762:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4762:

TnGCCAAATC TTAGTAGTCG CTTGGTTCGG TTGTGGTGCG ACAGCTGTGA AATCATCACT 60  
 ACGTTGCTCA TCACTCACTG TCTCTCCGCT TCCTTGCCTT GCAACAGCTT GAATTGTATC 120  
 AGCAGGGTTG 130

## (2) INFORMATION FOR SEQ ID NO: 4763:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4763:

CAACTCGTAG TCAGGGTCGA AAGACGGGAC TTAGTGATCC GGTGGTTCCG TCATGGGTAG 60  
10 GGCCATCGTC TCAACGGTAT AAAAGCTACC CCGGGGATAA CAGGCTTATC TnCCCCAAGA 120  
GTTACATCG ACGGGGAGGT TTGGCACCTC G 151

(2) INFORMATION FOR SEQ ID NO: 4764:

15

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 128 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4764:

ACCCCAACTT GCATTGnCTG TAGAAATTGG GAATCCAATT TCTCTTTGTT GGGGCCCCGC 60  
25 CGGCAAGGTT GACTAGAATT GACCAAAAGC TTGTACAAG CGCATTTTCG TTCAGTCAAC 120  
TACTGCCA 128

30 (2) INFORMATION FOR SEQ ID NO: 4765:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 135 base pairs  
(B) TYPE: nucleic acid  
35 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4765:

40 AATACAGCCC CAGAGCGATG AGCCGACATC GAGGTGCCAA ACCTCCCCGT CGATGTGAAC 60  
TCTTGGGGGA GATAAGCCTG TTATCCCCGG GGTAGCTTTT ATCCGTTGAG CGGATGGCCC 120  
45 TTTCCATGTG GnAAC 135

(2) INFORMATION FOR SEQ ID NO: 4766:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 126 base pairs  
50 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

55

GATTCTCACC CGTCTTTGCG TACTCACACC GGCATTCTCA CTTCTAAGCG CTCCACATGT 60  
 CCTTACGATC ATGCTTCAAC GCCCTTAGAA CnCTCTCCTA CCATTGTCCA AAGGACAATC 120  
 5 CACAGC 126

## (2) INFORMATION FOR SEQ ID NO: 4767:

(i) SEQUENCE CHARACTERISTICS:  
 10 (A) LENGTH: 130 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4767:

TTAATAGTTT TATAAGAGAG GTGTTTGATC TTGAGCTAAC CACnTCATTC GAGTACTGTC 60  
 20 ATGAAGTAAT TTCTCTATTC TACGACCAGA AAATACAGAT GGGGTATATG CATATAAGAT 120  
 GATTTTTAAC 130

## (2) INFORMATION FOR SEQ ID NO: 4768:

25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 142 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4768:

35 GTTAACCCTA AAGAGCACCC CTTATACCGA AGTTACGGGG TCATTTTGCC GAGTTCCTTA 60  
 AnGCGCGTTC GATCGCTCAC CTTAGGAATT CTCATCTTGA CTACCTGTGT CGGTTTGCGG 120  
 TAGGGCACCT ATTTTCCTAT CT 142

## 40 (2) INFORMATION FOR SEQ ID NO: 4769:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 136 base pairs  
 45 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4769:

CCTTGGGACC GACTACAGCC CCAGGATGCG ATGAGCCGAC ATCGAGGTGC CAAACCTCCC 60  
 CGTCGATGTG AACTCTTGnG TGGAGATAAG CCTGTTATCC CCGGGGTGAG CTTTGTATCC 120

55

## (2) INFORMATION FOR SEQ ID NO: 4770:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4770:

CTAAAAGTTG TATTTTAAAA ATAGTTCTTT AAATTATATA CCCACCACAT TTGGTGGAGA 60  
 ACCGTAAAC AATGCATAGT TTGCTTAACT TCCAATATTG ACTCATCATT ACAATTGACA 120  
 TAGAGCTATT AAGCGTnGCC ATGAG 145

## (2) INFORMATION FOR SEQ ID NO: 4771:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4771:

TCGAGTGACA CTGTCGCCGA AAATGTACCG GGGCTAAACA TATTACCGAA GCTGTGGATT 60  
 GTGCCTTTGG AAATGGTGAG GnGAGCGTTC TAAGGGCGTT GGAAGCATGA TCGTAAGGAC 120  
 ATGTGGGA 128

## (2) INFORMATION FOR SEQ ID NO: 4772:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4772:

GGGCAGATGT TCCTGCAGTC ATAGTGCCGT CAACTTTAAA TACTGTACGT AATTGGCTA 60  
 ATGCCTCCAT CGTGnTGTC AGGGCGTATA AATTCATCTT GGGTCAAAGA TATTGGTGT 120  
 GTACTT 126

## (2) INFORMATION FOR SEQ ID NO: 4773:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 base pairs



- (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4773:

GTCTTTTCTC GTTTCGTTCA GATTCAAACG TTTTCACTTC GCCAAGCCAT TTTTCTTTGT 60  
10 GTTTACTTTT TATTTTGACG TTTTAGGATA AAAAAAAGAn ACCTTGCGGT CTCATGCGG 120  
CTCATC 126

(2) INFORMATION FOR SEQ ID NO: 4774:

15

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 124 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4774:

25 ATTTCAATAT CAGGCTACAG TAAAGCTCCA CGGGGTCTTT CCGTCCTGTC GCGGGTAACC 60  
TGATCTTTnA CAGGTACTAT GATTTACCG AGTCTCTCGT TGAGACAGTG CCCAAATCGT 120  
TACG 124

30

(2) INFORMATION FOR SEQ ID NO: 4775:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 124 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4775:

40 ACCAAGTGAG CCGGAAACAC CAACGCCACC AACACCAGAA GTACCAAGTG AGCCGGAAAC 60  
ACCAACACCA CCGACACCAG AAGTGCCGAG TGAnCCAGAA ACTCCAACAC CGCCAACACC 120  
45 AGAG 124

(2) INFORMATION FOR SEQ ID NO: 4776:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 135 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

50

55

CCCCCTAGTC TCCACCATTT ATTTTTTACA CGATGAACAT TGAAAACtA ATACAATATG 60  
 CAACGTTAAT TCCAAAAAAC GTAACATAA GTTACAAACA TTATTTAGTA TTTATGAGCT 120  
 5 AATCAAACAT CATAA 135

(2) INFORMATION FOR SEQ ID NO: 4777:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4777:

AGTGCAGAAG AGGAAAGTGG AATAnCCCCA ACATAGCGGT GAAATGCGCA GAGATATGGA 60  
 20 GGAACACCAG TGGCGAAGGC GACTTTCTGG TCTGTAAC TG GACGCTGGAT GTGCGAAACG 120  
 TTGGGGGTTC AAACAGGATT TAGA 144

(2) INFORMATION FOR SEQ ID NO: 4778:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4778:

AATTTTTGAT GACGGGTCCC TTCCTAGGGT GCCGTCTCAG CCACCCCAAC CGGCACATTG 60  
 TTGTAAGCTG ACTATATGTC nTTCATGTGT TGGGGCCCCT GTCTTCGACT GGCAC TGCTC 120  
 CCT 123

(2) INFORMATION FOR SEQ ID NO: 4779:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4779:

GCGCATTAACTATCGCGATA TTAATCGCTA TTCTATATCG TCACTTTAGA GGATATCCTG 60  
 AACAAATATAG CTCAGGTATT ACGTTTTTCAT CTAAATATTT ATTAAGATTT GCAATCATCC 120

## (2) INFORMATION FOR SEQ ID NO: 4780:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4780:

GGTAATATGT TTAGCCCCGG TACATTTTCG GCGCantGTC CTCGACTAGT GAGCTATTAC 60  
 GCACTCTTTA AATGATGGCT GCTTCTAAGC CAACATCCTA GTTGTCTGGG CAACGTCACA 120  
 TCCTTTT 127

## (2) INFORMATION FOR SEQ ID NO: 4781:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4781:

ACACnGGGTG AGAATTTGTC GCTATTTGTA AATTGTATCC TGGCTTAAGT TGGCCAAAGT 60  
 GTCTTATTTT TTAAAGTAT TTAAAGTAA AATTACATGT TAATACGTAG TATTAAATGG 120  
 CGAGACTCC 129

## (2) INFORMATION FOR SEQ ID NO: 4782:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4782:

CTCATTCCCG TTGCATTTTA TCTTCTGCAA CAACAACATT TCGTCTTTAT CGTCTTCCAT 60  
 AGTAGTAGGA TTTTCTACTA CTTGACCATT CATAATCTGT TGCATTTTCAT GTTTGnTTTG 120  
 GTCAGATTTA GGACCA 136

## (2) INFORMATION FOR SEQ ID NO: 4783:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4783:

CATCAACATC GCGCATTAA AAGATGGACG TTTTGATGAT GTACAACAAG ACATTGAAGC 60  
10 AGTGTTAAA GCTGCGAAAG GTCACACAGT AAAAGTGATT ATTGnGACGG TATTGTTGG 119

(2) INFORMATION FOR SEQ ID NO: 4784:

(i) SEQUENCE CHARACTERISTICS:  
15 (A) LENGTH: 127 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4784:

ATCACTAATC CATTGTGGTA AGTCTCCAAG TTCGTCTTCC ATACGTGTTT TAACCTGCGT 60  
25 nATCCATTG CATCCATAA TTGTGAATGG ACCAAGTTTC CAGTTGAACC CCCAGACAAG 120  
CGCACGG 127

(2) INFORMATION FOR SEQ ID NO: 4785:

(i) SEQUENCE CHARACTERISTICS:  
30 (A) LENGTH: 119 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4785:

ACACCGGCAT GCTGAATACT CGTTTTGGGT GAAGCCCCTG nACCACCATC GTAACCACTG 60  
40 ATGACAATTT TATCTGCAA TGCTTTTGCC ACCCCAGATG CAATGGTACC AACACCTGT 119

(2) INFORMATION FOR SEQ ID NO: 4786:

(i) SEQUENCE CHARACTERISTICS:  
45 (A) LENGTH: 137 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4786:

CTTTCTAAAC CCGnCAACAC TTTATCGTGG TGGGGAGACA GTGTTcAGGC GGGCCAGTTT 60  
55

AATCATTTCAT AGAGTGT

137

(2) INFORMATION FOR SEQ ID NO: 4787:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 119 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4787:

GTTTTAAACA CTGTTACCGT TTTCATCTTT TAATGTTACC GTTACGCCAG AATACCTTT 60  
 TTCATCTTGG TCTTGGATAC CATTTTTTATT TGTATCTTCC CAGACATAGT CACCTAAGT 119

(2) INFORMATION FOR SEQ ID NO: 4788:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 141 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4788:

CATGCTTCCA CCTCGAACCT ATTAACCTnC ATCATCTTTG AGGGATCTTA TAACCGCACT 60  
 TGGGAAATCT CATCTTGTAG GGGGGCTTCA TGCTTCAGAT GCTTTGCAGC ACTTAGCCCCG 120  
 GCCACACATA GCTACCCAGC T 141

(2) INFORMATION FOR SEQ ID NO: 4789:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 139 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4789:

CTGGGTTTCAG AACGTCTAAG CAGTTCGGTC CCTATCCGTC GTGGGCGTAA GAAATTTGAG 60  
 AGGAGCTGTC CTTAGTACGA GAAGACCGGG ATGGACTACC TCTnGTGTAC CAATTGTCGT 120  
 GCCAACGCAT AGCTGGGTA 139

(2) INFORMATION FOR SEQ ID NO: 4790:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 129 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4790:

10

CATTATTTAG TATTTATGAG CTAATCAAAC AncATAATTT TTATGGAGAG TTTGATCCTG 60  
GCTCAGGATG AGCGCTGGCG GCGTGCCTAA TACATGCAAG TCGAGCGAAC GGACGAGATG 120  
CTTGCTTCG 129

(2) INFORMATION FOR SEQ ID NO: 4791:

15

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 120 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4791:

25

GGGTGCTCTT TAGGGTTAAC GCCCAGAAGA GCCGCAGTGC AATAGGCCCA AGCGACTGTT 60  
TATCAAAAnC ACAGGTCTCT GCTAAACCGT AAGGTGATGT ATAGGGGCTG ACGGCTTCCC 120

(2) INFORMATION FOR SEQ ID NO: 4792:

30

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 123 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4792:

40

CAAATTCTTT CGCTACTTGA ATGACAACAC TTTGTTTTAC GCCTGAAATG GCTTCTTGCC 60  
AAGCAGGTGT ATATTTTGAT TCTGCATCGT CGTATCCTTT TGATCTAATT ATGATCAAAC 120  
CGn 123

45

(2) INFORMATION FOR SEQ ID NO: 4793:

50

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 130 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4793:

AGTTTTGAAT GTTTGTTTCAT TCAAATTAAT GGGCCTATAG CTCAGCTGGT TAGAGCGCAC 120  
nCTGATAAC 130

5 (2) INFORMATION FOR SEQ ID NO: 4794:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 115 base pairs  
(B) TYPE: nucleic acid  
10 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4794:

CACAGCCACA AGTGATTAAA GGCTTACCCA ATGATCCTGA AATGACGATA GAGTCAGTAT 60  
TAACTCATTT TTCAATAGAT CAGGAAGACT ACCAAGCTTA TGTnGAAGGA CATCT 115

20 (2) INFORMATION FOR SEQ ID NO: 4795:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 224 base pairs  
(B) TYPE: nucleic acid  
25 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4795:

nTTAAAAAA ATTCCCAATT TTTTnTGGGG GGTnGGGAAT TTAAAAATTT GGTnTTTAAC 60  
CCAAAGGCC TTTTCCCAA AATTAAATT CCCTTAAAAA TTAAAAATTT GGAATTTTTT 120  
35 TTTnGGCCC AAAATTTTTT CCCTTTTTTT AAAGGCCCCA ATTTTnAATT TAACCCTTAA 180  
AACCCCCAAA CCTTTTTTCC TTTTnTAAAA TTTTnTTAAA TGGA 224

40 (2) INFORMATION FOR SEQ ID NO: 4796:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 120 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4796:

50 TCGCGTACCG CTTTAATGGG CGAACAGCAA GACCTTGGGC ACCGACTACA GCCCCAnGAT 60  
GCGATGAGCC GACATCGAGG TGCCAAACCT CCCCnTCGAT GTGAACnCTT GGGGGCAGAT 120

55 (2) INFORMATION FOR SEQ ID NO: 4797:

- (A) LENGTH: 125 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4797:

10 AATTCGATTC CCTTAGTAGC GGCGAGCGAA ACGTGAAGAG CCCCAnACCA ACAAGCTTGG 60  
 CTGTTGTGGT TGTAGGACAC TCTATAACGG GAGTTACAAA GGACCGACAT TAGACGAATC 120  
 ATCTG 125

15 (2) INFORMATION FOR SEQ ID NO: 4798:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4798:

CAAAATAATG ACTCCTACGG GnCTCGAACC CGTGTTACCG CCGTGAAAGG GCGGTGTCTT 60  
 AACCGCTTGA CCAAGGAGCC ATGGCTCCAC AGGTAGGACT CGAACCTACG ACC 113

30 (2) INFORMATION FOR SEQ ID NO: 4799:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4799:

CCGGTGGGAG GTAACCTTTT AGGAGCTAGC CGTCGnAGGT GGGACAAATG ATTGGGGTGA 60  
 AGTCGTAACA AGGTAGCCGT ATCGGAAGGT GCGGCTGGAT CACCTCCTTT CTAAGG 116

45 (2) INFORMATION FOR SEQ ID NO: 4800:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

50

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4800:



TCAGTGGGAT GATTCGTGAA ATTGAAACGC AAGATTTTGA TATCGAnCAC CT

112

(2) INFORMATION FOR SEQ ID NO: 4801:

- 5 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 110 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4801:

15 ATAGGATAGG CGACGTGCGA TTGGATTGCA CGTCTAAGCA nTAAGGCTGA GTATTAGGAA 60  
 ATCCGGTACT CGTTAAGGCT GACTGTGATG GGGAGAAACA TTGTGTCTTC 110

(2) INFORMATION FOR SEQ ID NO: 4802:

- 20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 237 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4802:

30 GAACCAAGTT GTTATTGAAA AntCGTTCGT AAAGTTACGG TACGCCCACC GTGAGTGCTT 60  
 TTACTIONCTAT ATCAGCACCT ACTGTATCTT TCATTAAATT AACGTCTTCT GCAGTCGCAC 120  
 CGCCACCTGC AAAACCTGTT GAATTTTACG AGTCCGCACC GCGCTTTGTA ATCATnCTTA 180  
 35 CATTCTCTGT CACAACGCCA TACCTTCGGG ACTGACTCAC AGCTCAGCGG AACACAA 237

(2) INFORMATION FOR SEQ ID NO: 4803:

- 40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 114 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4803:

CTTGAACCCC CAACCTACTG ATTACAAGTC AGTTGCTCTA CCAATTGAGC TAAGCCGGGC 60  
 50 AATATGTAAG AATAAATGGT GGAGAATTGA CGGGTTCGAA CCGCCGAnCC TCTG 114

(2) INFORMATION FOR SEQ ID NO: 4804:

- 55 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 113 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4804:

GGATCAAACA GGATTAGATA CCCTGGnTAG TCCACGCCGT TAAACGCATG AGTGCTAAGT 60  
GTTAGGGGTT TCCGCCCCCTT AGTGCTGCAG CTAACGCATT AAGCACTCCG CCT 113

10

(2) INFORMATION FOR SEQ ID NO: 4805:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 108 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4805:

TACCAGGTA TCTAATCCTG TTTGATCCCC ACGCTTTCGC GCATCAGCGT CnGTTACAGA 60  
CCAGGAAAGT CGCCTTCGCC ACTGGTGTTC CTCCATATCT CTGCGCAT 108

25

(2) INFORMATION FOR SEQ ID NO: 4806:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 115 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4806:

TTTCAGCACT TATCCCGTCC ACACATAGTC TACCCAGGCT ATGCCGTTGG CACGACAACT 60  
GGTACACCAG AGGTATGTCC ATCCCGGTCC TCTCGTACTA AGGAnAGCTC CTCTC 115

40

(2) INFORMATION FOR SEQ ID NO: 4807:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 167 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

45

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4807:

CAGCCACATA ACATAACTAA GTTTAAGATT GAACGATAAA TCGTATCTGA GTTAAACCAA 60  
TGGTTAATAC CCGCACCCAT GATAATCATT GAACGCCTTC AGTATCGTAG GTTTGGAATT 120

55

## (2) INFORMATION FOR SEQ ID NO: 4808:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4808:

TGCTTACATC ATTAGCTAAT TGAGCACATG TTGCCATTGC TTGCAGCTAA ATTACCTTGC 60  
 ATCATTGCTA GCTTTTCTTG TATTAAGTGA TATTACTAA TTGGTTTGCC GAATTGCT 118

## (2) INFORMATION FOR SEQ ID NO: 4809:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4809:

TTGAGGTAGC CTAAAGCTAT TTCGGAGAGA CCAGCTATCT CCAGGTTTGA TTGGAATTTTC 60  
 TCCATACCT CAGTTCATCC GCTCACTTTC AACGTAAGTC GGTTCCGGTCC TCATCAGTGG 120  
 TACCTGACTT CAACTGACCA GGGTAGACAC 150

## (2) INFORMATION FOR SEQ ID NO: 4810:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4810:

AAGAAGGCGA CGATACATTA TCACCTGGTG TAACAATTAG TACGTGTATA TATCGTTCA 60  
 AAACGTAAAT TCATGTTGGT GATAAGATGT GTGGTCGACA TGGTACA 107

## (2) INFORMATION FOR SEQ ID NO: 4811:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4811:

AGAGTGnATT AGGTTATGAA GGTGGGCAAA ATAGGGTAAC CAGTCATTCTG AGGAAGACAC 60  
 5 AGAAGAAGAC AAACCTAAAT ATGAACCAAG GTGGCATATC GTAGATATCG ATTCCA 117

## (2) INFORMATION FOR SEQ ID NO: 4812:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4812:

CTTTTATCCG TTGAACGATG GCCCTTCCAT GCGGAACCAC CCGATnACTA AATCCGTCTT 60  
 20 TCGACCCTGC TCGACTTGTA AGTCTCGCAA TCAAGTCCCT TATGCCTTTA CACTCTATGA 120  
 ATG 123

## (2) INFORMATION FOR SEQ ID NO: 4813:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4813:

TAACCCGAGA GGGTCCCCTn GTCCAAACAG TGCTCTACCT CCAATATCAT CACTTGAGGC 60  
 35 TAGCCCTAAA GCTATTTTCGG AGAGAACCAG CTATCTCCAG GTTCGA 106

## (2) INFORMATION FOR SEQ ID NO: 4814:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4814:

CTATTGCTTT AGATGCATAT GAATCATTGA nTGACGCGAT GCCGATGATT TCTGAACACG 60  
 50 GAATCGCGAA CGTTGGCCAA CTGCCAACGA TTGGCGTGGG AATCATCCAG TG 112

## (2) INFORMATION FOR SEQ ID NO: 4815:

- (A) LENGTH: 125 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4815:

10 ACGTGGAGAG CATGTCCGTT CAAGCAGAGG GCGGCGGTT GAACCCGTCA TTCTGCACCA 60  
 TTTATTCTTA CATATTGCCG GACTAGCTCA ATTGGTAGAG CAACTGACCT TGTATCAGT 120  
 AGGTT 125

15

(2) INFORMATION FOR SEQ ID NO: 4816:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 104 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4816:

25

GTGCTGGCGC AGTTGCGATG GTTATTGCAC ATAATCCAAG CATGGCATT AATGAAGATG 60  
 CTGTTGCTTA CACTGAAGAC GTTTATGnTT TCTGGCGTCC AACT 104

30

(2) INFORMATION FOR SEQ ID NO: 4817:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 117 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4817:

40

GTCGGGTAAG TTCCGGCCCG CACGAAAGGC GTAACGATTT GGGCACTGTC TCAACGnGAG 60  
 ACTCGGTGAA ATCATAGTAC CTGTGAAGAT GCAGGTTACC CGCGGCAGGG CGGAAAG 117

45

(2) INFORMATION FOR SEQ ID NO: 4818:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 121 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4818:

55

TCGCTTACTC ATTTAGCTCT ACTAAACTCG TTGACGCTCT TTTCTCGnTT CGTCAGATTG 120

A 121

5 (2) INFORMATION FOR SEQ ID NO: 4819:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 118 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4819:

TCAGTTCGGT ATTGTGAGTC TGCAACTCGA CTGACATGAA GCTGGAATCG CTAGTAATCG 60

TAGATCAGCA TGCTACGGTG AATACGTTCC CGGGTCTTGT ACACAACGCC CGTnAAGA 118

20 (2) INFORMATION FOR SEQ ID NO: 4820:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 104 base pairs

(B) TYPE: nucleic acid

25 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4820:

30 CAAACAGTGC TCTACCTACA ATAATCATCA CTTGAGGCTA GCCCTAAAGC TATTTCCGAG 60

AGAACCAGCT ATCTnAGGT TCGATTGGAA TTTCTCCGCT ACCC 104

35 (2) INFORMATION FOR SEQ ID NO: 4821:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 165 base pairs

(B) TYPE: nucleic acid

40 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4821:

45 TCGTAGTGGT TTCCAACCAA GTTTTTATAA GTCAAACGCT CACATACGGC TTCGTTTTCA 60

TTATTTTAAA TGCTCATTTA CATAGTnAAC TCGCTTTAAA ATAATTTAAC TCATGTCGCT 120

AACGTTTTCT TTTATAAAAG TTTAACGGTT TTATCTGTGG TGTCT 165

50 (2) INFORMATION FOR SEQ ID NO: 4822:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 base pairs

55

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4822:

GAGTTTGATC CGGGCTCAGG ATGAACGCTG GCGGCGTGCC TAATACATGG CAATCGAGCG 60  
AACGGACGAG AAGCTTGCTT CnCTGAGGTA GCGGCGGACG GGTGAGTAAC ACG 113

(2) INFORMATION FOR SEQ ID NO: 4823:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 106 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4823:

CCGGCAACGT TCTACTCTAG CGGAACGTAA GTTGGCTACC ATCGACGCTA AGAACCTTTC 60  
TTTGAnTTGT GACAAATCGCT TGCTTCTTTC CTCTTCTTCG GCTCTC 106

(2) INFORMATION FOR SEQ ID NO: 4824:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 108 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4824:

TAAACGGCGG CCGTAACTAT AACGGTCCTA AGGTAGCGAA ATTCCTTGTC GGGTAAGTTC 60  
CGACCCGCAC GAAAGGCGTA ACGATTGCGG CACTGTCTCA ACTAGAGn 108

40

(2) INFORMATION FOR SEQ ID NO: 4825:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 116 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4825:

TCTAGTGACC GATAGTGAAC CAGTACCGTG AGGATAAGGT GAAAAGCACC CCGGAAGTAG 60  
nTGTAATAG AACCTGAAAC CGTGTGCTTA CAAGTAGTCA GAGCCCGTA ATGGGT 116

55

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4826:

ATAATATTGT AAATTAATCC ATTGATGCCA CAAGTGCCGG ACCAGAAATG ATGGTATTTA 60  
 ATAATGTGCC ATCTTTATCT TTACGCCAAT CATAATTGGT AAAAATTCCC CCTTCTAATA 120  
 ATCCTTGTAT TGCGTGT CAT AAAGTCTTTG CTCCTTGAC 160

## (2) INFORMATION FOR SEQ ID NO: 4827:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4827:

CGCATTGAGA CCGCAAGCTC TTTTTTTTAT GTCTAAAACG TCAAAATAAA AAGTAAACAC 60  
 AAAGAAAATG GTTGGCCnAG TGAAAACGTT TGAATCTGAC GAAACGAGAA AGAGC 115

## (2) INFORMATION FOR SEQ ID NO: 4828:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4828:

CCAAAATAGC CTTTATAATC CAAAACAGG CTCCTTTGAC TATAGATTTT CGTTTCTGGT 60  
 TCAGAAAGCT TTTGATTAACTTTAAAGTAT nCCCAATTAT AAT 103

## (2) INFORMATION FOR SEQ ID NO: 4829:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear



GGACCGAACT GTCTCAGAC GTTCThAACC CATCTCGCGT ACCGCTTTAA TGGGCGAACA 60  
 GCCAACCCTT GGGACCGACT ACAGCCCCAT GATGCGATGA GCCGACATCG A 111

(2) INFORMATION FOR SEQ ID NO: 4830:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 105 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4830:

GTTGTTGGGG CCCC GCCGC AAGGTTGACT AGAATTGAGA AAAGCTTGTT ACAACGCTAT 60  
 TTTGTTTCAG TCAACnACTG CCAATATAAC TTTGTAGAGC ATTGA 105

(2) INFORMATION FOR SEQ ID NO: 4831:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 102 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4831:

ACATTGAGTC TTCGAGTCGT TGCATTTTAC ACTGCCGnGA AAAGCCTCTA GATAGAAAAT 60  
 AGGTGCCCCGT ACCGCAAACC GACACAGGTA GTCAAGATGA GA 102

(2) INFORMATION FOR SEQ ID NO: 4832:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 107 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4832:

TTnTAGAATG AACCGGCGAG TTACGATTG ATGCAAGGTT AAGCAGTAAA TGTGGAGCCG 60  
 TAGCGATAAG GAGGTCTGAA TAGGGCGTTT AGTATTTGGT CGTAGCC 107

(2) INFORMATION FOR SEQ ID NO: 4833:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 144 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4833:

5 TGCAACTAAT GAAAAGTAGA GTTCCGGGGA GTTAAAACCA GTGACTGTTG ACCTTGTTGT 60  
 CTCCATTGGA ATGTACTACC TGATGCAAGA TAATTATCAT CACTTTGTTG ACGTGCTTnA 120  
 TTTTCAGCAT CAATTTGATC AATC 144

10 (2) INFORMATION FOR SEQ ID NO: 4834:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 108 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4834:

20 GGCTCAGATG nACGCTGGCG GCGTGCCTAA TACATGCAAG TCGAGCGAAC GGCACCAGAA 60  
 GCTTGCTTCT CTGGATGTTA GCGGCGGACG GGTGTAGTAA CACGTGGG 108

25 (2) INFORMATION FOR SEQ ID NO: 4835:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 102 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4835:

35 GACAATGGTA GgGAGCGTT CTAAGGGCGT TGAAGCATGA TCGTAAGGAC ATGTGGAGCG 60  
 CTTAGAAGTG AGAATGCCCG TGTGAGTAGC GAAAGACGCA GT 102

(2) INFORMATION FOR SEQ ID NO: 4836:

40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 109 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4836:

50 TTGCAGACTA CAATCCGGAA CTGGAGTAAC AACTTTATGG GATTnGnCTT GACCTCGCGG 60  
 TTTGCTGGC CCTTTGGTAT TGTCCATTGT AGCACGTGTG TAGCCCAA 109

55

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 103 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4837:

CTCCACGTAA GCTAGCGCTC ACGTTTCAAA GGCTCCTACC TATCCTGGTA CAAGCTGTGC 60  
CGGAATTTC AATTGCAAGC TACAGTAAAG CTCCACGGGG GTC 103

(2) INFORMATION FOR SEQ ID NO: 4838:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 121 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4838:

TCAAACACTC nCATACTGCT TTATTTTCAT AAACAATATC ACTTTAACCA AAAAATATTT 60  
GAATGTAA TAAACATTCA AACTGAATA CAATATGTCA CGTTATTCCA CATCTTCTGG 120  
A 121

(2) INFORMATION FOR SEQ ID NO: 4839:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 104 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4839:

AAACCATGAA TTAAGAATCC AGAAACAGGA GATGTAGTTA GACCACCGGT CGATTAGCGT 60  
ACCAAAATAT GGACCTGTAA AAGGAGACTC GATTGTAGAN AAAG 104

(2) INFORMATION FOR SEQ ID NO: 4840:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 127 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

CCGTGGAGTT TATGTAGCCT GATATTGAAT TCGGCACAGT TGTACAGGTA GGTAGGAGCC 60  
 TTGAAACGTG AGCGCTATTA GTGnAGGCGT GGTGGGTACT ACCCTAGCTG TGTGGCCTTT 120  
 CTAACCC 127

## (2) INFORMATION FOR SEQ ID NO: 4841:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 125 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4841:

CATCCCACCC CGGGCAAGGT TGACTAGAAT TGGAAAAAAA CTTGGTTACA ACGTTATTTT 60  
 CATTCACTCA ACTACTGCCA ATATAATATT GnaAACTATA GGACATTTAT TAGTGTTC 120  
 GTTCT 125

## (2) INFORMATION FOR SEQ ID NO: 4842:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 108 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4842:

TGGTACGGCA TCTCACCCGT CTTTCGCTAC TCACACCGGC ATTCTCACTT CTAnGCGCTC 60  
 CACATGATCC TTACGATCAT GACTTCAACG CCCTTAGAAC GCTCGTCC 108

## (2) INFORMATION FOR SEQ ID NO: 4843:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 108 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4843:

TAATGAAGGT CTTCCGATCG TAAAACTCTG TTATTAAGnA GGAACATGTG TGTAAGTAGC 60  
 TGTGCACATC TTGACGGTAC CTAATCAGAA AGCCACGGCT AACTACGT 108

## (2) INFORMATION FOR SEQ ID NO: 4844:

- (A) LENGTH: 117 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4844:

10 CGGTCTCAAT GCGGCTCATC GCATCCATTT TTTGACCTGG GCAACGTTCT ACTCTAGCGG 60  
 AACCTAAGTT GGGCTACCAT CGACGnCTAA GAACCTTTCT TGACTTGTGT ACAATCG 117

(2) INFORMATION FOR SEQ ID NO: 4845:

15

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 108 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4845:

25 GACTGTTTAT CAAAAACACA GGTCTCTGCT AAACCGTAAG TGATGTATAG GGGGCTGACG 60  
 CCTGnCCGGG TTCTGGTAAG GTTAAGAGGA GTGGTTAGCT TCTGCGAA 108

(2) INFORMATION FOR SEQ ID NO: 4846:

30

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 118 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4846:

40 CAATATTTGA AGCGATTGGC TTGTCTCATG ATGTGATTGA TCGTTATTTT ACTGGGACAC 60  
 AGTCTAAGTT ATCTGGTATT TCGATTGATC AAATTTnGCC TGAAAAAGAC GCACAAGT 118

(2) INFORMATION FOR SEQ ID NO: 4847:

45

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 104 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4847:

55 GATCCCCGGA CGGAGTGCTT AATGCGTTAC TGACAGCACT AAGGGGCGGA AACCCCTAA 60

## (2) INFORMATION FOR SEQ ID NO: 4848:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4848:

CTGGCGATTA TGCTCTGTAA CGTGCTTTCC AATTGGGAAC GCACGTGnCC CTGCCCATAC 60  
 CTACGGGACT TGAATTATAT TGTTTGGCTT TGTACGTCAT TTCAACAATA GACGCCCCATG 120  
 CCAGCAACGC GATTACC 137

## (2) INFORMATION FOR SEQ ID NO: 4849:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4849:

GTTTAGGCTC ATCTTAAGAT GTTAGGTCCA CTCGGTTTAC ACCATATTTT TTACTTACCG 60  
 TTTTGGCAGA CGGCACTTGG TGGTACTTTA GAAGTCAAAG ACAnGGGGGG GGGGGG 116

## (2) INFORMATION FOR SEQ ID NO: 4850:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4850:

TCCTTTCGTG ACGGGCTCGG TAACTTACCC GACAAGGTAA TTTCGCTACC TTAGGnACCG 60  
 TTATAGTTAC GGTCCGCCGT TTA CTGGGGC TTCGATTCTG ATCTTCGCAG CTATATCTCA 120  
 CTCCT 125

## (2) INFORMATION FOR SEQ ID NO: 4851:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4851:

5 AAGTTGTATT TTAAAAATAG TTCTTTAAAT TATATACCCA CCACATTTGG TGGGAGAACC 60  
 TAAAAAAAG CACTTTCCCC AAAAATGGGA AAGTGC 96

## (2) INFORMATION FOR SEQ ID NO: 4852:

10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 100 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4852:

20 ACCGTGTGCT TACAAGTAGT CAGAGCCCGT TAATGGGTGA TGGCGTGCCT TTTGTAGnAT 60  
 GAACCGGCGA GTTCACGATT TAGATGCAAG GTTGAAGCAG 100

## (2) INFORMATION FOR SEQ ID NO: 4853:

25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 101 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4853:

30 CCGACAGCGT AGnCGATGGA TAACAGGTTG ATATTCCTGG TACCACCTAT AATCGTTTnTA 60  
 35 ATCGATGGGG GACCCATAGG ATAGCGAACC TGCGATTGGA T 101

## (2) INFORMATION FOR SEQ ID NO: 4854:

40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 102 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4854:

45 GGACATCTCC TAAGGCTAAA TACTCTCTAG TGACCGTAGT GAACCAGACC GTGAGGAAAG 60  
 50 GTGAAAnACC CCGGAGGGGA GTGAATAGAC CTGAAACCGT GT 102

## (2) INFORMATION FOR SEQ ID NO: 4855:

55

- (A) LENGTH: 104 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4855:

10 ATAACCGCAA TTGGCGAAAT CTCATCTTGA GGGGGGCTTC ATGCTTAGAT GCTTTCAGCA 60  
CTTATCCCGT CCACACATAn CTACCCAGCT ATGCCGTTGG CACG 104

## (2) INFORMATION FOR SEQ ID NO: 4856:

- 15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 138 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4856:

CTACTGTCTT CATTCTTTCA GTTCTTTTTT ACGGGTCTGT TTTCTAATTT GAGCACATCT 60  
25 TCGATTCTTT ATCAAATGAC TACCAATTAA ATCTATTCCT CTnTGGTAAA TCGCTAACTC 120  
CATCTCCTTA ACCCGGTA 138

## (2) INFORMATION FOR SEQ ID NO: 4857:

30

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 100 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4857:

40 TCAAACGnTT GTCATCTATT AAAGAAGTAG GTCTAGATAT ATCACGTACG TAATGTGTAA 60  
TGGATGGCGC TATTGCTTTA GGTATCCAT TAGGTGCTAC 100

## (2) INFORMATION FOR SEQ ID NO: 4858:

45

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 106 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4858:

55



CCTGTGTGTT TGATAAACAG TCGGTTGGGC CTATTCAC TG CGGCTT

106

## (2) INFORMATION FOR SEQ ID NO: 4859:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 152 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4859:

GTAACGCGCC GGTTCAATTCT ACAAAGGGC ACGCCAATCA CCCATTAACG GGCTCCTGAA 60

CTACTTGTTA AGCAACACGG TTTCCAGGGT TCTATTTCCA CTTCCCTTT CCGGGGTnGC 120

TTTTTCAACC TTTTTCCTCC TCCACGGTTA CT 152

## (2) INFORMATION FOR SEQ ID NO: 4860:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 100 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4860:

GCCCGTACCG CAAACCGACA CAGGTAGTCA AGATGAGGAA TTCTAAGGTG AGCGAGCGAA 60

CTCTCGTTAA GGAACGCGC AAACGACCC CGTCACTTCG 100

## (2) INFORMATION FOR SEQ ID NO: 4861:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 104 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4861:

CAGGTAACAC TGAATGGAGG ACCGAACCGA CTTACGTTAA AAAGTAAGCG GATGAACTAA 60

AGGTAGCnGA GAAATTCCAA TCGAACCTGG AGATAGCTGG TTCT 104

## (2) INFORMATION FOR SEQ ID NO: 4862:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 87 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4862:

TTACTTATCT AGTTTTCAAT GTACAAATAA TGGTGGAGAC TAGCGGGATC GAACCGCTGA 60

CCTCCTGCGT GCAAAGCAGG CGCTCTG 87

(2) INFORMATION FOR SEQ ID NO: 4863:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 105 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4863:

ACCGTTTGAT TTCTTATCTA ATTCAAGCTT ATTTAAACT CTTTATTCAC TCGGTTTTGG 60

CTTGGTAAAA TCTATATTTT ACTTACTTAT CTANTTTTCA ATGTA 105

(2) INFORMATION FOR SEQ ID NO: 4864:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 129 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4864:

AGGGAATCGA ATTTTCTTTC TCTTCCTCCG GGGTACTAAG ATGTTTCAGT TCTCCGGGTG 60

TGCCTTGCTG GATGATGCTA TGATATTGCA CATATCGAAT CAACAGTGGT GCATGAACCT 120

GCAATGGCT 129

(2) INFORMATION FOR SEQ ID NO: 4865:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 100 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4865:

AAACCGCAAG GTCAAGCAAA TCCATAAAG TTGTTCTCAG TTCGGATTGT AGTCTGCAAC 60

TCGACTACTT GAAGCTGGAA ATCGCTATAA ATCGTAGATC 100

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 115 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4866:

GTGATAAGAT TAGCAGAAAA TGGATGGTGT TAAGAGAGTT AATTGGTTTG GnGGTATGCT 60  
TATTTTAAAT GGCATTGTGT ACGAGAGCAT TAGAGTTTGT ACTTGTGAGG TTATT 115

(2) INFORMATION FOR SEQ ID NO: 4867:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 90 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4867:

ACACCACTCC TCATTACCT TCCAGCACCG CAGCAGGCGT CACCCCTATA CATCACCTTA 60  
CGGTTTAGCA GAGACCTGTG TTTTGTGATAA 90

(2) INFORMATION FOR SEQ ID NO: 4868:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 87 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4868:

CACGAACGAT TGTCTTGCCT GCGGGGATTA TCTGACACGG TACCGGTCAA ACAGTGAATC 60  
GCTACTGCTC ATCAGGGATT ACAAACC 87

(2) INFORMATION FOR SEQ ID NO: 4869:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 165 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4869:

CGCTCACCTT AGAATCTATT TACTACTGGTG TTGGTAGGCA CTTTTTTCAA GCTTCCGATT 120

AACACATGAA AAGCTTCCAA AGTACTAGGA CGTTCAATAC ATGTA 165

5 (2) INFORMATION FOR SEQ ID NO: 4870:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 111 base pairs  
 (B) TYPE: nucleic acid  
 10 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4870:

AATATCATTT ATAACATTAA GTAATAACTT TTTTATCTT GTCCATTTTA TTTTThAACC 60

AAAATTTGAT TAAAAAAGTG CCTGGCAACG TTCTACTCTA GCGGAACTAA G 111

20 (2) INFORMATION FOR SEQ ID NO: 4871:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 84 base pairs  
 (B) TYPE: nucleic acid  
 25 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4871:

TAGCAGAGAC CTGTGTTTTT TGATAAACAG TCGCTTGGGC CTATTCCTG CGGCTCTTCT 60

GGGCGTTAAC CCTAAAGAGC ACCC 84

35 (2) INFORMATION FOR SEQ ID NO: 4872:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 101 base pairs  
 (B) TYPE: nucleic acid  
 40 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4872:

ACAGTAAAGC TCCACGGGTC TTTCCGTCCT GTCGCGGGTA ACTGCATCTT CACAGGTACT 60

ATGATTTTAC CGATCTCTCh ATGAACAGTG CCAAATCGTA C 101

50 (2) INFORMATION FOR SEQ ID NO: 4873:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 87 base pairs  
 (B) TYPE: nucleic acid  
 55 (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4873:

5 GACAGGCGTA GCGATGGAT AACAGGTTGT ATTCCTGTAC CACCTATGAT CGTTTTAATC 60  
 GATGGGGGGA AGCATAGGAT AGGCGAA 87

## (2) INFORMATION FOR SEQ ID NO: 4874:

10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 81 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4874:

20 GGGAGAGCGC CTGCTTTGCA CGCAGGAGGT CAGCGGTTCTG ATCCCGCTAG TCTCCACCAT 60  
 TATTTGTACA TTGAAACTA G 81

## (2) INFORMATION FOR SEQ ID NO: 4875:

25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 81 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4875:

30 TATGTTTCGA AATATCTTTA TCACTCTAAA ATGATATACA AGAAATCCAA GAAAAATAAG 60  
 35 CGAACTGAAT AAATAAGAT T 81

## (2) INFORMATION FOR SEQ ID NO: 4876:

40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 87 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4876:

45 AACGCGTTAA ATCTTTTAT AAAAGACGTA ACTTCATGTT AACGTTGCTT ATAAAAATGG 60  
 50 TGGACATAG ATTAAGTTAT TAAGGGC 87

## (2) INFORMATION FOR SEQ ID NO: 4877:

55

(A) LENGTH: 101 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4877:

10 ACAACGGATA AAAGCTACCC CGGGGATAAC AGGCTTATCT CCCCCAAGAG TTCACATCGA 60  
CGGGGAGGTT TgncCTCAAT GTGGCTCATC GGATCTTGGG G 101

(2) INFORMATION FOR SEQ ID NO: 4878:

15

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 79 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4878:

25 ATTTATTAGG TGTACAAATG ACCACCGCAT CAACAAGTTT AACAGCTCG CTAGGTGTCT 60  
CAACTGCATG AGGTATATT 79

(2) INFORMATION FOR SEQ ID NO: 4879:

30

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 83 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4879:

40 ACATCGTTTC AATGGGTCGC TAACGCTGCT AGGACATTAT AACAGACGTG TACAAAAAGA 60  
AAATTGGTAT GGTAATTGTG GCA 83

(2) INFORMATION FOR SEQ ID NO: 4880:

45

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 84 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4880:

55 CTTTCATCCTG ATCCAGATCA AACTCTCCAT AAAAATTATG ATGTTTGATT AGCTCATAAA 60

## (2) INFORMATION FOR SEQ ID NO: 4881:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4881:

TTGTGCAGTT GCATCGCCAT TGATCAATAA CACGTTGAGC TGCAGTTATT TCAGTTTCTG 60  
 CTTACAGCTT CTTCGCATT 80

## (2) INFORMATION FOR SEQ ID NO: 4882:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4882:

TCTGATGTGA AAGCCCACGG CTCAACCGTG GAGGGTCATT GGAAACTGGA AAAGTTGAGT 60  
 GCAGAAGAGG AAAGTGGGTT CCATGT 86

## (2) INFORMATION FOR SEQ ID NO: 4883:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4883:

TGATCGCATA TCTACGCAAC ATCGGCATAA GTnTGATGAC AAACAAGCTT CCATGACAAA 60  
 AGTAATGGAC GAATATCGCA TTTGGGGAAA GTCCTCTAAA AATGCCTTTT GAAGGAACGT 120  
 CGGTAA 127

## (2) INFORMATION FOR SEQ ID NO: 4884:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4884:

AGTAGGAATC GAACCCACAC CAAAGTTTTG GAGACCTCTA TTCTACCTTG AACTATGCCC 60  
CTATTAAAAA TAATAAAT 78

(2) INFORMATION FOR SEQ ID NO: 4885:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 84 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4885:

CTCACTATTC GAGTGACACT GCGCCGAAAA TGTACCGGGG CTAAACATAT TACCGAAGCT 60  
GTGGATTGTC CTTTGGAAT GGGT 84

(2) INFORMATION FOR SEQ ID NO: 4886:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 117 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4886:

GGTATCTGTT CACTCTTCCG GTGGTGCACT TGCGACCAAC AATGGGTTGG AGATTGGATT 60  
TCATCCTTCT CAATTAATCG TTGCCGTACT TTTCAANTGG TACCCCATCC AAAAGGG 117

(2) INFORMATION FOR SEQ ID NO: 4887:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 80 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4887:

CGGATCTGGG AGGAAATCTC CTAAGGCTAA ATACTCTCTA GTGACCGATA GTGAACCAGT 60  
ACCGTGAGGA AAGGTGAAAA 80

(2) INFORMATION FOR SEQ ID NO: 4888:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 77 base pairs



- (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4888:

AATATGCAAG CACATGGTGA ATATGACGAG GTTGCAACTT CAACGGCGAA GATGATGGAA 60

10

GGCCTTACGT TTGCGTG 77

(2) INFORMATION FOR SEQ ID NO: 4889:

15

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 76 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4889:

TCTTCTGGGC GTTAACCCTA AAGAGCACCC CTTCTCCCGA GTTACGGGGT CTTTGTCCGA 60

GTTCCCTTAAC GAGAGT 76

25

(2) INFORMATION FOR SEQ ID NO: 4890:

30

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 117 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4890:

GTGGGGGGCCC CAACATAGGA GCTGATTTTC TGTCAGCTTA CCATnATGTG GCAAGTTGGC 60

GGGGGGCCCC AAACCAAGGA GCTGGCTTTC TGTCACCTTA CCATTAAATGT GGCAAGT 117

40

(2) INFORMATION FOR SEQ ID NO: 4891:

45

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 109 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4891:

TTAATCCnCC TGCATATGAT GACTTTGTTG AACCGTCATT GCATACTTTC AACATGAATA 60

CGCTGAACAC CTTCACTTAC TGCATATCTT AGTTCTCTCGG TCTGTCTTA 109

55

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 88 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4892:

CTCTTAACCT TGCAGCACCG GGCAGGCGTC AGCCCGTATA CATCACCTTA CGGTTTGCAG 60  
AGACCGTGTG TTTTGTAGAA ACAGGTGC 88

(2) INFORMATION FOR SEQ ID NO: 4893:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 102 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4893:

TAGCGAATGA GATAAACGCG GCGGACTGTA AATCCGCTCC TTCGGGTTCC GCAGTTTCGAA 60  
TCTGCCCCCC TCCATTTATT ATTTTAAAAA AAAGCATAGT TC 102

(2) INFORMATION FOR SEQ ID NO: 4894:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 78 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4894:

CGAGCGATTC CGACTCAGAC AATGACTCGG AATTCAGATA ACGAATCTGA CTCAGACAGT 60  
GACTCAGATT CCGACAGT 78

(2) INFORMATION FOR SEQ ID NO: 4895:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 141 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4895:

TTAGTATTCG CACTCACATG TCACATGCTT CACTCGACCT ATTACCTCAC ACTTGGGGAC 120  
TTATACCGAG TnGGAATCTC A 141

5 (2) INFORMATION FOR SEQ ID NO: 4896:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 80 base pairs  
(B) TYPE: nucleic acid  
10 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4896:

GTTCGGATTT AATTTGATTC ATTTGTTGCG TAATTTTACA AGCCATTTTA TGAAAAGAGT 60  
GATTTAATTC ATAAATTTCT 80

20 (2) INFORMATION FOR SEQ ID NO: 4897:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 73 base pairs  
(B) TYPE: nucleic acid  
25 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4897:

30 GGTATGGCTG GCGCTTTACG TGCCACATTA GATTATGTCA CTGAGCGTAA GAAGTTCGGC 60  
AAACCAATTA GTA 73

35 (2) INFORMATION FOR SEQ ID NO: 4898:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 71 base pairs  
(B) TYPE: nucleic acid  
40 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4898:

45 GTGCCGAGGA CCGGAATCGA ACCGGTACGG TGATCACTCA CCGCAGGATT TTAAGTCCTG 60  
TGCGTCTGCC A 71

(2) INFORMATION FOR SEQ ID NO: 4899:

50 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 116 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4899:

AGCCGCTGGA TTCCACGGTG TAAGCAGTAA GGCTGAGTAT TAGGCAAATC CGGTACTCGT 60  
TAAGGCTGGA GCTGTnGATG GGGAGAAGAC ATGTGTGCTT ACGTAGTGCG TGGTTT 116

(2) INFORMATION FOR SEQ ID NO: 4900:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 113 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4900:

TTCCGGCCCC TGGCGGTnTC CTAGGAGTTC CACGGAACCC CAGGATTTTG TAGGACCCCC 60  
CGGGCAGAGT CCCCTTCGAC TAAGAAAATC TCACATTCTT CAGGGACTTT TAC 113

(2) INFORMATION FOR SEQ ID NO: 4901:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 78 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4901:

ACTTAATGGA TTGATTAAGT AGTGGGTTCT TAACATTAGG CCTCAGCTAA TGTGGTACTT 60  
AAAAATAGGG AATACATG 78

(2) INFORMATION FOR SEQ ID NO: 4902:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 84 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4902:

ATGGGACATG GTGTGCCTCC TTGCTATAGT CACCAGACAT ATGAATGTAA TTTATACATT 60  
CAAAACTAGA TAGTAAGTAA AAGT 84

(2) INFORMATION FOR SEQ ID NO: 4903:

- (A) LENGTH: 70 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4903:

10 TTGTCGGGTA AGTTCGGACC CGCACGAAAG GCGTAACGAT TTTGGCACTG TCTCAACGAG 60  
 AGACTCGGTG 70

(2) INFORMATION FOR SEQ ID NO: 4904:

- 15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 151 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4904:

25 TAAGTTGGCT ACCATCGACG CTAAGAACCT TTCTTGACTT GTGACAATCG CTGCTTCTT 60  
 TCCTCTTCTT GGCTCTGCTT CTATTTGCCT CTAATGTGGC TTTTGTGTGT AATAAGTTAT 120  
 GCGCTTCGGT GTTATnGTGA AAAAGCGGTC A 151

(2) INFORMATION FOR SEQ ID NO: 4905:

- 30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 75 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4905:

40 TGACTTGTAG GCGCTGGTGG GATACTACCC TAGCTGTGTT GGCTTTCTAA CCCGCACCAC 60  
 TTATCGTGGT GGGGA 75

(2) INFORMATION FOR SEQ ID NO: 4906:

- 45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 112 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4906:

55

ACTCAGACAG TGA CTCAGAT CAGATAGTGr CTCGGATTCA GCGATTATTC AG

112

(2) INFORMATION FOR SEQ ID NO: 4907:

5

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 70 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4907:

15

GTAAAAACAC CCCAGCCAGG TCACTTTACG CCTACGCATC GCTTGACAC GTGCTACTAA  
AGGTTTACCA

60

70

(2) INFORMATION FOR SEQ ID NO: 4908:

20

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 121 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4908:

30

AGAAGATACA AATAAGnTA AACCCAAATT ATTCAATTTT GGTGGGACAC AATAGTGTG  
ACTTTGAAGA AGATACTT TCCCACCAAG TTAAGTGGGT CCATAATTGA AGGGTCCAAC  
C

60

120

121

35

(2) INFORMATION FOR SEQ ID NO: 4909:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 70 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4909:

45

GGGAACAAAG TGGACAGGTG GTGCATGGTT GTCGTCAACT CGTGTCGTGA GATGTTGGGG  
TTAAGTCCCG

60

70

50

(2) INFORMATION FOR SEQ ID NO: 4910:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 100 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

55

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4910:

5 GGACACCCCG AGAACTGAAA CATTAGTAC CCGGAGAAGA GAAGAAATTC GTTCCCTTAG 60  
 TAGCGGGACG AACGGGAGAG CCCAAACCAC AGCTTGTGnG 100

## (2) INFORMATION FOR SEQ ID NO: 4911:

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 155 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4911:

15 ntCTGTGTTC GGCATGGGAA CAGGTGTGAC CTCCTTGCTA TAGTCACCAG ACAAATAAC 60  
 20 TTACTTATTC ATGATACACG CTTAATTAAT AAGGTGCAAT AGTTAATTTT AACTTTGAT 120  
 GTAACTTTG GCACATCAGC TTTTAGTGTG TTTTCG 155

## (2) INFORMATION FOR SEQ ID NO: 4912:

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 69 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4912:

30 CCCGTCACAC CACGAGATTT GTAACACCCG AAAGCCGGTG GAGTGAACCT TTTAGGAGCT 60  
 AGCCGTCGA 69

## (2) INFORMATION FOR SEQ ID NO: 4913:

## (i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 69 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4913:

45 TATGCTCTCC CAGCTGAGCT AATTCTCCGA TTAAAACTG CCTGGCAACG TTCTACTCTA 60  
 GCGGAACGT 69

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 69 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4914:

CAAATGCTTC TGTCAATTCG ATCAAATCAA TGTCTTCAAC AGATAGATTG CTGAGTGACA 60  
ATACTTCAT 69

(2) INFORMATION FOR SEQ ID NO: 4915:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 70 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4915:

TATTTTCGGAG AGAACCAGCT ATTTCCAGGC TCGATTGGAA TTTCTCCGGT ACCCTCAGTT 60  
CATCCGCTCA 70

(2) INFORMATION FOR SEQ ID NO: 4916:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 67 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4916:

TCACCCATTA ACGGGCTCTA ACTACTTGTA AGCACACGGT TTCAGGTTCT ATTCACTCC 60  
CCTTCCG 67

(2) INFORMATION FOR SEQ ID NO: 4917:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 161 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4917:



TCCACCGTTG ACTAAGGTTT CAGAGAGGCT CGTCCCTCTG GGTAGTCGGG CCTAAGCTGA 120  
GGCGCACGTA GGCGATGATA CAGGTTATAT CCTACACCT A 161

(2) INFORMATION FOR SEQ ID NO: 4918:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4918:

GCACGTAGTT AGCCGTTGGC TTTCTGATTA GGTACCGGCA AGATGTGCAC AGTTACTTAC 60  
ACATATGT 68

(2) INFORMATION FOR SEQ ID NO: 4919:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4919:

GAAAGCAAAT GTCTTCGTTG CAATTCGATC AAATCAATGT CTTCAACAGA TAGATTGCTG 60  
AGTGACAATA CTTCAGGG 78

(2) INFORMATION FOR SEQ ID NO: 4920:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4920:

AATTTGCTA CCTTAGGGAC CGTTATAGTT ACGGCCGACG TTTACTGGGG CTTTCGATTTCG 60  
TACTTCGC 68

(2) INFORMATION FOR SEQ ID NO: 4921:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4921:

5 AATCATAGTA CCTGTAAAGA TGCAGGTTAC CCGCAACAAG ACGGAAAGAC CCCGTGGAGC 60  
TTTACTG 67

## (2) INFORMATION FOR SEQ ID NO: 4922:

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 66 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4922:

15 GGGAGCTGTA ATAAGCTTTG ATCCAGAGAT TTCCGAATGG GGAAACCCAG CATGAGTTAT 60  
20 GTCATG 66

## (2) INFORMATION FOR SEQ ID NO: 4923:

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 73 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4923:

30 GTGGAGGCGC TGGTGGGATA CTACCCTAGC TGTGTTGGCT TTCTAACCCG CAACCACTTA 60  
35 TCGTGGGTGG GAG 73

## (2) INFORMATION FOR SEQ ID NO: 4924:

## (i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 89 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4924:

45 GAGGTCAGCG GTTCGATCCC GCTAGTCTCA CCATTTATTT TTTACACGAT GACATGAAAC 60  
50 TGATGACATA TGCACCGTAA TTCCAAAAA 89

## (2) INFORMATION FOR SEQ ID NO: 4925:

- (A) LENGTH: 68 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4925:

10 AATGGCATCG GAGTTGTCTG AATTCGGTAA CCCGAGAGGC CCCTCGTCCA AACAGGCTCT 60  
ACCTCCAA 68

(2) INFORMATION FOR SEQ ID NO: 4926:

- 15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 73 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4926:

25 ACGAAAGGCG TAACGATTTG GGCAC TGATC TCGACGAGAG ACTCGTGAAA ATCATAGATA 60  
CCTGTGAAGA TGC 73

(2) INFORMATION FOR SEQ ID NO: 4927:

- 30 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 69 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4927:

40 ATTTCTATTA ATTATTTGCA TAGAAATCAG CTTTTTGAT ATGTATTTTA TAATGTACAG 60  
CTCGTTGAG 69

(2) INFORMATION FOR SEQ ID NO: 4928:

- 45 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 70 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4928:

55 AGGTATGTCC ATCCCGGTCC TCTCGTACTA AGGACATCTC CTCTCAAATT TCCTACGCCC 60

## (2) INFORMATION FOR SEQ ID NO: 4929:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4929:

GGCGGGGCCC CAACACAGAG GCTGGCGGAA AGTGCAGCTT ACAATAGTGT GCAAGTTGGG 60  
GTGGGTCCCG ACACAGAGAA ATT 83

## (2) INFORMATION FOR SEQ ID NO: 4930:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4930:

CTTGGTAGAG CACTTGGTTT GGGACCAAGG GGTGCGAGTT CGAATCCTGT CTTCCCGATT 60  
ACTCTA 66

## (2) INFORMATION FOR SEQ ID NO: 4931:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4931:

AAGAAGCTTG TTATGCTGCA ACACCAGCAA TTCAAGTAGC TAAAGATTAT TTAGCAACTA 60  
GACCG 65

## (2) INFORMATION FOR SEQ ID NO: 4932:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

TGCAGAAGAG GAAAGTGGAA TTCCATGTGT AGGGTGAAAT GCGCATAGAT ATGGCAGGAA 60  
CACCAGTGGG CGA 73

(2) INFORMATION FOR SEQ ID NO: 4933:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4933:

TCGCTATCCG AGTCTGGGTC GCTATCTGAG TCTGAGTCGC TATCTGAGTC TGAAATCGCT 60  
GTCTG 65

(2) INFORMATION FOR SEQ ID NO: 4934:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4934:

GAGCATGTGG GTTTAATTCG AAGCAACGCA GAGAACCTTG ACCAAATCTT GGACATCCnT 60  
TGACAACTCT GAGAGATTAG AGCCTTGCCC CTTGCGGGGT AACAAATGTA CAGGTTGGTG 120

(2) INFORMATION FOR SEQ ID NO: 4935:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4935:

GAAGGCTCGT CCGCTCTGGG TTAGTCGGGT CCTAAGCTGA GGCCGAGCAG GTACGGCGAT 60  
GGATAACGGT TG 72

(2) INFORMATION FOR SEQ ID NO: 4936:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4936:

5 CACATCAGCG TCAGTTACAT ACCAGAAAGT CGCCTTCGCC ACTGGTGTTC CTCCATATCT 60  
CTGC 64

## (2) INFORMATION FOR SEQ ID NO: 4937:

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 64 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4937:

15 ATCACCTGGT GTAAACCAAT TAGTACGTGT ATATATCGTT CAAAACCGTA AAATTCATGT 60  
20 TGGT 64

## (2) INFORMATION FOR SEQ ID NO: 4938:

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 63 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4938:

30 CTGGGTAGCT ATGTGTGGAC GGGATAAGTG CTGAAACATC TAAGCATGAA GCCCCCTCAA 60  
35 GAT 63

## (2) INFORMATION FOR SEQ ID NO: 4939:

## (i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 63 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4939:

45 TAGAAATCAG CTTTTTGGCA TATGTATTTT ATAATGTACA GCTCGTTGAG CTGCTATTTT 60  
50 CCT 63

## (2) INFORMATION FOR SEQ ID NO: 4940:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4940:

GGTAGTCGAA CTTACGTTCC GCTAGAGTAG AACTTGCCAG CAAATGACAA ATCGGAGAAT 60  
 TAGCTCAG 68

(2) INFORMATION FOR SEQ ID NO: 4941:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 62 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4941:

CTGAAACATC TTAGTACCCG GAGAAGAGAA AGAAAATTCG ATTCCCTTAG TAGCGGCGAG 60  
 CG 62

(2) INFORMATION FOR SEQ ID NO: 4942:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 89 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4942:

TTAGAACAAAT GCAATTGGCG GGGCCCAACA TAGAACTGGC AATAGTTACT TTCAATAATG 60  
 TGCAAGTTGG GGTAGGGCCC AACACAGAA 89

(2) INFORMATION FOR SEQ ID NO: 4943:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 69 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4943:

AATGGACAAT ATGTCAACGT TAATTCCAAA AAACGGTAAC TATAATTTAC AAACATTATT 60

55

## (2) INFORMATION FOR SEQ ID NO: 4944:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 77 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4944:

CCCGTGAAAG ATGATGAGGT TAATAGGTTT GAGGTGGAAG CATGGTGACA TGTGGAGCGT 60  
 GACGAATACG TAATTGA 77

15

## (2) INFORMATION FOR SEQ ID NO: 4945:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 75 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

20

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4945:

GAATAGGTCG ATGTATTTGG CGACCGAAAC CAGGAATCTA CCCTTGGTCA GGTGAAGTT 60  
 CAGGTAACAC TGAAT 75

30

## (2) INFORMATION FOR SEQ ID NO: 4946:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 135 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

35

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4946:

ATCAGAAGGC ACACCCGAGA ATGAAACATC TAGTACCCGG AGAAGAGAAA GAAATTCGAT 60  
 TCCCTATAGC GGCgncGAAA CGGAAGAGCC AACCACAGCT GCTTTGGTTT GACCCATCGG 120  
 TACAGCGCTG AACT 135

45

## (2) INFORMATION FOR SEQ ID NO: 4947:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 61 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

50

55



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4947:

5 GATTTGGGCT CTTCCATTTC GCTCGCCGCT ACTAAGGGAA TCGAATTTC TTTCTCTTCC 60  
T 61

(2) INFORMATION FOR SEQ ID NO: 4948:

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4948:

20 GCTTTTGAGG AATTAAATAT CAATATATAT TCTGTGTATG AAAATATTTT TCATAAAAAT 60  
TGTTTGAATC 70

(2) INFORMATION FOR SEQ ID NO: 4949:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4949:

CTTCGACCTG ACCAAGGGTA GATCACCTGG TTTCGGGTCT ACGACCAAGT ACTAAACGCC 60  
35 CTATTC 66

(2) INFORMATION FOR SEQ ID NO: 4950:

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4950:

GGGTGTTACA AAATATCGTG GTGTGACGGG GCGGTGTGTA CAAGACCCCG GGTACGTTTT 60  
50 TCACCGTAGG CATGCTGG 78

(2) INFORMATION FOR SEQ ID NO: 4951:

55 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 base pairs

- (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4951:

CCGCGATAAT AAAAAATAAT GCGGGAGGAA GAGGGATTCG AACCCCCGTG GCCCGTTAAG 60

10

G 61

(2) INFORMATION FOR SEQ ID NO: 4952:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 68 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4952:

ACTTATCTAG TTTTCAATGT ACAATGTCTT TTTAGTCAGC GCTCGCATAA GCAATATCAC 60

25

TGTAACCA 68

(2) INFORMATION FOR SEQ ID NO: 4953:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 59 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4953:

ACTGACGCTG ATGTGCGAAA GCGTGGGGAT CAAACAGGAT TAGATACCCT GGTAGTCCA 59

40

(2) INFORMATION FOR SEQ ID NO: 4954:

(i) SEQUENCE CHARACTERISTICS:

45

- (A) LENGTH: 60 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4954:

50

CGTGAGCGCT AGCTGTACGT GGAGGCGCTG GTGGGATACT ACCCTAGCTG TGTTGGCTTT 60

(2) INFORMATION FOR SEQ ID NO: 4955:

(i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 59 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4955:

AAGGCGTAAC GATTGGGCA CTGTCTCAAC GAGAGACTCG GTGAAATCAT AGTACCTGT 59

10

(2) INFORMATION FOR SEQ ID NO: 4956:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 59 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4956:

20

AATAGGTGCC CGTACCGCAA ACCGACACAG GTAGTCAAGA TGAGAATTCT AAGGTGAGC 59

(2) INFORMATION FOR SEQ ID NO: 4957:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 77 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4957:

ACACGTTTAG TTCACGCGGG TTTTGCTTGG TAAAATCTAT ATTTTACTTA CTTATCTAGT 60

35

TTTCAATGTA CAATTC 77

(2) INFORMATION FOR SEQ ID NO: 4958:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 59 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4958:

TGTCGTCAGC TCGTGTCGTG AGATGTTGGG TTAAGTCCCG CAACGAGCGC AACCTTAA 59

50

(2) INFORMATION FOR SEQ ID NO: 4959:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 59 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4959:

GACTTGAACC CCCAACCTAC TGATTACAAG TCAGTTGCTC TACCAATTGA GCTAGGCCG 59

(2) INFORMATION FOR SEQ ID NO: 4960:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4960:

TATTAAGTGG TGACTTAGCG AGATGGACAA CGATGGCGAT ATATTTATTA TTGACCGCA 59

(2) INFORMATION FOR SEQ ID NO: 4961:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4961:

ATGATTATCA TATTGCCTTA AATATCGCCA CAATTTTAGC GGGTGGTGAT TTACCAAGA 59

(2) INFORMATION FOR SEQ ID NO: 4962:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4962:

CGCCGAAAAT TGTACCGGGG CTAAACATAT TACCGAAGCT GTGGATTGTC CTTTGGACA 59

(2) INFORMATION FOR SEQ ID NO: 4963:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

TTAAGCTTAG TTGCCATCAT TAAGTTGGGC ACTCTAATGT TGACTGCCGG TGACAAACCG

60

(2) INFORMATION FOR SEQ ID NO: 4964:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 59 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4964:

TAGTTTTGGT ACGGTAACAA ATTTATTTGA AGAAACAATC TCAAATAAAG AATTGTTTG

59

(2) INFORMATION FOR SEQ ID NO: 4965:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 59 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4965:

AGTTCGGTCC CTATCCGTCG TGGGGCGTAG GAAATTTTAG AGGAGCTGTC CTTAGTACG

59

(2) INFORMATION FOR SEQ ID NO: 4966:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 59 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4966:

TACAAAGGGC AGCGAAACCG TGAGTCAAAG CAAATCCCAT AAAGTTGTTC TCAGTTCGG

59

(2) INFORMATION FOR SEQ ID NO: 4967:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 65 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4967:

CCATTGCAGC ACCGACAGCC ACACCATTTA TTTTGGCGCT ATGTATATCG CATTAAACGT

60

## (2) INFORMATION FOR SEQ ID NO: 4968:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 60 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4968:

GCCTCCGTTA CTTT TAGAGG CGA GCGCCAG TCAA ACTGCC CGCTGACACT GTCTCCCACC 60

## (2) INFORMATION FOR SEQ ID NO: 4969:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 59 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4969:

CAAGGAATTT CGCTACCTTA GGACCGTTAT AGTTACGGCC GCCGTTTACT GGGGCTTCG 59

## (2) INFORMATION FOR SEQ ID NO: 4970:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 65 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4970:

CATCTGTCAC AGGTACTATG GATTTCACCG GAGTCTCTCG TTGAGACAGT GCCCAAATCG 60  
TTACG 65

## (2) INFORMATION FOR SEQ ID NO: 4971:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 100 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4971:

CTAGAGTTGG CATACCAGTC CGTCGCTAAG GAACCTTTCT TGA CTTGATG ACAATCGACT 60

(2) INFORMATION FOR SEQ ID NO: 4972:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4972:

AGACCCCGTG GAGCTTTACT GTAGCCTGCA TATTCGAATT CGGCACAGCT TGTACAGGAT 60  
AGGTAGG 67

(2) INFORMATION FOR SEQ ID NO: 4973:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4973:

TGTGTACTTA AAAATATGAA TACATGAGTA AAACATGTC ATAAGAAATA CTAATTTTC 58

(2) INFORMATION FOR SEQ ID NO: 4974:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4974:

ACCTCCAATA ATCATCACTT GAGGCTAGCC CTAAAGCTAT TTCGGAGAGA ACCAGCTA 58

(2) INFORMATION FOR SEQ ID NO: 4975:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4975:

GACGCCACAT CCTTTTCCAC TTGGCGTGTG TTTTGGGACC TTGGCTGGTG GTCTGGGCTG 60

(2) INFORMATION FOR SEQ ID NO: 4976:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 59 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4976:

TCACTAAGTC CGTCTTTCGA CCCTGACTCG ACTTG TAGGT CTCGCAGTCA AGCTCCCTT

59

(2) INFORMATION FOR SEQ ID NO: 4977:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 58 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4977:

TAAGTAAGTA AAATATAGAT TTTACCAAGC AAAACCGAGT GAATAAAGAG TTTTAAAT

58

(2) INFORMATION FOR SEQ ID NO: 4978:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 58 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4978:

GTGAGGTACG TCCAGAATGG GGATTGGCTA AAAATGCATC ATTTATAATT GGACGACG

58

(2) INFORMATION FOR SEQ ID NO: 4979:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 60 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4979:

TCGCTATCTG AATCCGAGGT CGCTATCCGA ATCTGGAGTC GCTATCTGGA GTCTGGAATC

60

(2) INFORMATION FOR SEQ ID NO: 4980:



- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4980:

10 AAGAAGGTAA TAATCCTGTA GTCGAAAATG TTGTCTCTCT TGAGTGGATC CTGAGTAC 58

(2) INFORMATION FOR SEQ ID NO: 4981:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 75 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4981:

GTGGTGTGTT AGGGCACTCT ATACGGGTGA CAAAGTACGA CATTAGACGG ATCATCTGGA 60

25 AAGATGAATC AAAGT 75

(2) INFORMATION FOR SEQ ID NO: 4982:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4982:

GTTTTTCATT TTCATTTATA TTTATATTAG TGTTAATCCA ATCATAGATT TATCTATA 58

(2) INFORMATION FOR SEQ ID NO: 4983:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4983:

50 TGACAGCTAA CTATTGGCCA GCTTCTATGT TGGGGCCCCG CCAACTTGCA TTGTCTGTAG 60

A 61

(2) INFORMATION FOR SEQ ID NO: 4984:

55

- (A) LENGTH: 64 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4984:

10 GGTGTTTTTA AGTCTGATGT GAAAACCCAC GGCTCAACCG GTAGAGGTCA TTGGAAACTG 60  
GAAA 64

(2) INFORMATION FOR SEQ ID NO: 4985:

15

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 59 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4985:

25 CAGCATACAA TAATGTGCAA GTTGGTCGGG GCCCCAACAT AGAGAATTTC AAAAGAAAT 59

(2) INFORMATION FOR SEQ ID NO: 4986:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 57 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4986:

TGATGAAGGT CTTGGATCG TAAACTCTG TTATTAGGGA AGAACATATG TGTAAGT 57

(2) INFORMATION FOR SEQ ID NO: 4987:

40

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 57 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4987:

50 AAAGAATTTG CGCAAACGC TATCGATACT GAAGGCGTT CAATGATTAT CATGGGT 57

(2) INFORMATION FOR SEQ ID NO: 4988:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 57 base pairs

55

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4988:

TTGTCACAAG TCAAGAAAGG TCTTTAGCGA CGATGGTAGC CAACTTACGT TCCGCTA 57

10

(2) INFORMATION FOR SEQ ID NO: 4989:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 57 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4989:

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TAGGACCGTT ATAGTTACGG CCGCCGTTTA CTGGGGCTTC GATTCGTAGC TTCGCAG 57

(2) INFORMATION FOR SEQ ID NO: 4990:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 61 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4990:

30

AAAGTCAACG TTAATTCCAA AAAACGTAAC TATAAGTTAC TAACATTATT TAGTATTTAT 60

35

G 61

(2) INFORMATION FOR SEQ ID NO: 4991:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 65 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4991:

45

TCCACGGGGT CTTTCCATCG TGTCTCGGGT AACCTGCATC TTCACAGGTA CTATGATTTC 60

50

ACCGA 65

(2) INFORMATION FOR SEQ ID NO: 4992:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 57 base pairs

55

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4992:

GTGCGGCTGG ATCACCTCCT TTCTAAGGAT ATATTCGGAA CATCTTCTTC AGAAGAT

57

10

(2) INFORMATION FOR SEQ ID NO: 4993:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4993:

20

CCAATGCGGC TCATCGCATC CATTTTTTGC CTGGCAACGT TCTACTCTAG CGGAACG

57

(2) INFORMATION FOR SEQ ID NO: 4994:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4994:

CTGGTTTCGG GTCTACGACA AATACTAAAC GCCTATTTCAG ACTCGCTTTC GCTACGG

57

35

(2) INFORMATION FOR SEQ ID NO: 4995:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4995:

45

CAAACCTCTCG TGGTGTGACG GCGGGTGTGG TACAAGCCCC GGGAACGTAT TCACCGTAGC

60

ATGCCGGTCT ACG

73

50

(2) INFORMATION FOR SEQ ID NO: 4996:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4996:

5 ACTAATTCT ATAGGAAAAG TATTCTTTAT CGTCGTCCCA CCCCAACTCG CACATTATTG 60  
TAAGC 65

(2) INFORMATION FOR SEQ ID NO: 4997:

10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 58 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4997:

20 ATTGGATTCC CAATTCTAC AGACAATGCA GTTGGGGTGG GACGTCGAAA TAAATTTT 58

(2) INFORMATION FOR SEQ ID NO: 4998:

25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 56 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4998:

AACTTCAACA GGTTTTGCAG GTGGCGGTGC GACTGCAGGA AGACGTTAAA TTAATG 56

(2) INFORMATION FOR SEQ ID NO: 4999:

35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 56 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4999:

45 GGGCAGGCGT CAGCCCTATA CATCACCTTA CGGTTTAGCA GAGACCTGTG TTTTGG 56

(2) INFORMATION FOR SEQ ID NO: 5000:

50 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 56 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5000:

TTAGGACCCG ACTAACCCAG AGCGGACGAG CCTTCCTCTG GAAACCTTAG TCAATC

56

(2) INFORMATION FOR SEQ ID NO: 5001:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5001:

GACGGGATTC TCACCCGTCT TCGCTACTC ACACCGGCAT TCTCACTTCT AAGCGC

56

(2) INFORMATION FOR SEQ ID NO: 5002:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5002:

CCTGTCCGCC TCAGCTTAGG ACCCGACTAA CCCAGAGCGG ACGAGCCTTC CTCTGG

56

(2) INFORMATION FOR SEQ ID NO: 5003:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5003:

TTACTCATTT AGCTCTACTA AACTCGTTGC GCTCTTTTCT CGTTTCGTCA GATTCA

56

(2) INFORMATION FOR SEQ ID NO: 5004:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5004:

## (2) INFORMATION FOR SEQ ID NO: 5005:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 57 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5005:

GACATAGATT AAGTTATTAA GGGCGCACGG TGGATGCCTT GGCAC TAGAA GCCGATG

## (2) INFORMATION FOR SEQ ID NO: 5006:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 57 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5006:

GGAACCACTA CATAATAAAT CATTAGTGGC TCTTTATCAT TCTGTCCCAC TCCCCTG

## (2) INFORMATION FOR SEQ ID NO: 5007:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 69 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5007:

CGCTACGTTT TTCCTCAACA TTTAAGAAAA TAAAGAATGC TACAATTACG ATTGCAATCA

AACCAAAGA

## (2) INFORMATION FOR SEQ ID NO: 5008:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 57 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5008:

AAAAGCTTGT TACAAGCGCT ATTTTCGTTT AGTCAACTAC TGCCAATATA ACTTCGT

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 56 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

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- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5009:

10

ACATCTTAGT ACCCGGAGAA GAGAAAGAAA ATTCGATTCC CTTAGTAGCG GCGAGC

56

- (2) INFORMATION FOR SEQ ID NO: 5010:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 65 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

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- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5010:

25

GTTTGGACGA GGGGCCCTCT CGGGTTACGA TTCAGACAAA CTCCGATGCA ATTAATTTAC

60

TTGGG

65

- (2) INFORMATION FOR SEQ ID NO: 5011:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 56 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

30

35

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5011:

40

TTTACTTGTA TTGAATAAT TTCATCTTTG AACCGACCAT CACGTTGTGC GTCATA

56

- (2) INFORMATION FOR SEQ ID NO: 5012:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 60 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

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- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5012:

CCTTATACAT CACCTTTACG GTTTTAGCAG AAACCTGTGT TTTTIGATAA ACAGTCGCTT

60

- (2) INFORMATION FOR SEQ ID NO: 5013:

55



- (A) LENGTH: 63 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5013:

10 GGGCCCAACA CAGAAGCTGG CGAAAAGTCA GCATACAAA TTGTGCAAGT TGGCGGGTCC 60  
ACA 63

(2) INFORMATION FOR SEQ ID NO: 5014:

15

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 58 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5014:

25 TAGGGTAGTA TCCCACCACT GGCCTCCACG TAAGCTAGCG CTTACGTTT CAAAGGCT 58

(2) INFORMATION FOR SEQ ID NO: 5015:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 105 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5015:

CAACTCCGAT GCAATTAATT TAACTTGGGA nCAGACATGG GTGATAAGGT CGTGTTGAA 60  
GGGAACAGCC AGACACAGCT AAGTCCAGAT ATATGTAAGT GGAAA 105

40

(2) INFORMATION FOR SEQ ID NO: 5016:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 56 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5016:

CAAACGATTT ATTTATATGC TTATTTCTTT ATTTATTATT ATTACAATTA CTTTT 56

55

(2) INFORMATION FOR SEQ ID NO: 5017:

- (A) LENGTH: 65 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5017:

10 TCTGTAGAAA TTGGGGAATC CAATTTCTCT TGGTTTGGGT CCCATCCCCA ACTTGACAT 60  
TATTG 65

(2) INFORMATION FOR SEQ ID NO: 5018:

15

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 56 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5018:

25 GGGGATGGGC CCCAACAAAG AGAAATTGGA TTCCCAATTT CTACAGACAA TGCAAC 56

(2) INFORMATION FOR SEQ ID NO: 5019:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 55 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5019:

CGATTGGATT GCACGTCTAA GCAGTAAGGC TGAGTATTAG GCAAAATCCGG TACTC 55

40

(2) INFORMATION FOR SEQ ID NO: 5020:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 58 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5020:

50

TACGGCGTTT AGTATTGGT CGTAGCCGGA AACCAGGTGA TCTACCCTTG GTCAGGTT 58

(2) INFORMATION FOR SEQ ID NO: 5021:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 55 base pairs

55

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5021:

TTGTGCGGGT CCCCGTCAAT TCCTTTGAGT TTCAACCTTG CGGTCGTACT CCCCCA 55

10

(2) INFORMATION FOR SEQ ID NO: 5022:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 55 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5022:

20

AGAGTTCACA TCGACGGGGA GGTTTGGCAC CTCGATGTCG GCTCATCGCA TCCTG 55

(2) INFORMATION FOR SEQ ID NO: 5023:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 58 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5023:

CCTTAGCTGG TGGTCTGGGC TGTTTCCCTT TCGAACACGG ACCTTATCAC CCATGGTC 58

35

(2) INFORMATION FOR SEQ ID NO: 5024:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 55 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5024:

TAAAGGCTAA ACTACCAATG TTTTCAATGG ATTTCCAAAA TGAATCATCT GGGAT 55

(2) INFORMATION FOR SEQ ID NO: 5025:

50

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 63 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

55

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5025:

TCAAACCGGA GGGGTCATTG GAAACTGGAA AACTTGAGTG CAGAAGAGGA AAGTGAATT 60  
CCA 63

## (2) INFORMATION FOR SEQ ID NO: 5026:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5026:

GCTTGCGTAC CTAAAGAGCA CCCCTTCTCC GAATTACGGG GTCATTTTGC CGAGTTCCTT 60  
AACG 64

## (2) INFORMATION FOR SEQ ID NO: 5027:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5027:

AATACATAGC ATATCATAAG GCACACCCGG AGAACTGAAA CATCTTAGTA CCCGGA 56

## (2) INFORMATION FOR SEQ ID NO: 5028:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5028:

GGGCCCCTCT CGGGTTACCA ATTCAGACAA ACTCCGAATG CCAATTAATT TAACT 55

## (2) INFORMATION FOR SEQ ID NO: 5029:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5029:

CGTAACTATA ACGGTCCTAA GGTAGCCGAA ATTCCTTGTC GGGTAAGTTC CGAC

54

(2) INFORMATION FOR SEQ ID NO: 5030:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5030:

ATCCCCGGGG CCCCAACACA GAGAATTTTCG AAAAGAAATT CTACAGGCAA TGCAAGT

57

(2) INFORMATION FOR SEQ ID NO: 5031:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5031:

TGCTTGGTAA AATCTATATT TTACTTACTT ATCTAGTTTT CAATGTACAA TTTC

54

(2) INFORMATION FOR SEQ ID NO: 5032:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5032:

TCCCTATCCG TCGTGGGCGT AGGAAATTTG AGAGGAGCTG TCCTTAGTAC GAGA

54

(2) INFORMATION FOR SEQ ID NO: 5033:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5033:

(2) INFORMATION FOR SEQ ID NO: 5034:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 54 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5034:

TATCTGAATC TGAGTCGCTG TCTGAATCTG AATCGCTATC CGAGTCTGAG TCGC

54

(2) INFORMATION FOR SEQ ID NO: 5035:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 54 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5035:

CACCAGCAAT TCAATTAGCT AAAGATTATT TAGCAACTAG ACCGGAATGA AAAA

54

(2) INFORMATION FOR SEQ ID NO: 5036:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 54 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5036:

CTACCATCGA CGCTAAGAGC TTAAGTTCTG TGTTCCGGCAT GGGAACAGGT GTGA

54

(2) INFORMATION FOR SEQ ID NO: 5037:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 56 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5037:

CGGCGAGTTA CGATTTGATG CAAGGTTAAG CAGTAAATGT GGAGCCGTAG CGGAAG

56

(2) INFORMATION FOR SEQ ID NO: 5038:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5038:

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GACCGGGATG GACATACCTC TGGTGTACCA GTTGTGCGTG CCAACGCATA AGCT

54

(2) INFORMATION FOR SEQ ID NO: 5039:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5039:

TTTCACCGAG TCTCTCGTTG AGCAGTGCCC AAATCGTTAC GCCTTTCGTG CGGG

54

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(2) INFORMATION FOR SEQ ID NO: 5040:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 105 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5040:

35

TTATAACACG TATGCTTGGG GAGTGTAAATA AGCTTGATCA GAGATTCCnA TGGGAACCAG

60

CATGAGTTAT GTCATTTATC ATATGTGATC ATAGCATATC AAAGG

105

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(2) INFORMATION FOR SEQ ID NO: 5041:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5041:

50

GGCACCTATT TTCTATCTAG AGGCTTTTCT CGGCAGTGTG GAAATCAACG ACTC

54

(2) INFORMATION FOR SEQ ID NO: 5042:

(i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 54 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5042:

ACTTATCTAG TTTTCAATGT ACAAATAATG GTGGAGACTA GCGGGATCGA ACCG

54

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(2) INFORMATION FOR SEQ ID NO: 5043:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 53 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5043:

20

CGTTCAGTCA ACTACTGCCA ATATAACATC GTAGAGCATA GAACATTGAT TTA

53

(2) INFORMATION FOR SEQ ID NO: 5044:

25

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 59 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5044:

ACTAGAGAGT ATTTAGACTT AGGAGTGGTC CTCCCAGATT CCGACGGATT TCACGTGCT

59

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(2) INFORMATION FOR SEQ ID NO: 5045:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 62 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5045:

45

TTTCGTCGTC CCACCCCAAC TTGCACGCTA TTGTGAGCTG ACTTTTCGCC AGCTTCTGTG

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TT

62

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(2) INFORMATION FOR SEQ ID NO: 5046:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 53 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

55



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5046:

CGTCATCCCC ACCTTCCTCC GGTTCGTCAC CGGCAGTCAA CTTAGAGTGC CCA

53

(2) INFORMATION FOR SEQ ID NO: 5047:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5047:

TATTTATTAA ACCTAATAAA GATGAATTAG AAGTGATGTT TAATACAACA GTG

53

(2) INFORMATION FOR SEQ ID NO: 5048:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5048:

CCTCGGCACC ATTTTCAATA AAAACATATG CGCCCGTAGC TCAATTGGAT AGA

53

(2) INFORMATION FOR SEQ ID NO: 5049:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5049:

AAATGGCCAA CTTAAGCCAG GATACAATTT ACAAATAGCG ACAAATTCTC AATGTGTTT

59

(2) INFORMATION FOR SEQ ID NO: 5050:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

CGAAAGACAC nCACAAGATT AATAACGCGT TTGAGTCTTT TTATAAGAC GTACTTCATG 60  
TTACGTTGAC TTTAAGATGG TGGAACATAG TTAGTTTTAG GGCCACGGGG G 111

5 (2) INFORMATION FOR SEQ ID NO: 5051:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 53 base pairs  
(B) TYPE: nucleic acid  
10 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5051:

ACGTTGACAT ATTGTCATTC AGTTTTCAAT GTTCATTAAT GTTCAATCTC TTT 53

(2) INFORMATION FOR SEQ ID NO: 5052:

20 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 53 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5052:

CTGAATTCGG TAACCCGAGA GGGCCCCTCG TCCAAACAGT GCTCTACCTC CAA 53

30

(2) INFORMATION FOR SEQ ID NO: 5053:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 53 base pairs  
(B) TYPE: nucleic acid  
35 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5053:

TACATAGCAT ATCAGAAGGC ACACCCGGAG AACTGAAACA TCTTAGTACC CGG 53

(2) INFORMATION FOR SEQ ID NO: 5054:

45 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 54 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5054:

55

(2) INFORMATION FOR SEQ ID NO: 5055:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 53 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5055:

TAGGGCTAGC CTCAAGTGAT GATTATTGGA GGTAGAGCAC TGTTCGGACG AGG

53

(2) INFORMATION FOR SEQ ID NO: 5056:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 63 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5056:

ACTGCTTTGA AATGTTGTTG TCTCAGTTAA TATTCAATTG CTTTTCTTTT GCATAATTGA  
 CAA

60

63

(2) INFORMATION FOR SEQ ID NO: 5057:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 54 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5057:

CTATGTTGGG GCCCCGCCAA CTTGCATTGT CTGTAGAATT CCTTTTCGAA ATTC

54

(2) INFORMATION FOR SEQ ID NO: 5058:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 53 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5058:

CTGAATCCGA GTCGCTATCC GAGTCTGAGT CGCTATCTGA GTCTGAATCG CTG

53

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 59 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5059:

TTTGGGCTAC ACACGTGCTA CAATGGACAA TACAAAGGGC AGCGAAACCG TGATGTCAA

(2) INFORMATION FOR SEQ ID NO: 5060:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 53 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5060:

AAATAACTAA TAACATTTAG AGGCTGGGAC ATAAATCCCT AAAAAACAGC AGT

(2) INFORMATION FOR SEQ ID NO: 5061:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 55 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5061:

TTAAAGAGTG CGTAATAGCT CACTAATCGA GTGACAATGG CGCCGAAAAT GTACC

(2) INFORMATION FOR SEQ ID NO: 5062:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 52 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5062:

TACCAGGGTA TCTAATCCTG TTTGATCCCC ACGCTTTCGC ACATCAGCGT, CA

(2) INFORMATION FOR SEQ ID NO: 5063:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 52 base pairs

- (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5063:

TCGCCAAGCC ATTTTCTTT GTGTTTCTTT TTATTTGAC GTTTAGACA TA

52

10

(2) INFORMATION FOR SEQ ID NO: 5064:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 76 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5064:

20

CTCAAGCTCC CTTGTGCCTT TACACTCTAT GTGTGCTTTC CGACCGTTCT GGGGGGAAC

60

TTGGAGCGCC TCCGTT

76

25

(2) INFORMATION FOR SEQ ID NO: 5065:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 54 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5065:

35

CCACCGCTTG TCGGGTCCC CGTCAATTCC TTTGAGTCGC AACCTTGCGG TCGT

54

(2) INFORMATION FOR SEQ ID NO: 5066:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 55 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5066:

45

TCCCCGGGCT AAACATATTA CCGAAGCTGT GGATTGTCCT TTGACAATG GTAGG

55

50

(2) INFORMATION FOR SEQ ID NO: 5067:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 52 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5067:

GCTCATCGCA TCCACTTTTT GCCTGGCAAC GTTCTACTCT AGCGGAACGT AA

52

(2) INFORMATION FOR SEQ ID NO: 5068:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5068:

CGGACACCAG AAGTACCAAG CGAGCCGGAA ACACCAACAC CACCGACACC AGACGTACAA

60

GCGAGCGGAA ACAACAACAA CG

82

(2) INFORMATION FOR SEQ ID NO: 5069:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5069:

TCCATAACGT GCTGTATCTG TAGCAATAAC TAATACTTTT TCATTCGGTC TA

52

(2) INFORMATION FOR SEQ ID NO: 5070:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5070:

CGACTCGAAG ACTCAATGTC TTCTCCCAT CACAGCTCAG CCTTAACGAG TA

52

(2) INFORMATION FOR SEQ ID NO: 5071:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5071:

GCGATGGATA ACAGGTTGAT ATTCTGTAC CACCTATAAT CGTTTTAATC GA

52

(2) INFORMATION FOR SEQ ID NO: 5072:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5072:

CACTTCACCA CAGCCGCCAT GGCATGGGCA GTAGGAATCG AACCCACACC AAA

53

(2) INFORMATION FOR SEQ ID NO: 5073:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5073:

GTCCAGACTC CTACGGGAGG CAGCAGTAGG GAATCTTCCG CAATGGGCGA AA

52

(2) INFORMATION FOR SEQ ID NO: 5074:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5074:

TGTTGGCTTA GAATCAGCCA TCATTAAAG AGTGCCTAAT AGCTCACTAG TCGC

54

(2) INFORMATION FOR SEQ ID NO: 5075:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 74 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5075:

AAACTTCCCT TTGG

74

(2) INFORMATION FOR SEQ ID NO: 5076:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 53 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5076:

TGAGCTAATC AGACATCATA ATTTTATGG AGAGTTTGAT CCTGGCTCAA GAT

53

(2) INFORMATION FOR SEQ ID NO: 5077:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 52 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5077:

GTTAAGCTCC TTAGCGTCGA TGGTAGTCGA ACTTACGTTT CGCTAGAGTA GA

52

(2) INFORMATION FOR SEQ ID NO: 5078:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 52 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5078:

GGGTAAGTTC CGACCCGCAC GAAAGGCGTA ACGATTGTTGG CACTGTCTCA AC

52

(2) INFORMATION FOR SEQ ID NO: 5079:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 52 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5079:

ATTAATCCAT TGTGCCACAA GTGCCGACC AGAAATGATG GTATTTAATA AT

52



## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5080:

AATAGCGACG AATCACACCT TCTGCGGCAC CACGGAATAA TACACCATGT GG

## (2) INFORMATION FOR SEQ ID NO: 5081:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5081:

CTTTCGCTAC TCACACCGGC ATTCTCACTT CTAAGCGCTC CACATGTCCT TA

## (2) INFORMATION FOR SEQ ID NO: 5082:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5082:

CAGACAGCGA CTCAGATCAG ATAGCGATCG GACTCAGACA ACGACTCAGA TTCAGA

## (2) INFORMATION FOR SEQ ID NO: 5083:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5083:

AGGGTATGAT CCATCCCGGG TCCTCTCGGT ACTAAGGGAC AGCTCCTCTC AAATTCCTA

CG

## (2) INFORMATION FOR SEQ ID NO: 5084:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5084:

10

GTGTACCACT TGTCGTGCCA ACGGCATAGC TGGGTAGCTA TGTGTGGACG AG

52

(2) INFORMATION FOR SEQ ID NO: 5085:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 78 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5085:

TTGCTTACGC TTGCTATAGC CAATATATAG ATGTTGGAGG GGGCAGATTC GAATGCGAAC

60

CCGAGGAGCG GATTAACA

78

25

(2) INFORMATION FOR SEQ ID NO: 5086:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5086:

ACTGACGCTG ATGTGCGAAG CGTGGGGATC ACACAGGATT AGATACCCTG GT

52

(2) INFORMATION FOR SEQ ID NO: 5087:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5087:

50

AAGTTGTTCT CAGTTCGGAT TGTAAGTCTGC AACTCGACTA CATGAAGCTG G

51

(2) INFORMATION FOR SEQ ID NO: 5088:

(i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 51 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5088:

AATACTTTAA AAAAATAAGA CACTTTGGCC AACTTAAGCC AGGATACAAT T

51

10

(2) INFORMATION FOR SEQ ID NO: 5089:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 51 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5089:

20

AGAACGTAAA TTAAATCCTG ATTTAGCACC AGGGACAGAA AAAGTAACAA G

51

(2) INFORMATION FOR SEQ ID NO: 5090:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 51 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5090:

CCGCTACCT CAGTTCATCC GCTCACTTTT CAACGTAAGT CGGTTCCGGTC C

51

35

(2) INFORMATION FOR SEQ ID NO: 5091:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 51 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5091:

CATGGGTGAT AAGGTCCGTG TTCGAAAGGG AAACAGCCCA GACCACCAGC T

51

(2) INFORMATION FOR SEQ ID NO: 5092:

50

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 55 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5092:

TTGTGCGGAT CCCCCTCAAT TCCTTTGAGT TTCAACCTTG CGGTCGTACT CCCCA

55

(2) INFORMATION FOR SEQ ID NO: 5093:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5093:

CCGCAAACCG ACACAGGTAG TCAAGATGAG AATTCTAAGG TGAGCGAGCG A

51

(2) INFORMATION FOR SEQ ID NO: 5094:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5094:

ACGAATACTA ATCGATCGAA GACTTAATCA AAATAAATGT TTTGCGACAA A

51

(2) INFORMATION FOR SEQ ID NO: 5095:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 77 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5095:

AATCGTTGTT ACCTTCATTA TACCACTTAC TTGTGGAGTG ATCTTCTTCA AAGTAACACT

60

ATTGTGCCAC CGATTGA

77

(2) INFORMATION FOR SEQ ID NO: 5096:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

TTCGTAAGGA CATGTGGAGC GCTTAGAAGT GAGAATGCCG GTGTGAGTAG CG

52

(2) INFORMATION FOR SEQ ID NO: 5097:

- 5 (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 51 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5097:

15 GGGTCTGTTT TCTAATTGA GCACAATCTT CGTTCTCAAT AGAATGATTT A

51

(2) INFORMATION FOR SEQ ID NO: 5098:

- 20 (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 51 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5098:

CTGTAGAAAT TGGGAATCCA ATTTCTCTAT GTTGGGGCCC ACACCCAAC T

51

(2) INFORMATION FOR SEQ ID NO: 5099:

- 30 (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 51 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5099:

40 CTGTGGATTG TCCTTTGGCA TGAGATAGGA GAGCGTTCTA AGGGCGTTGA A

51

(2) INFORMATION FOR SEQ ID NO: 5100:

- 45 (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 51 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5100:

GGTTCAGAAC GTCGTGAGAC AGTTCGGTCC CTATCCGTCG TGGGCGTAGG A

51

55

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5101:

TGACTGATAC GATCAATGCG CTTGTAACAA GCTTTTTTCA ATTCTAGTCA GGGGCCCCAA 60  
CACA 64

## (2) INFORMATION FOR SEQ ID NO: 5102:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5102:

TATTTGCATT TATATTGACG TTTTAAACAT AAAAAAAGAA ACCTTGCGGT CTCAATGG 58

## (2) INFORMATION FOR SEQ ID NO: 5103:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5103:

ATTACCATT TGGTATACCA CATCGTTATT CAACACATTA TCTTTTACTT 50

## (2) INFORMATION FOR SEQ ID NO: 5104:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5104:

GGACACTGCT CCCTCAGGAG TCTCGCCATT AATACTACGT ATTAACATGT AAT 53

## (2) INFORMATION FOR SEQ ID NO: 5105:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5105:

10 ATTTCTTCTT TTTCTACAAT CGAGTCTCCT TTTACAGGTC CATATTTTGT

50

(2) INFORMATION FOR SEQ ID NO: 5106:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5106:

TGGTCAAGCG GTTAAGACAC CGCCCTTTCA CGGCGGTAAC ACGGGTTCGA

50

(2) INFORMATION FOR SEQ ID NO: 5107:

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5107:

35

TTTTTAGCAG TAATTGCCAC ATCTGTGTGA CGATAATGAT ATGCGACAGT

50

(2) INFORMATION FOR SEQ ID NO: 5108:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5108:

CAAGCCATTT TTCTTTGTGT TTACTTTTAA TTTTGACGTT TTAGACATAA

50

(2) INFORMATION FOR SEQ ID NO: 5109:

(i) SEQUENCE CHARACTERISTICS:

50

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5109:

AGCCGATGAA GGACGTTACT AACGACGATA TGCTTTGGGG AGCTGTAAGT

50

(2) INFORMATION FOR SEQ ID NO: 5110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5110:

ATCCATAACG TTTGGTATCT GTAGCAATAA CTAATACTTT TTCATTCGGT CTA

53

(2) INFORMATION FOR SEQ ID NO: 5111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5111:

CCCTTAGTAC TGCAGCTAAC GCATTAAGCA CTCGCCTGA GGAGTACGAC CTC

53

(2) INFORMATION FOR SEQ ID NO: 5112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5112:

GGAGTCAAAG TCCGTTGCCT TACCGCTTGG CTATAGCCCA ATATATAGAT

50

(2) INFORMATION FOR SEQ ID NO: 5113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear



AGATTCTT TTCGAAATTC TTTATGTTGG GGCCCCGCCA ACTTGCAATG

50

(2) INFORMATION FOR SEQ ID NO: 5114:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5114:

GCTGTGATGG GGAGAAGACA TTGTGTCTTC GAGTCGTTGA TTTCACTG

50

(2) INFORMATION FOR SEQ ID NO: 5115:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 55 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5115:

CTTGATTAAC TCATTATCAA GTTATGCACG TGTAATGAA TTCGGCTTTA TCGAA

55

(2) INFORMATION FOR SEQ ID NO: 5116:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5116:

GTACTTAAAA AATGAATACA TGAGTAAAGC TCATGGCATA AGAAATACTA

50

(2) INFORMATION FOR SEQ ID NO: 5117:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5117:

CAGAAATCAGA TAGCGACTCA GAATCAGATA GTGAGTCAGA TTCAGCAGTn

50

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5118:

CGAATACTAA TCGATCGAAG ACTTAATCAA AATAAATGTT TTGCGACnAA

50

## (2) INFORMATION FOR SEQ ID NO: 5119:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5119:

AATCGTCGAA ACTTAATCAA AATAAATGTT TTGCGACAAA TCACTTTTAC TTACTATCTA

60

## (2) INFORMATION FOR SEQ ID NO: 5120:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5120:

CCGAAGTTTA CGGGGTCAAT TTGCCGAGTT CCTTAACGAG AGTTCGCTCG

50

## (2) INFORMATION FOR SEQ ID NO: 5121:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5121:

ATAATCCTGT AGTCGAAAAT GTTGTCTCTC TTGAGTGGAT CCTTAGTACG CCGGGGCACG

60

T

61

## (2) INFORMATION FOR SEQ ID NO: 5122:

- (A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5122:

10 TAGCGACTCA GATTGAGACA GCGATTGAGA CAGCGACTCA GACTGAGATA

50

(2) INFORMATION FOR SEQ ID NO: 5123:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5123:

TATTTGTAAA TTGTATCCTG GCTTAAGTTG GCCATTTTTC ATATGGTCTT

50

(2) INFORMATION FOR SEQ ID NO: 5124:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5124:

35

CACGAGCTGA CGACAACCAT GCACCACCTG TCACTTTGTC CCCCAGAGAAG GTCTCTATCT

60

(2) INFORMATION FOR SEQ ID NO: 5125:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 64 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5125:

AGAACACATT GCAGTCTTCG AGTCGTTGAT TTCACACTGC CGTAGTAAAA GCCTCTAGAT

60

50

AGAA

64

(2) INFORMATION FOR SEQ ID NO: 5126:

(i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 57 base pairs

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5126:

GGACGACATT AGACGAATCA TCTGGAAAAG ATGAGTCAAA GAAGGTAATA GTCCTGT

57

10

(2) INFORMATION FOR SEQ ID NO: 5127:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5127:

20

GTCCTTAGTA CGAGATGACC GGGATGGACA TACCTCTGGT GTACCAAGTTG

50

(2) INFORMATION FOR SEQ ID NO: 5128:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5128:

GCCGATTTTA GCACTTGTTG CTTGCTTCAA TTTTATGGGG CCATTTATGG

50

35

(2) INFORMATION FOR SEQ ID NO: 5129:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5129:

45

TCCACACATA GCTACCCAGT CTATGCCGTT TGCACTACAA CTGGTACACC A

51

(2) INFORMATION FOR SEQ ID NO: 5130:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

50

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5130:

CTCAGTTGGT TGAGCATCTG ACTTTTAATC AAAGGGTCAA GGTTCGAATC CTCTTTT

57

(2) INFORMATION FOR SEQ ID NO: 5131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5131:

TGATATTCAC TTCAATGTTA TCAATATTAG TGCCATCTAT GACATCTGCC A

51

(2) INFORMATION FOR SEQ ID NO: 5132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5132:

TCCTGTAGTC GAACGTGTTG TCTCTCTTGA GTGGATCCTG AGTACGACGG A

51

(2) INFORMATION FOR SEQ ID NO: 5133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5133:

ACTCAGACAT TGGATTCAGA TTCAGACAGC GACTCAGATT CAGATAGCGA CTCAGATTC

59

(2) INFORMATION FOR SEQ ID NO: 5134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5134:

## (2) INFORMATION FOR SEQ ID NO: 5135:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5135:

CAATACnAAG GGCAGCGAAA CCGTGATTCA AGCAAATCCC ATAAAGTTGG

50

## (2) INFORMATION FOR SEQ ID NO: 5136:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5136:

GAAGCTGGCG AAAAGTCAGC TTACAAAATG TGCCAGTTGG CGGGGGCCCA AC

52

## (2) INFORMATION FOR SEQ ID NO: 5137:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5137:

TTGTAAGGAA GATGCTCTCC CAGCTGAGCT AATTCTCCAA AATAATGAnT

50

## (2) INFORMATION FOR SEQ ID NO: 5138:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5138:

CTGTACAAGC TGTGCCGATA TTTCAATATC AnGnTACAGT AnAGCTCCAC

50

## (2) INFORMATION FOR SEQ ID NO: 5139:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5139:

10

GGTTCGAATC CTGTCTTCCC GATATACTGT AATTATTATG GGGGCTTTGC TC

52

(2) INFORMATION FOR SEQ ID NO: 5140:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5140:

GCTACTGAAC CTATAAAATG TATGATGGCG GTCTCGAGGG AATCGAACCC AGATCT

56

(2) INFORMATION FOR SEQ ID NO: 5141:

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5141:

35

AGGAGGCTCG TCCGCTCTAG GTTAGTCGGG TCCTAAGCTG AGGCCGACAG TA

52

(2) INFORMATION FOR SEQ ID NO: 5142:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5142:

CACGCTTTTCG ACATCAGCGT CAGTTACAGA CCAGAAAGTC GCCTTCGCAC TGGTGT

56

(2) INFORMATION FOR SEQ ID NO: 5143:

(i) SEQUENCE CHARACTERISTICS:

50

- (A) LENGTH: 75 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5143:

CTCCTAAAAC AATTTACATC CAAACCTTCA TCACTCACGC GGC GTTGCTC CGTCAGCTTT 60  
CGCCATTGCG AAGAT 75

(2) INFORMATION FOR SEQ ID NO: 5144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5144:

GAGGAGTGGT TAGCTTCTGC GGAGTACGAA TCGAGCCCCG TAAACGGCGG CCGGT 55

(2) INFORMATION FOR SEQ ID NO: 5145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5145:

GCCTAATACT CAGCCTGACT GCTTAGACGT GCAATCCATA TCAGCACGAT TCG 53

(2) INFORMATION FOR SEQ ID NO: 5146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5146:

AGCTGTGGAT TGTCTTTTG GCATGGGTAA GGAGAACGTT CTAAGGGCGT T 51

(2) INFORMATION FOR SEQ ID NO: 5147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5147:

CTCTTTGATC CGTAGTCAAA CGCTCTATCC AATTGAGCTA CGGGCGCATA.

50

5

(2) INFORMATION FOR SEQ ID NO: 5148:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5148:

GAACTAATTC TCCAAAATAA TGA CTCTAC AGGAACTCGA ACCCGTATAA CCGCCGTAAA

60

(2) INFORMATION FOR SEQ ID NO: 5149:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5149:

AAAGCACACC CGGAAACTG AAACATCTTA AGTACCCGGA GAAAGAGAAA

50

30

(2) INFORMATION FOR SEQ ID NO: 5150:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 56 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5150:

GTAAGTTCGC ACTACCATCG ACGCTAAGGG AGCTTAACTT CTGTGGTTCG GCATGG

56

(2) INFORMATION FOR SEQ ID NO: 5151:

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 56 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5151:

55

## (2) INFORMATION FOR SEQ ID NO: 5152:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 59 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5152:

CTATTCTCTG TGTCGGGCTC ACCCCAACCTT GCACACTATT GTAAGCTGAC TTTCCTCCA 59

## (2) INFORMATION FOR SEQ ID NO: 5153:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 65 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5153:

TAACCACATC ATTCGGATAC TGTTCATGGA AGTAATTTCT CTATTCTTCG GACCAGGAAA 60

ATACA 65

## (2) INFORMATION FOR SEQ ID NO: 5154:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 91 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5154:

CCATATGTGT CAGTCACTGT GCACATCTTG ACGGTACCTA ATCAGACAGC CACGGCTAAC 60

TCCGTGCCAG CCGCCGCGGT ACTACGTGGT G 91

## (2) INFORMATION FOR SEQ ID NO: 5155:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 52 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5155:

(2) INFORMATION FOR SEQ ID NO: 5156:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 58 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5156:

GACTCTGGGA GGACCATCTC CTAAGGCTAA ACTACTCTCT CGTGACCGAT AGTGAACC

58

(2) INFORMATION FOR SEQ ID NO: 5157:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 51 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5157:

TTGTAACTCC GGTATAGGAG TGTCTTACAA CCCCACAAG CAAGCTTGTT G

51

(2) INFORMATION FOR SEQ ID NO: 5158:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5158:

TAGTnACCGn TAGTGAACCA TTACCGTGAG GGAAAGGTGA AAAGCACCCC

50

(2) INFORMATION FOR SEQ ID NO: 5159:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 51 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5159:

TTCGCTCGCC GCTACTCAAG GGAATCGCAT TTCCTTTCTC TTCCTCCGGG T

51

(2) INFORMATION FOR SEQ ID NO: 5160:

(A) LENGTH: 61 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5160:

10 AACTGGAGAA ACAACTTTAT GGGGTTTGCT TGAACCTCGC GGTTTCGCTG CCCTTTGTAT 60  
T 61

(2) INFORMATION FOR SEQ ID NO: 5161:

15

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 51 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5161:

25 AGACCTCTGC CTTACCACTT GGCTATGCGC CAATAACTGG GCTACCTGGA T 51

(2) INFORMATION FOR SEQ ID NO: 5162:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 55 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5162:

CCGCTCACTT TTCAACGTAA GTCGGATCGG TCCTCCATTC AGTGTCACCT GAACT 55

40

(2) INFORMATION FOR SEQ ID NO: 5163:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 81 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5163:

50 CTTGATCTGT ATTTAAAATG ATATTTTCTA TCTTTTCTTT ATTATTAAACG TCTATGACGT 60  
CGTAGTATAA GATTCCGTGT A 81

55

(2) INFORMATION FOR SEQ ID NO: 5164:

- (A) LENGTH: 62 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5164:

10 GTTCGAATCC CGTCTTCTGC TCCATTATTT TGCCGGGGTG GCGGCAACTC TCACACGCAC 60  
AG 62

(2) INFORMATION FOR SEQ ID NO: 5165:

15

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 55 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5165:

25 CAGGGGTCTT TCGTCCTGTG TGGGTAAGTG CATCTTCACA GGTACTATGA TTTCA 55

(2) INFORMATION FOR SEQ ID NO: 5166:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 62 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5166:

35 AAGCTGAGGC CGACAGCGTA GGCGATGGAT GACAGGTTGA TATTGCCGGT ACCACCCGAT 60  
AA 62

40

(2) INFORMATION FOR SEQ ID NO: 5167:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 52 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5167:

50 CTTGCGTCTC CAGTTCCGCC ACCCCGGCAC TATAAAAATG GAGCAGAAGA CG 52

55

(2) INFORMATION FOR SEQ ID NO: 5168:

- (A) LENGTH: 56 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5168:

10

TCGTCCGCTA TCTCCACCAT TATTTGTACA TTGAAACTAG ATAAGTAGTA AATATA

56

(2) INFORMATION FOR SEQ ID NO: 5169:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 55 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5169:

CTTGGACGTC GGTGGGTAGT CGAACTTAC GTTCCGCTAG AGTAGAACGT TGCCA

55

25

(2) INFORMATION FOR SEQ ID NO: 5170:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 52 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5170:

35

CTACTGCTGC ATATGCGGGT GAAGGGAGTC GAACCCCCAC GCCGTAAGCA TA

52

(2) INFORMATION FOR SEQ ID NO: 5171:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5171:

GGGCTTnGGA CATTAGTTC TnAGGCAATG TAAAAAAGCT GATTCTATT

50

50

(2) INFORMATION FOR SEQ ID NO: 5172:

(i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 60 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5172:

AAATTACATG TTAATACGTA ATTAATGGCG AGACTCCTGA GGAACCATTG CCATTGGAAG

60

(2) INFORMATION FOR SEQ ID NO: 5173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5173:

GTTTTATTTT TTAAAGTAT GTAAAAGTAA AATTACATGn TAATACGTAn

50

(2) INFORMATION FOR SEQ ID NO: 5174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5174:

CAACTCTCGT TAAGGAACTC GGCAAATAC CCCGTAAGTT CGGAGTAGGT CTCTTTA

57

(2) INFORMATION FOR SEQ ID NO: 5175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5175:

GGAAACTGGA ATAAATAAAC ATTCAATTGA GCGCATCAGT ATTAGGATTC ACTCTAAAAA

60

(2) INFORMATION FOR SEQ ID NO: 5176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

GTAACGGACG CGCTCAAAGG TTCCTCACA ATGGTTGGAA ATCATTGATA

50

(2) INFORMATION FOR SEQ ID NO: 5177:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5177:

AGTTACGTTT TTTTATAAAG AGGTTTGAGA CGCGTTATTA ATCTTGTGAG

50

(2) INFORMATION FOR SEQ ID NO: 5178:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 53 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5178:

GTGTGGATCC TGAGTACGAC GGAGCACGTG ACAATCCGT CGGCAATCTG GGG

53

(2) INFORMATION FOR SEQ ID NO: 5179:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 83 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5179:

CGGTAACCTT ATACCTTTTA ACATATTTTG CATTGATTG CGTTTACCTT TTTTACCTTT

60

ACCGCCACCA GTGAAGTGT TCA

83

(2) INFORMATION FOR SEQ ID NO: 5180:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 66 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5180:



TTTAAA

66

(2) INFORMATION FOR SEQ ID NO: 5181:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 67 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5181:

GTTCGGTAAC TCGAGCGGGT CTCATAACCC GTAGGTCGGG TGGTTCAAAT CCGTCCTCCC  
GCAATAT

(2) INFORMATION FOR SEQ ID NO: 5182:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 55 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5182:

TAGCGGTGAA ATGCGCAGAG ATATGGAGGA ACACCAAGTAG CGAAGGCAAC TTTCT

(2) INFORMATION FOR SEQ ID NO: 5183:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5183:

GAATTCCATG TGTAGCGGTG AAATGCGCAG AGATATGnAC GAACACCAAT

(2) INFORMATION FOR SEQ ID NO: 5184:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 62 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5184:

CC

62

(2) INFORMATION FOR SEQ ID NO: 5185:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 55 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5185:

GAGACCTTGT CGGTCCATAT GCGGCTCATC GCATCCATT TTTGCCTGGC AACGT

(2) INFORMATION FOR SEQ ID NO: 5186:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5186:

CCATCATTAA GTTGGGCACT CTAAGTTGAC TGCCGGnGnC ACCnAAGAAG

(2) INFORMATION FOR SEQ ID NO: 5187:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5187:

TTAATACGTT GCAATCCAAT CGCACGCTTC GCCTATCCTA CTGCCnTCCC

(2) INFORMATION FOR SEQ ID NO: 5188:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5188:

AGTCGCTATC CGAATCTGAG TCGCTATCTG AGTCTnAGTC GCTAnnCCAG

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 54 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5189:

ATAGATGCCC TTACCGCAA CCGACACATG TAGTCAATAT GATAATTCTA AGGT

(2) INFORMATION FOR SEQ ID NO: 5190:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5190:

CTTTAATGGG CGAACAGnAC CCTTGGACCG ACTACAGCCC AGATCGATGA

(2) INFORMATION FOR SEQ ID NO: 5191:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 60 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5191:

ACATAGCACC CAGCGAGCCG TTGGACGACA ACTGGTACAC CAGAGGATGC CATCCGGCCT

(2) INFORMATION FOR SEQ ID NO: 5192:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 320 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5192:

Met Lys Met Ile Asn Lys Leu Ile Val Pro Val Thr Ala Ser Ala Leu  
 1 5 10 15

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	20	25	30
5	Leu Ile Ser Ser Lys Ala Gly Asp Val Thr Val Ala Asp Thr Met Lys 35 40 45		
	Lys Ile Gly Lys Asp Gln Ile Ala Asn Ala Ser Phe Thr Glu Met Leu 50 55 60		
10	Asn Lys Ile Leu Ala Asp Lys Tyr Lys Asn Lys Val Asn Asp Lys Lys 65 70 75 80		
	Ile Asp Glu Gln Ile Glu Lys Met Gln Lys Gln Tyr Gly Gly Lys Asp 85 90 95		
15	Lys Phe Glu Lys Ala Leu Gln Gln Gln Gly Leu Thr Ala Asp Lys Tyr 100 105 110		
	Lys Glu Asn Leu Arg Thr Ala Ala Tyr His Lys Glu Leu Leu Ser Asp 115 120 125		
20	Lys Ile Lys Ile Ser Asp Ser Glu Ile Lys Glu Asp Ser Lys Lys Ala 130 135 140		
	Ser His Ile Leu Ile Lys Val Lys Ser Lys Lys Ser Asp Xaa Glu Gly 145 150 155 160		
25	Leu Asp Asp Lys Glu Ala Lys Gln Lys Ala Glu Glu Ile Gln Lys Glu 165 170 175		
	Val Ser Lys Asp Pro Ser Lys Phe Gly Glu Ile Ala Lys Lys Glu Ser 180 185 190		
30	Met Asp Thr Gly Ser Ala Lys Lys Asp Gly Glu Leu Gly Tyr Val Leu 195 200 205		
	Lys Gly Gln Thr Asp Lys Asp Phe Glu Lys Ala Leu Phe Lys Leu Lys 210 215 220		
35	Asp Gly Glu Val Ser Glu Val Val Lys Ser Ser Phe Gly Tyr His Ile 225 230 235 240		
	Ile Lys Ala Asp Lys Pro Thr Asp Phe Asn Ser Glu Lys Gln Ser Leu 245 250 255		
40	Lys Glu Lys Leu Val Asp Gln Lys Val Gln Lys Asn Pro Lys Leu Leu 260 265 270		
	Thr Asp Ala Tyr Lys Asp Leu Leu Lys Glu Tyr Asp Val Asp Phe Lys 275 280 285		
45	Asp Arg Asp Ile Lys Ser Val Val Glu Asp Lys Ile Leu Asn Pro Glu 290 295 300		
50	Lys Leu Lys Gln Gly Gly Ala Gln Gly Gly Gln Ser Gly Met Ser Gln 305 310 315 320		

55

(2) INFORMATION FOR SEQ ID NO:5193:

(A) LENGTH: 330 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5193:

Met	Asn	Lys	Val	Ile	Lys	Met	Leu	Val	Val	Thr	Leu	Ala	Phe	Leu	Leu	1	5	10	15
Val	Leu	Ala	Gly	Cys	Ser	Gly	Asn	Ser	Asn	Lys	Gln	Ser	Ser	Asp	Asn	20	25	30	
Lys	Asp	Lys	Glu	Thr	Thr	Ser	Ile	Lys	His	Ala	Met	Gly	Thr	Thr	Glu	35	40	45	
Ile	Lys	Gly	Lys	Pro	Lys	Arg	Val	Val	Thr	Leu	Tyr	Gln	Gly	Ala	Thr	50	55	60	
Asp	Val	Ala	Val	Ser	Leu	Gly	Val	Lys	Pro	Val	Gly	Ala	Val	Glu	Ser	65	70	75	80
Trp	Thr	Gln	Lys	Pro	Lys	Phe	Glu	Tyr	Ile	Lys	Asn	Asp	Leu	Lys	Asp	85	90	95	
Thr	Lys	Ile	Val	Gly	Gln	Glu	Pro	Ala	Pro	Asn	Leu	Glu	Glu	Ile	Ser	100	105	110	
Lys	Leu	Lys	Pro	Asp	Leu	Ile	Val	Ala	Ser	Lys	Val	Arg	Asn	Glu	Lys	115	120	125	
Val	Tyr	Asp	Gln	Leu	Ser	Lys	Ile	Ala	Pro	Thr	Val	Ser	Thr	Asp	Thr	130	135	140	
Val	Phe	Lys	Phe	Lys	Asp	Thr	Thr	Lys	Leu	Met	Gly	Lys	Ala	Leu	Gly	145	150	155	160
Lys	Glu	Lys	Glu	Ala	Glu	Asp	Leu	Leu	Lys	Lys	Tyr	Asp	Asp	Lys	Val	165	170	175	
Ala	Ala	Phe	Gln	Lys	Asp	Ala	Lys	Ala	Lys	Tyr	Lys	Asp	Ala	Trp	Pro	180	185	190	
Leu	Lys	Ala	Ser	Val	Val	Asn	Phe	Arg	Ala	Asp	His	Thr	Arg	Ile	Tyr	195	200	205	
Ala	Gly	Gly	Tyr	Ala	Gly	Glu	Ile	Leu	Asn	Asp	Leu	Gly	Phe	Lys	Arg	210	215	220	
Asn	Lys	Asp	Leu	Gln	Lys	Gln	Val	Asp	Asn	Gly	Lys	Asp	Ile	Ile	Gln	225	230	235	240
Leu	Thr	Ser	Lys	Glu	Ser	Ile	Pro	Leu	Met	Asn	Ala	Asp	His	Ile	Phe	245	250	255	

Val Val Lys Ser Asp Pro Asn Ala Lys Asp Ala Ala Leu Val Lys Lys  
 260 265 270

Thr Glu Ser Glu Trp Thr Ser Ser Lys Glu Trp Lys Asn Leu Asp Ala  
 275 280 285

Val Lys Asn Asn Gln Val Ser Asp Asp Leu Asp Glu Ile Thr Trp Asn  
 290 295 300

Leu Ala Gly Gly Tyr Lys Ser Ser Leu Lys Leu Ile Asp Asp Leu Tyr  
 305 310 315 320

Glu Lys Leu Asn Ile Glu Lys Gln Ser Lys  
 325 330

(2) INFORMATION FOR SEQ ID NO:5194:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 314 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5194:

Met Thr Arg Lys Phe Arg Thr Leu Ile Leu Ile Leu Ile Ala Thr Ile  
 1 5 10 15

Ala Leu Ser Gly Cys Ala Asn Asp Asp Gly Ile Tyr Ser Asp Lys Gly  
 20 25 30

Gln Val Phe Arg Lys Ile Leu Ser Ser Asp Leu Thr Ser Leu Asp Thr  
 35 40 45

Ser Leu Ile Thr Asp Glu Ile Ser Ser Glu Val Thr Ala Gln Thr Phe  
 50 55 60

Glu Gly Leu Tyr Thr Leu Gly Lys Gly Asp Lys Pro Val Leu Gly Val  
 65 70 75 80

Ala Lys Ala Phe Pro Glu Lys Ser Lys Asp Gly Lys Thr Leu Lys Val  
 85 90 95

Lys Leu Arg Ser Asp Ala Lys Trp Ser Asn Gly Asp Lys Val Thr Ala  
 100 105 110

Gln Asp Phe Val Tyr Ala Trp Arg Lys Thr Val Asp Pro Lys Thr Gly  
 115 120 125

Ser Glu Phe Ala Tyr Ile Met Gly Asp Ile Lys Asn Ala Ser Asp Ile  
 130 135 140

Ser Thr Gly Lys Lys Pro Val Glu Gln Leu Gly Ile Lys Ala Leu Asn  
 145 150 155 160

Asp Glu Thr Leu Gln Ile Glu Leu Glu Lys Pro Val Pro Tyr Ile Asn  
 165 170 175  
 5 Gln Leu Leu Ala Leu Asn Thr Phe Ala Pro Gln Asn Glu Lys Val Ala  
 180 185 190  
 Lys Lys Tyr Gly Lys Asn Tyr Gly Thr Ala Ala Asp Arg Ala Val Tyr  
 195 200 205  
 10 Asn Gly Pro Phe Lys Val Asp Asp Trp Lys Gln Glu Asp Lys Thr Leu  
 210 215 220  
 Leu Ser Lys Asn Gln Tyr Tyr Trp Asp Lys Lys Asn Val Lys Leu Asp  
 225 230 235 240  
 15 Lys Val Asn Tyr Lys Val Ile Lys Asp Leu Gln Ala Gly Ala Ser Leu  
 245 250 255  
 Tyr Asp Thr Glu Ser Val Asp Asp Ala Phe Ile Thr Ala Asp Gln Val  
 260 265 270  
 20 Asn Lys Tyr Lys Asp Asn Lys Gly Leu Asn Phe Val Leu Thr Thr Gly  
 275 280 285  
 Thr Phe Phe Val Lys Met Asn Glu Lys Gln Tyr Pro Asp Phe Lys Asn  
 290 295 300  
 25 Lys Asn Leu Arg Leu Xaa Ser His Lys Gln  
 305 310

## (2) INFORMATION FOR SEQ ID NO:5195:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5195:

Met Lys Arg Leu Ile Gly Leu Val Ile Val Ala Leu Val Leu Leu Ala  
 1 5 10 15  
 45 Ala Cys Gly Gly Asn Asn Asp Lys Lys Val Thr Ile Gly Val Ala Ser  
 20 25 30  
 Asn Asp Thr Lys Ala Trp Glu Lys Val Lys Glu Leu Ala Lys Lys Asp  
 35 40 45  
 50 Asp Ile Asp Val Glu Ile Lys His Phe Ser Asp Tyr Asn Leu Pro Asn  
 50 55 60  
 55 Lys Ala Leu Asn Asp Gly Asp Ile Asp Met Asn Ala Phe Gln His Phe  
 65 70 75 80

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Ala Phe Leu Asp Gln Tyr Lys Lys Ala His Lys Gly Thr Lys Ile Ser  
85 90 95

5 Ala Leu Ser Thr Thr Val Leu Ala Pro Leu Gly Ile Tyr Ser Asp Lys  
100 105 110

Ile Lys Asp Val Lys Lys Val Lys Asp Gly Ala Lys Val Val Ile Pro  
115 120 125

10 Asn Asp Val Ser Asn Gln Ala Arg Ala Leu Lys Leu Leu Glu Ala Ala  
130 135 140

Gly Leu Ile Lys Leu Lys Lys Asp Phe Gly Leu Ala Gly Thr Val Lys  
145 150 155 160

15 Asp Ile Thr Ser Asn Pro Lys His Leu Lys Ile Thr Ala Val Asp Ala  
165 170 175

Gln Gln Thr Ala Arg Ala Leu Ser Asp Val Asp Ile Ala Val Ile Asn  
180 185 190

20 Asn Gly Val Ala Thr Lys Ala Gly Lys Asp Pro Lys Asn Asp Pro Ile  
195 200 205

Phe Leu Glu Lys Ser Asn Ser Asp Ala Val Lys Pro Tyr Ile Asn Ile  
210 215 220

25 Val Ala Val Asn Asp Lys Asp Leu Asp Asn Lys Thr Tyr Ala Lys Ile  
225 230 235 240

30 Val Glu Leu Tyr His Ser Lys Glu Ala Gln Lys Ala Leu Gln Glu Asp  
245 250 255

Val Lys Asp Gly Glu Lys Pro Val Asn Leu Ser Lys Asp Glu Ile Lys  
260 265 270

35 Ala Ile Glu Thr Ser Leu Ala Lys  
275 280

(2) INFORMATION FOR SEQ ID NO:5196:

40 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 273 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: protein

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5196:

Met Lys Lys Leu Phe Gly Leu Ile Leu Val Leu Thr Phe Ala Val Val  
1 5 10 15

55 Leu Ala Ala Cys Gly Asn Gly Asn Lys Ser Gly Ser Asp Asp Lys Lys  
20 25 30



Ile Thr Val Ser Ala Ser Pro Ala Pro His Ala Glu Ile Leu Glu Lys  
 35 40 45  
 5 Ala Lys Pro Leu Leu Glu Lys Lys Gly Tyr Glu Leu Asp Ile Lys Thr  
 50 55 60  
 Ile Asn Asp Tyr Thr Thr Pro Asn Lys Leu Leu Asp Lys Gly Glu Ile  
 65 70 75 80  
 10 Asp Ala Asn Tyr Phe Gln His Thr Pro Tyr Leu Asn Thr Glu Lys Lys  
 85 90 95  
 Asp Lys Gly Tyr Lys Ile Val Ser Ala Gly Asp Val His Leu Glu Pro  
 100 105 110  
 15 Met Ala Val Tyr Ser Lys Lys Tyr Lys Ser Leu Lys Glu Leu Pro Lys  
 115 120 125  
 Gly Ala Thr Val Tyr Val Ser Asn Asn Pro Ala Glu Gln Gly Arg Phe  
 130 135 140  
 20 Leu Lys Phe Phe Val Asp Ala Gly Leu Ile Lys Ile Lys Lys Gly Val  
 145 150 155 160  
 Lys Ile Glu Asp Ala Lys Phe Ser Asp Ile Thr Glu Asn Lys Lys Asp  
 165 170 175  
 25 Ile Lys Phe Asn Asn Lys Gln Ser Ala Glu Phe Leu Pro Lys Ile Tyr  
 180 185 190  
 Gln Asn Glu Asp Ala Asp Ala Val Ile Ile Asn Ser Asn Phe Ala Ile  
 195 200 205  
 30 Glu Gln Lys Leu Asn Pro Lys Lys Asp Ser Ile Ala Val Glu Ser Ala  
 210 215 220  
 Lys Asp Asn Pro Tyr Ala Asn Leu Ile Ala Val Lys Glu Gly His Gln  
 225 230 235 240  
 Asp Asp Lys Lys Ile Lys Ala Leu Ile Glu Val Leu Gln Ser Lys Asp  
 245 250 255  
 40 Ile Gln Asp Phe Ile Asn Glu Lys Tyr Asn Gly Ala Val Ile Pro Ala  
 260 265 270  
 Lys

## (2) INFORMATION FOR SEQ ID NO:5197:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5197:

5	Met	Lys	Lys	Ile	Lys	Tyr	Ile	Leu	Val	Val	Phe	Val	Leu	Ser	Leu	Thr	1	5	10	15
	Val	Leu	Ser	Gly	Cys	Ser	Leu	Pro	Gly	Leu	Gly	Ser	Lys	Ser	Thr	Lys	20	25	30	
10	Asn	Asp	Val	Lys	Ile	Thr	Ala	Leu	Ser	Thr	Ser	Glu	Ser	Gln	Ile	Ile	35	40	45	
	Ser	His	Met	Leu	Arg	Leu	Leu	Ile	Glu	His	Asp	Thr	His	Gly	Lys	Ile	50	55	60	
15	Lys	Pro	Thr	Leu	Val	Asn	Asn	Leu	Gly	Ser	Ser	Thr	Ile	Gln	His	Asn	65	70	75	80
	Ala	Leu	Ile	Asn	Gly	Asp	Ala	Asn	Ile	Ser	Gly	Val	Arg	Tyr	Asn	Gly	85	90	95	
20	Thr	Asp	Leu	Thr	Gly	Ala	Leu	Lys	Glu	Ala	Pro	Ile	Lys	Asn	Pro	Lys	100	105	110	
	Lys	Ala	Met	Ile	Ala	Thr	Gln	Gln	Gly	Phe	Lys	Lys	Lys	Phe	Asp	Gln	115	120	125	
25	Thr	Phe	Phe	Asp	Ser	Tyr	Gly	Phe	Ala	Asn	Thr	Tyr	Ala	Phe	Met	Val	130	135	140	
30	Thr	Lys	Glu	Thr	Ala	Lys	Lys	Tyr	His	Leu	Glu	Thr	Val	Ser	Asp	Leu	145	150	155	160
	Ala	Lys	His	Ser	Lys	Asp	Leu	Arg	Leu	Gly	Met	Asp	Ser	Ser	Trp	Met	165	170	175	
35	Asn	Arg	Lys	Gly	Asp	Gly	Tyr	Glu	Gly	Phe	Lys	Lys	Glu	Tyr	Gly	Phe	180	185	190	
	Asp	Phe	Gly	Thr	Val	Arg	Pro	Met	Gln	Ile	Gly	Leu	Val	Tyr	Asp	Ala	195	200	205	
40	Leu	Asn	Ser	Glu	Lys	Leu	Asp	Val	Ala	Leu	Gly	Tyr	Ser	Thr	Asp	Gly	210	215	220	
	Arg	Ile	Ala	Ala	Tyr	Asp	Leu	Lys	Val	Leu	Lys	Asp	Asp	Lys	Gln	Phe	225	230	235	240
45	Phe	Pro	Pro	Tyr	Ala	Ala	Ser	Ala	Val	Ala	Thr	Asn	Glu	Leu	Leu	Arg	245	250	255	
50	Gln	His	Pro	Glu	Leu	Lys	Thr	Thr	Ile	Asn	Lys	Leu	Thr	Gly	Lys	Ile	260	265	270	
	Ser	Thr	Ser	Glu	Met	Gln	Arg	Leu	Asn	Tyr	Glu	Ala	Asp	Gly	Lys	Gly	275	280	285	
55	Lys	Glu	Pro	Ala	Val	Val	Ala	Glu	Glu	Phe	Leu	Lys	Lys	His	His	Tyr	290	295	300	

Phe Asp Lys Gln Lys Gly Gly His Lys  
305 310

## (2) INFORMATION FOR SEQ ID NO:5198:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5198:

Met Lys Lys Leu Thr Thr Leu Leu Leu Ala Ser Thr Leu Leu Ile Ala  
1 5 10 15  
Ala Cys Gly Asn Asp Asp Ser Lys Lys Asp Asp Ser Lys Thr Ser Lys  
20 25 30  
Lys Asp Asp Gly Val Lys Ala Glu Leu Lys Gln Ala Thr Lys Ala Tyr  
25 35 40 45  
Asp Lys Tyr Thr Asp Glu Gln Leu Asn Glu Phe Leu Lys Gly Thr Glu  
50 55 60  
Lys Phe Val Lys Ala Ile Glu Asn Asn Asp Met Ala Gln Ala Lys Ala  
30 65 70 75 80  
Leu Tyr Pro Lys Val Arg Met Tyr Tyr Glu Arg Ser Glu Pro Val Ala  
85 90 95  
Glu Ala Phe Gly Asp Leu Asp Pro Lys Ile Asp Ala Arg Leu Ala Asp  
35 100 105 110  
Met Lys Glu Glu Lys Lys Glu Lys Glu Trp Ser Gly Tyr His Lys Ile  
115 120 125  
Glu Lys Ala Leu Tyr Glu Asp Lys Lys Ile Asp Asp Val Thr Lys Lys  
40 130 135 140  
Asp Ala Gln Gln Leu Leu Lys Asp Ala Lys Glu Leu His Ala Lys Ala  
45 145 150 155 160  
Asp Thr Leu Asp Ile Thr Pro Lys Leu Met Leu Gln Gly Ser Val Asp  
165 170 175  
Leu Leu Asn Glu Val Ala Thr Ser Lys Ile Thr Gly Glu Glu Glu Ile  
50 180 185 190  
Tyr Ser His Thr Asp Leu Tyr Asp Phe Lys Ala Asn Val Glu Gly Ala  
195 200 205  
Gln Lys Ile Tyr Asp Leu Phe Lys Pro Ile Leu Glu Lys Lys Asp Lys  
55 210 215 220

EP 0 786 519 A2

Lys Leu Ser Asp Asp Ile Gln Met Asn Phe Asp Lys Val Asn Gln Leu  
225 230 235 240

Leu Asp Lys Tyr Lys Asp Asn Asn Gly Gly Tyr Glu Ser Phe Glu Lys  
245 250 255

Val Ser Lys Lys Asp Arg Lys Ala Phe Ala Asp Ala Val Asn Ala Leu  
260 265 270

Gly Glu Pro Leu Ser Lys Met Ala Val Ile Thr Glu  
275 280

(2) INFORMATION FOR SEQ ID NO:5199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5199:

Met Lys Lys Leu Thr Thr Leu Leu Leu Ala Ser Thr Leu Leu Ile Ala  
1 5 10 15

Ala Cys Gly Asn Asp Asp Ser Lys Lys Asp Asp Ser Lys Thr Ser Lys  
20 25 30

Lys Asp Asp Gly Val Lys Ala Glu Leu Lys Gln Ala Thr Lys Ala Tyr  
35 40 45

Asp Lys Tyr Thr Asp Glu Gln Leu Asn Glu Phe Leu Lys Gly Thr Glu  
50 55 60

Lys Phe Val Lys Ala Ile Glu Asn Asn Asp Met Ala Gln Ala Lys Ala  
65 70 75 80

Leu Tyr Pro Lys Val Arg Met Tyr Tyr Glu Arg Ser Glu Pro Val Ala  
85 90 95

Glu Ala Phe Gly Asp Leu Asp Pro Lys Ile Asp Ala Arg Leu Ala Asp  
100 105 110

Met Lys Glu Glu Lys Lys Glu Lys Glu Trp Ser Gly Tyr His Lys Ile  
115 120 125

Glu Lys Ala Leu Tyr Glu Asp Lys Lys Ile Asp Asp Val Thr Lys Lys  
130 135 140

Asp Ala Gln Gln Leu Leu Lys Asp Ala Lys Glu Leu His Ala Lys Ala  
145 150 155 160

Asp Thr Leu Asp Ile Thr Pro Lys Leu Met Leu Gln Gly Ser Val Asp  
165 170 175

Leu Leu Asn Glu Val Ala Thr Ser Lys Ile Thr Gly Glu Glu Glu Ile  
 180 185 190  
 Tyr Ser His Thr Asp Leu Tyr Asp Phe Lys Ala Asn Val Glu Gly Ala  
 195 200 205  
 Gln Lys Ile Tyr Asp Leu Phe Lys Pro Ile Leu Glu Lys Lys Asp Lys  
 210 215 220  
 Lys Leu Ser Asp Asp Ile Gln Met Asn Phe Asp Lys Val Asn Gln Leu  
 225 230 235 240  
 Leu Asp Lys Tyr Lys Asp Asn Asn Gly Gly Tyr Glu Ser Phe Glu Lys  
 245 250 255  
 Val Ser Lys Lys Asp Arg Lys Ala Phe Ala Asp Ala Val Asn Ala Leu  
 260 265 270  
 Gly Glu Pro Leu Ser Lys Met Ala Val Ile Thr Glu  
 275 280

## (2) INFORMATION FOR SEQ ID NO:5200:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5200:

Met Lys Phe Lys Ala Ile Val Ala Ile Thr Leu Ser Leu Ser Leu Leu  
 1 5 10 15  
 Thr Ala Cys Gly Ala Asn Gln His Lys Glu Asn Ser Ser Lys Ser Asn  
 20 25 30  
 Asp Thr Asn Lys Lys Thr Gln Gln Thr Asp Asn Thr Thr Gln Ser Asn  
 35 40 45  
 Thr Glu Lys Gln Met Thr Pro Gln Glu Ala Glu Asp Ile Val Arg Asn  
 50 55 60  
 Asp Tyr Lys Ala Arg Gly Val Asn Glu Tyr Gln Thr Leu Asn Tyr Lys  
 65 70 75 80  
 Thr Asn Leu Glu Arg Ser Asn Glu His Glu Tyr Tyr Val Glu His Leu  
 85 90 95  
 Val Arg Asp Ala Val Gly Thr Pro Leu Lys Arg Cys Ala Ile Val Asn  
 100 105 110  
 Arg His Asn Gly Thr Ile Ile Asn Ile Phe Asp Asp Met Ser Glu Lys  
 115 120 125

Asp Lys Glu Glu Phe Glu Ala Phe Lys Lys Arg Ser Pro Lys Tyr Asn  
130 135 140

Pro Gly Met Asn Asn His Asp Glu Thr Asp Gly Glu Ser Glu Asp Ile  
145 150 155 160

Gln His His Asp Ile Asp Asn Asn Lys Ala Ile Gln Asn Asp Ile Pro  
165 170 175

Asp Gln Lys Val Asp Asp Lys Asn Asp Lys Asn Ala Val Asn Lys Glu  
180 185 190

Glu Lys His Asp Asn Gly Ala Asn Asn Ser Glu Glu Thr Lys Val Lys  
195 200 205

(2) INFORMATION FOR SEQ ID NO:5201:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 184 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5201:

Met Leu Lys Gly Cys Gly Gly Cys Leu Ile Ser Phe Ile Leu Leu Ile  
1 5 10 15

Ile Leu Leu Ser Ala Cys Ser Met Met Phe Ser Asn Asn Asp Asn Ser  
20 25 30

Thr Asn Asn Gln Ser Ser Lys Thr Gln Leu Thr Gln Lys Asp Glu Asn  
35 40 45

Lys Asn Glu Asp Lys Pro Glu Glu Lys Ser Glu Thr Ala Thr Asp Glu  
50 55 60

Asp Leu Gln Ser Thr Glu Glu Val Pro Ala Asn Glu Asn Thr Glu Asn  
65 70 75 80

Asn Gln His Glu Ile Asp Glu Ile Thr Thr Lys Asp Gln Ser Asp Asp  
85 90 95

Asp Ile Asn Thr Pro Asn Val Ala Glu Asp Lys Ser Gln Asp Asp Leu  
100 105 110

Lys Asp Asp Leu Lys Glu Lys Gln Gln Ser Ser Asn His His Gln Ser  
115 120 125

Thr Gln Pro Lys Thr Ser Pro Ser Thr Glu Thr Asn Thr Gln Gln Ser  
130 135 140

Phe Ala Asn Cys Lys Gln Leu Arg Gln Val Tyr Pro Asn Gly Val Thr

Ala Asp His Pro Ala Tyr Arg Pro His Leu Asp Arg Asp Lys Asp Lys  
                                   165                                  170                                  175

Arg Ala Cys Glu Pro Asp Lys Tyr  
                                   180

(2) INFORMATION FOR SEQ ID NO:5202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5202:

Met Lys Lys Arg Leu Leu Leu Ser Thr Phe Leu Ala Ser Thr Leu Ile  
 1                                  5                                  10                                  15

Leu Thr Gly Cys Ala Ser Asp Gln Ser Asp Asn Glu Asp His His Thr  
                                   20                                  25                                  30

Ser Thr Gly Ile His Ala Pro Lys Ser Ala Lys Lys Leu Glu Thr Lys  
                                   35                                  40                                  45

Asp Ile Phe Xaa Ser Asp Lys Lys Asn Ser Asp Ile Ser Asp Ala Glu  
                                   50                                  55                                  60

Met Lys Gln Ala Ile Glu Lys Tyr Leu Ser Val Asn Ser Asp Ile Leu  
                                   65                                  70                                  75                                  80

Asp Asn Lys Tyr Ile Met Gln His Lys Leu Asp Lys Gln Ile Asp Ser  
                                   85                                  90                                  95

Gln Thr Lys Val Thr Glu Lys Gln Ala Glu Thr Leu Ser His Leu Ser  
                                   100                                  105                                  110

Asn Leu Ala Val Lys Asn Asp Leu His Phe Lys Lys Phe Val Thr Glu  
                                   115                                  120                                  125

Asn Asn Ile Pro Lys Glu Tyr Lys Lys Pro Val Glu Leu Met Met Asn  
                                   130                                  135                                  140

Tyr Phe Lys Ala Leu Asn Ser Thr Ile Ala Asn Val Asp Glu Asp Ile  
                                   145                                  150                                  155                                  160

Glu Lys Leu Ser Tyr Gln Pro Gln Asn Lys Ile Asn Val Val Asp Val  
                                   165                                  170                                  175

Pro Thr Lys Tyr Ala Gly Asp Val Asn Lys Lys Gln Gln Asp Lys Ile  
                                   180                                  185                                  190

Lys Asp Phe Leu Lys Ser Lys Gly Ile Lys Ser Asp Val Ile Asp Lys

## (2) INFORMATION FOR SEQ ID NO:5203:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 283 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5203:

```

Met Lys Ser Lys Ile Tyr Ile Leu Leu Leu Xaa Leu Ile Phe Leu Ser
 1           5           10           15
Ala Cys Ala Asn Thr Arg His Ser Glu Ser Asp Lys Asn Val Leu Thr
20           25           30
Val Tyr Ser Pro Tyr Gln Ser Asn Leu Ile Arg Pro Ile Leu Asn Glu
35           40           45
Xaa Glu Lys Gln Glu His Val Lys Ile Glu Ile Lys His Gly Ser Thr
25           50           55           60
Gln Val Leu Leu Ser Asn Leu His Asn Glu Asp Phe Ser Glu Arg Gly
65           70           75           80
Asp Val Phe Met Gly Gly Val Leu Ser Glu Thr Ile Asp His Pro Glu
30           85           90           95
Asp Phe Val Pro Tyr Gln Asp Thr Ser Val Thr Gln Gln Leu Glu Asp
100          105          110
Tyr Arg Ser Asn Asn Lys Tyr Val Thr Ser Phe Leu Leu Met Pro Thr
35          115          120          125
Val Ile Val Val Asn Ser Asp Leu Gln Gly Asp Ile Lys Ile Arg Gly
40          130          135          140
Tyr Gln Asp Leu Leu Gln Pro Ile Leu Lys Gly Lys Ile Ala Tyr Ser
145          150          155          160
Asn Pro Asn Thr Thr Thr Thr Gly Tyr Gln His Met Arg Ala Ile Tyr
45          165          170          175
Ser Met His His Arg Val Ser Asp Val His Gln Phe Gln Asn His Ala
180          185          190
Met Gln Leu Ser Lys Thr Ser Lys Val Ile Glu Asp Val Ala Lys Gly
50          195          200          205
Lys Tyr Tyr Ala Gly Leu Ser Tyr Glu Gln Asp Ala Arg Thr Trp Lys
210          215          220

```



225                      230                      235                      240  
 Leu Asn Val Asp Gly Ile Ala Leu Val Lys Asn Ala His Pro His Pro  
                                  245                      250                      255  
 5                      Lys Arg Lys Lys Leu Val Gln Tyr Leu Thr Ser Arg Ser Val Gln Gln  
                                  260                      265                      270  
 Arg Leu Val Ala Glu Phe Asp Ala Lys Ser Ile  
 10                      275                      280

## (2) INFORMATION FOR SEQ ID NO:5204:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5204:

25                      Met Lys Lys Phe Ile Gly Ser Val Leu Ala Thr Thr Leu Ile Leu Gly  
                                  1                      5                      10                      15  
 Gly Cys Ser Thr Met Glu Asn Glu Ser Lys Lys Asp Thr Lys Thr Glu  
                                  20                      25                      30  
 30                      Thr Lys Ser Val Pro Glu Glu Met Glu Ala Ser Lys Tyr Val Gly Gln  
                                  35                      40                      45  
 Gly Phe Gln Pro Pro Ala Glu Lys Asn Ala Ile Glu Phe Ala Lys Lys  
 35                      50                      55                      60  
 His Arg Lys Glu Phe Glu Lys Val Gly Glu Gln Phe Phe Lys Asp Asn  
                                  65                      70                      75                      80  
 Phe Gly Leu Lys Val Lys Ala Thr Asn Val Val Gly Lys Asp Asp Gly  
 40                      85                      90                      95  
 Val Glu Val Tyr Val His Cys Glu Asp His Gly Ile Val Phe Asn Ala  
                                  100                      105                      110  
 45                      Ser Leu Pro Leu Tyr Lys Asp Ala Ile His Gln Lys Gly Ser Met Arg  
                                  115                      120                      125  
 Ser Asn Asp Asn Gly Asp Asp Met Ser Met Met Val Gly Thr Val Leu  
                                  130                      135                      140  
 50                      Ser Gly Phe Glu Tyr Arg Ala Gln Lys Glu Lys Tyr Asp Asn Leu Tyr  
                                  145                      150                      155                      160  
 Lys Phe Phe Lys Glu Asn Glu Lys Lys Tyr Gln Tyr Thr Gly Phe Thr  
                                  165                      170                      175  
 55

180 185 190

Phe Tyr Ile Thr Tyr Ser Ser Arg Ser Leu Lys Glu Tyr Arg Lys Tyr  
195 200 205

Tyr Glu Pro Leu Ile Arg Lys Asn Asp Lys Glu Phe Lys Glu Gly Met  
210 215 220

Glu Arg Ala Arg Lys Glu Val Asn Tyr Ala Ala Asn Thr Asp Ala Val  
225 230 235 240

Ala Thr Leu Phe Ser Thr Lys Lys Asn Phe Thr Lys Asp Asn Thr Val  
245 250 255

Asp Asp Val Ile Glu Leu Ser Asp Lys Leu Tyr Asn Leu Lys Asn Lys  
260 265 270

Pro Asp Lys Ser Thr Ile Thr Ile Gln Ile Gly Lys Pro Thr Ile Asn  
275 280 285

Thr Lys Lys Ala Phe Tyr Asp Asp Asn Arg Pro Ile Glu Tyr Gly Val  
290 295 300

His Ser Lys Asp Glu  
305

(2) INFORMATION FOR SEQ ID NO:5205:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 193 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5205:

Met Lys Lys Leu Val Ser Ile Val Gly Ala Thr Leu Leu Leu Ala Gly  
1 5 10 15

Cys Gly Ser Gln Asn Leu Ala Pro Leu Glu Glu Lys Thr Thr Asp Leu  
20 25 30

Arg Glu Asp Asn His Gln Leu Lys Leu Asp Ile Gln Glu Leu Asn Gln  
35 40 45

Gln Ile Ser Asp Ser Lys Ser Lys Ile Lys Gly Leu Glu Lys Asp Lys  
50 55 60

Glu Asn Ser Lys Lys Thr Ala Ser Asn Asn Thr Lys Ile Lys Leu Met  
65 70 75 80

Asn Val Thr Ser Thr Tyr Tyr Asp Lys Val Ala Lys Ala Leu Lys Ser  
85 90 95

100 105 110  
 Val Gln Ser Lys Leu Asn Gln Ile Ser Asn Asp Ile Gln Ser Ala His  
 115 120 125  
 5 Thr Ser Tyr Lys Asp Ala Ile Asp Gly Leu Ser Leu Ser Asp Asp Asp  
 130 135 140  
 Lys Lys Thr Ser Lys Asn Ile Asp Lys Leu Asn Ser Asp Leu Asn His  
 10 145 150 155 160  
 Ala Phe Asp Asp Ile Lys Asn Gly Tyr Gln Asn Lys Asp Lys Lys Gln  
 165 170 175  
 15 Leu Thr Lys Gly Gln Gln Ala Leu Ser Lys Leu Asn Leu Asn Ala Lys  
 180 185 190  
 Ser

## (2) INFORMATION FOR SEQ ID NO:5206:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5206:

Met Lys Arg Leu Leu Phe Val Met Ile Ala Phe Val Phe Ile Leu Ala  
 1 5 10 15  
 Ala Cys Gly Asn Asn Ser Ser Lys Asp Lys Glu Ala Ser Lys Asp Ser  
 20 25 30  
 Lys Thr Ile Asn Val Gly Thr Glu Gly Thr Tyr Ala Pro Phe Ser Phe  
 35 40 45  
 His Asp Lys Asp Gly Lys Leu Thr Gly Tyr Asp Ile Asp Val Ile Lys  
 50 55 60  
 Ala Val Ala Lys Glu Glu Gly Leu Lys Leu Lys Phe Asn Glu Thr Ser  
 65 70 75 80  
 Trp Asp Ser Met Phe Ala Gly Leu Asp Ala Gly Arg Phe Asp Val Ile  
 85 90 95  
 50 Ala Asn Gln Val Gly Ile Asn Pro Asp Arg Glu Lys Lys Tyr Lys Phe  
 100 105 110  
 Ser Lys Pro Tyr Thr Phe Ser Ser Ala Val Leu Val Ile Arg Glu Asn  
 115 120 125

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130 135 140

Gln Thr Phe Thr Ser Asn Tyr Gly Lys Leu Ala Lys Asp Lys Gly Ala  
145 150 155 160

Asp Ile Thr Lys Val Asp Gly Phe Asn Gln Ser Met Asp Leu Leu Leu  
165 170 175

Ser Lys Arg Val Asp Gly Thr Phe Asn Asp Ser Leu Ser Tyr Leu Asp  
180 185 190

Tyr Lys Lys Gln Lys Pro Asn Ala Lys Ile Lys Ala Ile Lys Gly Asn  
195 200 205

Ala Glu Gln Ser Arg Ser Ala Phe Ala Phe Ser Lys Lys Ala Asp Asp  
210 215 220

Glu Thr Val Gln Lys Phe Asn Asp Gly Leu Lys Lys Ile Glu Glu Asn  
225 230 235 240

Gly Glu Leu Ala Lys Ile Gly Lys Lys Trp Phe Gly Gln Asp Val Ser  
245 250 255

Lys Ser Lys

(2) INFORMATION FOR SEQ ID NO:5207:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 203 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5207:

Met Gly Val His Ser Met Lys Leu Lys Arg Leu Phe Ala Val Val Ile  
1 5 10 15

Ala Met Leu Leu Val Leu Ala Gly Cys Ser Asn Ser Asn Asp Asn Asn  
20 25 30

Glu Ser Lys Lys Asp Asp Ala Asp Asn Gly Lys Lys Gln Glu Ile Gln  
35 40 45

Val Ala Ala Ala Ala Ser Leu Thr Asp Val Thr Lys Lys Leu Ala Ser  
50 55 60

Glu Phe Lys Lys Glu His Lys Asn Ala Asp Ile Lys Phe Asn Tyr Gly  
65 70 75 80

Gly Ser Gly Ala Leu Arg Lys Gln Ile Glu Ser Gly Ala Pro Val Asp  
85 90 95

100 105 110  
 Asn Lys Ala His Asp Thr Tyr Lys Tyr Ala Lys Asn Ser Leu Val Leu  
 115 120 125  
 Ile Gly Asp Lys Asp Ser Asn Tyr Thr Ser Val Lys Asp Leu Lys Asp  
 130 135 140  
 Asn Asp Lys Leu Ala Leu Gly Glu Val Lys Thr Val Pro Ala Gly Lys  
 145 150 155 160  
 Tyr Ala Lys Gln Tyr Leu Asp Asn Asn Asn Leu Phe Lys Glu Val Glu  
 165 170 175  
 Ser Xaa Ile Val Tyr Ala Lys Asp Val Lys Gln Val Leu Asn Tyr Val  
 180 185 190  
 Xaa Lys Gly Asn Ala Lys Gln Gly Phe Val Tyr  
 195 200

(2) INFORMATION FOR SEQ ID NO:5208:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 327 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5208:

Met Lys Lys Trp Gln Phe Val Gly Thr Thr Ala Leu Gly Ala Thr Leu  
 1 5 10 15  
 Leu Leu Gly Ala Cys Gly Gly Gly Asn Gly Gly Ser Gly Asn Ser Asp  
 20 25 30  
 Leu Lys Gly Glu Ala Lys Gly Asp Gly Ser Ser Thr Val Ala Pro Ile  
 35 40 45  
 Val Glu Lys Leu Asn Glu Lys Trp Ala Gln Asp His Ser Asp Ala Lys  
 50 55 60  
 Ile Ser Ala Gly Gln Ala Gly Thr Gly Ala Gly Phe Gln Lys Phe Ile  
 65 70 75 80  
 Ala Gly Asp Ile Asp Phe Ala Asp Ala Ser Arg Pro Ile Lys Asp Glu  
 85 90 95  
 Glu Lys Gln Lys Leu Gln Asp Lys Asn Ile Lys Tyr Lys Glu Phe Lys  
 100 105 110  
 Ile Ala Gln Asp Gly Val Thr Val Ala Val Asn Lys Glu Asn Asp Phe  
 115 120 125

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130 135 140

Ala Lys Thr Trp Lys Asp Val Asn Ser Lys Trp Pro Asp Lys Lys Ile  
145 150 155 160

Asn Ala Val Ser Pro Asn Ser Ser His Gly Thr Tyr Asp Phe Phe Glu  
165 170 175

Asn Glu Val Met Asn Lys Glu Asp Ile Lys Ala Glu Lys Asn Ala Asp  
180 185 190

Thr Asn Ala Ile Val Ser Ser Val Thr Lys Asn Lys Glu Gly Ile Gly  
195 200 205

Tyr Phe Gly Tyr Asn Phe Tyr Val Gln Asn Lys Asp Lys Leu Lys Glu  
210 215 220

Val Lys Ile Lys Asp Glu Asn Gly Lys Ala Thr Glu Pro Thr Lys Lys  
225 230 235 240

Thr Ile Gln Asp Asn Ser Tyr Ala Leu Ser Arg Pro Leu Phe Ile Tyr  
245 250 255

Val Asn Glu Lys Ala Leu Lys Asp Asn Lys Val Met Ser Glu Phe Ile  
260 265 270

Lys Phe Val Leu Glu Asp Lys Gly Lys Ala Ala Glu Glu Ala Gly Tyr  
275 280 285

Val Ala Ala Pro Glu Lys Thr Tyr Lys Ser Gln Leu Asp Asp Leu Lys  
290 295 300

Ala Phe Ile Asp Lys Asn Gln Lys Ser Asp Asp Lys Lys Ser Asp Asp  
305 310 315 320

Lys Lys Ser Glu Asp Lys Lys  
325

(2) INFORMATION FOR SEQ ID NO:5209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5209:

Met Lys Arg Leu Ser Ile Ile Val Ile Ile Gly Ile Phe Ile Ile Thr  
1 5 10 15

Gly Cys Asp Trp Gln Arg Thr Ser Lys Glu Arg Ser Lys Asn Ala Gln  
20 25 30

	35	40	45
5	Asn Leu Met Met Thr Lys 50	Lys Leu Leu Ser Gln Tyr 55	Asn His Pro Lys 60
	Tyr Lys Leu Glu Leu Val 65	Lys Phe Asn Asn Trp 70	Pro Asp Leu Met Asp 80
10	Ala Leu Asn Ser Gly Arg Ile 85	Asp Gly Ala Ser Thr 90	Leu Ile Glu Leu 95
	Ala Met Lys Ser Lys Gln Lys 100	Gly Ser Asn Ile Lys 105	Ala Val Ala Leu 110
15	Gly His His Glu Gly Asn Val 115	Ile Met Gly Gln Lys 120	Gly Met His Leu 125
	Asn Glu Phe Asn Asn Asn 130	Gly Asp Asp Tyr His 135	Phe Gly Ile Pro His 140
20	Arg Tyr Ser Thr His Tyr 145	Leu Leu Leu Glu Glu 150	Leu Arg Lys Gln Leu 155
	Lys Ile Lys Pro Gly His Phe 165	Ser Tyr His Glu Met Ser 170	Pro Ala Glu 175
25	Met Pro Ala Ala Leu Ser 180	Glu His Arg Ile Thr 185	Gly Tyr Ser Val Ala 190
	Glu Pro Phe Gly Ala Leu 195	Gly Glu Lys Leu Gly 200	Lys Gly Lys Thr Leu 205
30	Lys His Gly Asp Asp Val 210	Ile Pro Asp Ala Tyr 215	Cys Cys Val Leu Val 220
	Leu Arg Gly Glu Leu Leu 225	Asp Gln His Lys Asp 230	Val Ala Gln Ala Phe 235
35	Val Gln Asp Tyr Lys Lys 245	Ser Gly Phe Lys Met 250	Asn Asp Arg Lys Gln 255
	Ser Val Asp Ile Met Thr 260	His His Phe Lys Gln 265	Ser Arg Asp Val Leu 270
40	Thr Gln Ser Ala Ala Trp 275	Thr Ser Tyr Gly Asp 280	Leu Thr Ile Lys Pro 285
	Ser Gly Tyr Gln Glu Ile 290	Thr Thr Leu Val Lys 295	Gln His His Leu Phe 300
45	Asn Pro Pro Ala Tyr Asp 305	Asp Phe Val Glu Pro 310	Ser Leu Tyr Lys Glu 315
50	Ala Ser Arg Ser		

## (2) INFORMATION FOR SEQ ID NO:5210:

55 (i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: protein

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5210:

Met Lys Lys Thr Leu Gly Cys Leu Leu Leu Ile Met Leu Leu Val Val  
 1 5 10 15

Ala Gly Cys Ser Phe Gly Gly Asn His Lys Leu Ser Ser Lys Lys Ser  
 15 20 25 30

Glu Glu Ser Lys Gln Glu Thr Val Lys Lys Glu Ser Glu Glu Glu Lys  
 35 40 45

Asp Pro Asp Leu Glu Lys Tyr Glu Glu Ile Glu Lys Lys Met Lys Gly  
 20 50 55 60

Ile Lys Asp Ala Pro Ser Leu Asp Lys Leu Asp Pro Leu Met Thr Glu  
 65 70 75 80

Lys Ser Phe Thr Asn Ser Lys Gly Ile Gln Gly Trp Lys Asp Tyr Lys  
 25 85 90 95

Glu Leu Met Gly Lys Val Glu Leu Ala Asp Tyr Arg Phe Thr Lys Asp  
 100 105 110

Ser Lys Gly Ser Ser Ile Lys Asp Val Asp Ala Phe Phe Lys Gly Lys  
 30 115 120 125

Lys Gly Ile Lys Arg Lys Val Ile Glu Thr His Asp Asp Val Lys Gln  
 35 130 135 140

Val Asp Tyr Trp  
 145

(2) INFORMATION FOR SEQ ID NO:5211:

40

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 33 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

45

(ii) MOLECULE TYPE: protein

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5211:

Trp Pro Cys Ala Thr Xaa Gln Glx Glu Trp Trp Ser Arg His Xaa Trp  
 1 5 10 15

55



20

25

30

His

5

## (2) INFORMATION FOR SEQ ID NO:5212:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 490 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

10

## (ii) MOLECULE TYPE: protein

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5212:

20

Met Ser Ile Ile Met Glu Val Ala Thr Met Gln Ala Lys Leu Thr Lys  
 1 5 10 15

Asn Glu Phe Ile Glu Trp Leu Lys Thr Ser Glu Gly Lys Gln Phe Asn  
 20 25 30

25

Val Asp Leu Trp Tyr Gly Phe Gln Cys Phe Asp Tyr Ala Asn Ala Gly  
 35 40 45

Trp Lys Val Leu Phe Gly Leu Leu Leu Lys Gly Leu Gly Ala Lys Asp  
 50 55 60

30

Ile Pro Phe Ala Asn Asn Phe Asp Gly Leu Ala Thr Val Tyr Gln Asn  
 65 70 75 80

Thr Pro Asp Phe Leu Ala Gln Pro Gly Asp Met Val Val Phe Gly Ser  
 85 90 95

35

Asn Tyr Gly Ala Gly Tyr Gly His Val Ala Trp Val Ile Glu Ala Thr  
 100 105 110

Leu Asp Tyr Ile Ile Val Tyr Glu Gln Asn Trp Leu Gly Gly Gly Trp  
 115 120 125

40

Thr Asp Gly Ile Glu Gln Pro Gly Trp Gly Trp Glu Lys Val Thr Arg  
 130 135 140

Arg Gln His Ala Tyr Asp Phe Pro Met Trp Phe Ile Arg Pro Asn Phe  
 145 150 155 160

45

Lys Ser Glu Thr Ala Pro Arg Ser Val Gln Ser Pro Thr Gln Ala Pro  
 165 170 175

Lys Lys Glu Thr Ala Lys Pro Gln Pro Lys Ala Val Glu Leu Lys Ile  
 180 185 190

50

Ile Lys Asp Val Val Lys Gly Tyr Asp Leu Pro Lys Arg Gly Ser Asn  
 195 200 205

55

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	210	215	220
	Ala Glu Ala Tyr Arg Asn Gly Leu Val Asn Ala Pro Leu Ser Arg Leu		
	225	230	235 240
5	Glu Ala Gly Ile Ala His Ser Tyr Val Ser Gly Asn Thr Val Trp Gln		
	245	250	255
	Ala Leu Asp Glu Ser Gln Val Gly Trp His Thr Ala Asn Gln Ile Gly		
10	260	265	270
	Asn Lys Tyr Tyr Tyr Gly Ile Glu Val Cys Gln Ser Met Gly Ala Asp		
	275	280	285
	Asn Ala Thr Phe Leu Lys Asn Glu Gln Ala Thr Phe Gln Glu Cys Ala		
15	290	295	300
	Arg Leu Leu Lys Lys Trp Gly Leu Pro Ala Asn Arg Asn Thr Ile Arg		
	305	310	315 320
	Leu His Asn Glu Phe Thr Ser Thr Ser Cys Pro His Arg Ser Ser Val		
20	325	330	335
	Leu His Thr Gly Phe Asp Pro Val Thr Arg Gly Leu Leu Pro Glu Asp		
	340	345	350
	Lys Arg Leu Gln Leu Lys Asp Tyr Phe Ile Lys Gln Ile Arg Ala Tyr		
25	355	360	365
	Met Asp Gly Lys Ile Pro Val Ala Thr Val Ser Asn Glu Ser Ser Ala		
	370	375	380
	Ser Ser Asn Thr Val Lys Pro Val Ala Ser Ala Trp Lys Arg Asn Lys		
30	385	390	395 400
	Tyr Gly Thr Tyr Tyr Met Glu Glu Ser Ala Arg Phe Thr Asn Gly Asn		
	405	410	415
35	Gln Pro Ile Thr Val Arg Lys Val Gly Pro Phe Leu Ser Cys Pro Val		
	420	425	430
	Gly Tyr Gln Phe Gln Pro Gly Gly Tyr Cys Asp Tyr Thr Glu Val Met		
40	435	440	445
	Leu Gln Asp Gly His Val Trp Val Gly Tyr Thr Trp Glu Gly Gln Arg		
	450	455	460
	Tyr Tyr Leu Pro Ile Arg Thr Trp Asn Gly Ser Ala Pro Pro Asn Gln		
45	465	470	475 480
	Ile Leu Gly Asp Leu Trp Gly Glu Ile Ser		
	485	490	

50 (2) INFORMATION FOR SEQ ID NO:5213:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 299 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single

55

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5213:

5  
 10 Gly Asp Lys Met Asn Lys Ile Ser Lys Tyr Ile Ala Ile Ala Ser Leu  
 1 5 10 15  
 Ser Val Ala Val Thr Val Ser Ala Pro Gln Thr Thr Asn Ser Thr Ala  
 20 25 30  
 15 Phe Ala Lys Ser Ser Ala Glu Val Gln Gln Thr Gln Gln Ala Ser Ile  
 35 40 45  
 Pro Ala Ser Gln Lys Ala Asn Leu Gly Asn Gln Asn Ile Met Ala Val  
 50 55 60  
 20 Ala Trp Tyr Gln Asn Ser Ala Glu Ala Lys Ala Leu Tyr Leu Gln Gly  
 65 70 75 80  
 Tyr Asn Ser Ala Lys Thr Gln Leu Asp Lys Glu Ile Lys Lys Asn Lys  
 85 90 95  
 25 Gly Lys His Lys Leu Ala Ile Ala Leu Asp Leu Asp Glu Thr Val Leu  
 100 105 110  
 Asp Asn Ser Pro Tyr Gln Gly Tyr Ala Ser Ile His Asn Lys Pro Phe  
 115 120 125  
 30 Pro Glu Gly Trp His Glu Trp Val Gln Ala Ala Lys Ala Lys Pro Val  
 130 135 140  
 35 Tyr Gly Ala Lys Glu Phe Leu Lys Tyr Ala Asp Lys Lys Gly Val Asp  
 145 150 155 160  
 Ile Tyr Tyr Ile Ser Asp Arg Asp Lys Glu Lys Asp Leu Lys Ala Thr  
 165 170 175  
 40 Gln Lys Asn Leu Lys Gln Gln Gly Ile Pro Gln Ala Lys Lys Ser His  
 180 185 190  
 Ile Leu Leu Lys Gly Lys Asp Asp Lys Ser Lys Glu Ser Arg Arg Gln  
 195 200 205  
 45 Met Val Gln Lys Asp His Lys Leu Val Met Leu Phe Gly Asp Asn Leu  
 210 215 220  
 50 Leu Asp Phe Thr Asp Pro Lys Glu Ala Thr Ala Glu Ser Arg Glu Ala  
 225 230 235 240  
 Leu Ile Glu Lys His Lys Asp Asp Phe Gly Lys Lys Tyr Ile Ile Phe  
 245 250 255  
 55 Pro Asn Pro Met Tyr Gly Ser Trp Glu Ala Thr Ile Tyr Asn Asn Asn  
 260 265 270

275

280

285

Lys Gln Phe Asp Pro Lys Thr Gly Glu Val Lys  
290 295

## (2) INFORMATION FOR SEQ ID NO:5214:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5214:

Leu Asn Lys Cys Lys Ile Ile Ile Trp Arg Ile Ile Asn Met Lys Asn  
1 5 10 15  
Lys Leu Ile Ala Lys Ser Leu Leu Thr Leu Ala Ala Ile Gly Ile Thr  
20 25 30  
Thr Thr Thr Ile Ala Ser Thr Ala Asp Ala Ser Glu Gly Tyr Gly Pro  
35 40 45  
Arg Glu Lys Lys Pro Val Ser Ile Asn His Asn Ile Val Glu Tyr Asn  
50 55 60  
Asp Gly Thr Phe Lys Tyr Gln Ser Arg Pro Lys Phe Asn Ser Thr Pro  
65 70 75 80  
Lys Tyr Ile Lys Phe Lys His Asp Tyr Asn Ile Leu Glu Phe Asn Asp  
85 90 95  
Gly Thr Phe Glu Tyr Gly Ala Arg Pro Gln Phe Asn Lys Pro Ala Ala  
100 105 110  
Lys Thr Asp Ala Thr Ile Lys Lys Glu Gln Lys Leu Ile Gln Ala Gln  
115 120 125  
Asn Leu Val Arg Glu Phe Glu Lys Thr His Thr Val Ser Ala His Arg  
130 135 140  
Lys Ala Gln Lys Ala Val Asn Leu Val Ser Phe Glu Tyr Lys Val Lys  
145 150 155 160  
Lys Met Val Leu Gln Glu Arg Ile Asp Asn Val Leu Lys Gln Gly Leu  
165 170 175  
Val Lys

## (2) INFORMATION FOR SEQ ID NO:5215:

## (i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: protein

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5215:

Lys	Glu	Arg	Val	Leu	Met	Lys	Lys	Leu	Leu	Thr	Ala	Ser	Ile	Ile	Ala	1	5	10	15
Cys	Ser	Val	Val	Met	Gly	Val	Gly	Leu	Val	Asn	Thr	Ser	Ala	Glu	Ala	20	25	30	
Ala	Ser	Gly	Asn	Ser	Ile	Asp	Thr	Val	Lys	Gln	Leu	Ile	Lys	Gly	Asp	35	40	45	
Gln	Ser	Leu	Glu	Asn	Val	Lys	Ile	Gly	Glu	Ser	Ile	Lys	Asp	Val	Leu	50	55	60	
Thr	Lys	Tyr	Lys	Asn	Pro	Met	Tyr	Ser	Tyr	Asn	Glu	Asp	Gly	Thr	Glu	65	70	75	80
His	Tyr	Tyr	Glu	Phe	His	Thr	Lys	Lys	Gly	Met	Leu	Leu	Val	Thr	Thr	85	90	95	
Asp	Gly	Lys	Lys	Asn	Asn	Gly	Lys	Val	Thr	His	Ile	Ser	Met	Met	Tyr	100	105	110	
Asn	Asp	Ala	Asn	Gly	Pro	Thr	Tyr	Gln	Ala	Val	Lys	Asn	Tyr	Val	Gly	115	120	125	
Lys	Ala	Val	Thr	His	Thr	Glu	Tyr	Ser	Lys	Val	Ala	Gly	Asn	Phe	Gly	130	135	140	
Tyr	Ile	Glu	Lys	Gly	Lys	Thr	Thr	Tyr	Gln	Phe	Ala	Ser	Ala	Pro	Lys	145	150	155	160
Asp	Lys	Asn	Ile	Lys	Leu	Tyr	Arg	Ile	Asp	Leu	Glu	Lys	165	170					

(2) INFORMATION FOR SEQ ID NO:5216:

45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 167 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: protein

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5216:

1                      5                      10                      15  
 Asn Glu Asp Gly Ser Lys Lys Lys Met Ser Thr Thr Ala Lys Val Val  
                          20                      25                      30  
 5 Ser Ile Ala Thr Val Leu Leu Leu Leu Gly Gly Leu Val Phe Ala Ile  
                          35                      40                      45  
 10 Phe Ala Tyr Val Asp His Ser Asn Lys Ala Lys Glu Arg Met Leu Asn  
                          50                      55                      60  
 Glu Gln Lys Gln Glu Gln Lys Glu Lys Arg Gln Lys Glu Asn Ala Glu  
                          65                      70                      75                      80  
 15 Lys Glu Arg Lys Lys Lys Gln Gln Glu Glu Lys Glu Gln Asn Glu Leu  
    85                      90                      95  
 Asp Ser Gln Ala Asn Gln Tyr Gln Gln Leu Pro Gln Gln Asn Gln Tyr  
    100                      105                      110  
 20 Gln Tyr Val Pro Pro Gln Gln Gln Ala Pro Thr Lys Gln Arg Pro Ala  
    115                      120                      125  
 Lys Glu Glu Asn Asp Asp Lys Ala Ser Lys Asp Glu Ser Lys Asp Lys  
    130                      135                      140  
 25 Asp Asp Lys Ala Ser Gln Asp Lys Ser Asp Asp Asn Gln Lys Lys Thr  
    145                      150                      155                      160  
 30 Asp Asp Asn Lys Gln Pro Ala  
    165

## (2) INFORMATION FOR SEQ ID NO:5217:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5217:

Met Lys Arg Asn Phe Pro Lys Leu Ile Ala Leu Ser Leu Ile Phe Ser  
 1                      5                      10                      15  
 Leu Ser Val Thr Pro Ile Ala Asn Ala Glu Ser Asn Ser Asn Ile Lys  
                          20                      25                      30  
 Ala Lys Asp Lys Lys His Val Gln Val Asn Val Glu Asp Lys Ser Val  
                          35                      40                      45  
 55 Pro Thr Asp Val Arg Asn Leu Ala Gln Lys Asp Tyr Leu Ser Tyr Val  
                          50                      55                      60

65                      70                      75                      80

Gly Glu Pro Phe Lys Ile Tyr Lys Phe Asn Lys Lys Ser Asp Gly Asn  
                              85                      90                      95

Tyr Tyr Phe Pro Val Leu Asn Thr Glu Gly Asn Ile Asp Tyr Ile Val  
                              100                      105                      110

Thr Ile Ser  
                              115

(2) INFORMATION FOR SEQ ID NO:5218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5218:

	Asn	Phe	Lys	Met	Gln	Glu	Val	Lys	Tyr	Met	Thr	Glu	Ile	Thr	Phe	Lys	
	1																15
30	Gly	Gly	Pro	Ile	His	Leu	Lys	Gly	Gln	Gln	Ile	Asn	Glu	Gly	Asp	Phe	
				20					25					30			
	Ala	Pro	Asp	Phe	Thr	Val	Leu	Asp	Asn	Asp	Leu	Asn	Gln	Val	Thr	Leu	
			35					40					45				
35	Ala	Asp	Tyr	Ala	Gly	Lys	Lys	Lys	Leu	Ile	Ser	Val	Val	Pro	Ser	Ile	
		50					55					60					
	Asp	Thr	Gly	Val	Cys	Asp	Gln	Gln	Thr	Arg	Lys	Phe	Asn	Ser	Asp	Ala	
	65					70					75					80	
40	Ser	Lys	Glu	Glu	Gly	Ile	Val	Leu	Thr	Ile	Ser	Ala	Asp	Leu	Pro	Phe	
					85					90					95		
	Ala	Gln	Lys	Arg	Trp	Cys	Ala	Ser	Ala	Gly	Leu	Asp	Asn	Val	Ile	Thr	
				100					105						110		
45	Leu	Ser	Asp	His	Arg	Asp	Leu	Ser	Phe	Gly	Glu	Asn	Tyr	Gly	Val	Val	
			115					120					125				
	Met	Glu	Glu	Leu	Arg	Leu	Leu	Ala	Arg	Ala	Val	Phe	Val	Leu	Asp	Ala	
50		130					135					140					
	Asp	Asn	Lys	Val	Val	Tyr	Lys	Glu	Ile	Val	Ser	Glu	Gly	Thr	Asp	Phe	
	145					150					155					160	
55	Pro	Asp	Phe	Asp	Ala	Ala	Leu	Ala	Ala	Tyr	Lys	Asn	Ile				
					165					170							

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5219:

Ile Glu Ser Arg Phe Ile Met Ala Lys Ile Asn Phe Asp Ala Ala Thr  
 1 5 10 15  
 Lys Gly Asn Pro Gly Ile Ser Thr Cys Ala Ile Val Ile Lys Glu Asp  
 20 25 30  
 Glu Gln His Tyr Thr Tyr Thr His Glu Leu Gly Glu Met Asp Asn His  
 35 40 45  
 Thr Ala Glu Trp Ala Ala Cys Ile Tyr Ala Leu Glu His Ala Arg Glu  
 50 55 60  
 Leu Asn Val Gln Asn Ala Leu Leu Tyr Thr Asp Ser Lys Leu Ile Ala  
 65 70 75 80  
 Asp Ser Ile Glu Ala Gly Tyr Val Lys Asn Ala Asn Phe Lys Pro Tyr  
 85 90 95  
 Phe Asp Gln Ile Glu Ile Phe Glu Lys Asp Phe Asp Leu Leu Phe Val  
 100 105 110  
 Lys Trp Ile Pro Arg Glu Gln Asn Lys Glu Ala Asn Gln His Ala Gln  
 115 120 125  
 Gln Ala Leu Tyr Lys Leu Ile Lys Lys Asn Lys  
 130 135

## (2) INFORMATION FOR SEQ ID NO:5220:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5220:

Met Pro Gly Thr Val Leu Asp Pro Gln Met Ile Lys Asn Glu Asp Val  
 1 5 10 15



20                      25                      30  
 Gly Val Asn Thr Ser Met Asp Trp Asp Arg Lys Tyr Pro Tyr Gly Asp  
                     35                      40                      45  
 5 Thr Leu Arg Gly Ile Phe Gly Asp Val Ser Thr Pro Ala Glu Gly Ile  
                     50                      55                      60  
 10 Pro Lys Glu Leu Thr Glu His Tyr Leu Ser Lys Gly Tyr Ser Arg Asn  
                     65                      70                      75                      80  
 Asp Arg Val Gly Lys Ser Tyr Leu Glu Tyr Gln Tyr Glu Asp Val Leu  
                     85                      90                      95  
 15 Arg Gly Lys Lys Lys Glu Met Lys Tyr Thr Thr Asp Lys Ser Gly Lys  
                     100                      105                      110  
 Val Thr Ser Glu Val Leu Xaa Pro Gly Ala Arg Gly Gln Asp Leu  
                     115                      120                      125  
 20 Lys Leu Thr Ile Asp Ile Asp Leu Gln Lys Glu Val Glu Ala Leu Leu  
                     130                      135                      140  
 Asp Lys Gln Ile Lys Lys Leu Ala Val Lys Val Pro Lys Ile Trp Ile  
                     145                      150                      155                      160  
 25 Met Gln

## (2) INFORMATION FOR SEQ ID NO:5221:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 311 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5221:

Ile Met Ala Tyr Asp Gly Leu Phe Thr Lys Lys Met Val Glu Ser Leu  
 1                      5                      10                      15  
 45 Gln Phe Leu Thr Thr Gly Arg Val His Lys Ile Asn Gln Pro Asp Asn  
                     20                      25                      30  
 Asp Thr Ile Leu Met Val Val Arg Gln Asn Arg Gln Asn His Gln Leu  
                     35                      40                      45  
 50 Leu Leu Ser Ile His Pro Asn Phe Ser Arg Leu Gln Leu Thr Thr Lys  
                     50                      55                      60  
 55 Lys Tyr Asp Asn Pro Phe Asn Pro Pro Met Phe Ala Arg Val Phe Arg  
                     65                      70                      75                      80

	85	90	95
5	Asp Arg Arg Ile Glu Ile Asp Ile Lys Ser Lys Asp Glu Ile Gly Asp 100 105 110		
	Thr Ile Tyr Arg Thr Val Ile Leu Glu Ile Met Gly Lys His Ser Asn 115 120 125		
10	Leu Ile Leu Val Asp Glu Asn Arg Lys Ile Ile Glu Gly Phe Lys His 130 135 140		
	Leu Thr Pro Asn Thr Asn His Tyr Arg Thr Val Met Pro Gly Phe Asn 145 150 155 160		
15	Tyr Glu Ala Pro Pro Thr Gln His Lys Ile Asn Pro Tyr Asp Ile Thr 165 170 175		
	Gly Ala Glu Val Leu Lys Tyr Ile Asp Phe Asn Ala Gly Asn Ile Ala 180 185 190		
20	Lys Gln Leu Leu Asn Gln Phe Glu Gly Phe Ser Pro Leu Ile Thr Asn 195 200 205		
	Glu Ile Val Ser Arg Arg Gln Phe Met Thr Ser Ser Thr Leu Pro Glu 210 215 220		
25	Ala Phe Asp Glu Val Met Ala Glu Thr Lys Leu Pro Pro Thr Pro Ile 225 230 235 240		
	Phe His Lys Asn His Glu Thr Gly Lys Glu Asp Phe Tyr Phe Ile Lys 245 250 255		
30	Leu Asn Gln Phe Asn Asp Asp Thr Val Thr Tyr Asp Ser Leu Asn Asp 260 265 270		
	Leu Leu Asp Arg Phe Tyr Asp Ala Arg Gly Glu Arg Glu Arg Val Lys 275 280 285		
35	Gln Arg Ala Asn Asp Leu Val Arg Phe Val Gln Gln Gln Leu His Lys 290 295 300		
40	Tyr Gln Asn Lys Leu Ala Ser 305 310		

## (2) INFORMATION FOR SEQ ID NO:5222:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5222:

1	5	10	15
Glu Gln Leu Tyr Gly Glu Leu Ile Thr Ala Asn Ile Tyr Arg Ile Lys	20	25	30
Gln Gly Asp Lys Glu Val Thr Ala Leu Asn Tyr Tyr Thr Asn Glu Glu	35	40	45
Val Val Ile Pro Leu Asn Pro Thr Lys Ser Pro Ser Ala Asn Ala Gln	50	55	60
Tyr Tyr Tyr Lys Gln Tyr Xaa Arg Met Lys Thr Arg Xaa Arg Glu Leu	65	70	75
Gln His Gln Ile Gln Leu Thr Lys Asp Asn Ile Asp Tyr Phe Ser Thr	85	90	95
Ile Glu Gln Gln Leu His His Ile Ser Val His Asp Ile Asp Glu Ile	100	105	110
Arg Asp Glu Leu Ala Glu Gln Gly Phe Met Lys Gln Arg Lys Asn Gln	115	120	125
Thr Lys Lys Lys Lys Ala Gln Ile Gln Leu Gln His Tyr Val Ser Thr	130	135	140
Asp Gly Asp Asp Ile Tyr Val Gly Lys Asn Asn Lys Gln Asn Asp Tyr	145	150	155
Leu Thr Asn Lys Lys Ala Lys Lys Thr His Thr Trp Leu His Thr Lys	165	170	175
Asp Ile Pro Gly Ser His Val Val Ile Phe Asn Asp Ala Pro Ser Asp	180	185	190
Thr Thr Ile Lys Glu Ala Ala Met Leu Ala Gly Tyr Phe Ser Lys Ala	195	200	205
Gly Asn Ser Gly Gln Ile Pro Val Asp Tyr Thr Leu Ile Lys Asn Val	210	215	220
His Lys Pro Ser Gly Ala Lys Pro Gly Phe Val Thr Tyr Asp Asn Gln	225	230	235
Lys Thr Leu Tyr Ala	245		

## (2) INFORMATION FOR SEQ ID NO:5223:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5223:

Tyr Ile Thr Asn Pro Gln Asn Pro Lys Ile Lys Ile Thr Gly Ile Ser  
 1 5 10 15  
 Leu Ser Ser Gly Val Gly Asn Phe Phe Ile Ile Thr Asn Gly Lys Arg  
 20 25 30  
 Ile Ile Val Ala Lys Ile Lys Arg Asn Ala Asp Asn Asp Ser Ala Leu  
 35 40 45  
 Lys Ser Phe Asn Ala Ile Phe Ile Ile Gly Asn Ala Asp Pro His Asn  
 50 55 60  
 Met Ile Val Asn Lys Tyr Asp Arg Lys Val Val Ser Arg Ser Leu Phe  
 65 70 75 80  
 Ile Asn Ile Ile Thr Pro Leu Ile Met Cys Phe Tyr Ile Lys Lys Tyr  
 85 90 95  
 Asp Leu Lys

## (2) INFORMATION FOR SEQ ID NO:5224:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 131 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5224:

Glu Asn Val Leu Ala Lys Glu Tyr Ala Val Lys Tyr Asn Ala Val Glu  
 1 5 10 15  
 Ala Ile Gln His Arg Gly Glu Thr Val Thr Glu Gly Ser Ser Ser Asn  
 20 25 30  
 Ala Tyr Ala Ile Lys Asp Gly Val Ile Tyr Thr His Pro Ile Asn Asn  
 35 40 45  
 Tyr Ile Leu Asn Gly Ile Thr Arg Ile Val Ile Lys Lys Ile Ala Glu  
 50 55 60  
 Asp Tyr Asn Ile Pro Phe Lys Glu Glu Thr Phe Thr Val Asp Phe Leu  
 65 70 75 80  
 Lys Asn Ala Asp Glu Val Ile Val Ser Ser Thr Ser Ala Glu Val Thr  
 85 90 95  
 Pro Val Ile Lys Leu Asp Gly Glu Pro Val Asn Asp Gly Lys Val Gly  
 100 105 110

115

120

125

His Ser Ile  
130

5

## (2) INFORMATION FOR SEQ ID NO:5225:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 540 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

10

## (ii) MOLECULE TYPE: protein

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5225:

20

Asn His Leu Thr Ala Arg Ile Ile Asn Gln Glu Asp Asp Leu Met Asn  
1 5 10 15

25

Leu Phe Arg Gln Gln Lys Phe Ser Ile Arg Lys Phe Asn Val Gly Ile  
20 25 30

Phe Ser Ala Leu Ile Ala Thr Val Thr Phe Ile Ser Thr Asn Pro Thr  
35 40 45

30

Thr Ala Ser Ala Ala Glu Gln Asn Gln Pro Ala Gln Asn Gln Pro Ala  
50 55 60

Gln Pro Ala Asp Ala Asn Thr Gln Pro Asn Ala Asn Ala Gly Ala Gln  
65 70 75 80

35

Ala Asn Pro Thr Ala Gln Pro Ala Ala Pro Ala Asn Gln Gly Gln Pro  
85 90 95

Ala Val Gln Pro Ala Asn Gln Gly Gly Gln Ala Asn Pro Ala Gly Gly  
100 105 110

40

Ala Ala Gln Pro Asn Thr Gln Pro Ala Gly Gln Gly Asp Gln Ala Asp  
115 120 125

Pro Asn Asn Ala Ala Gln Ala Gln Pro Gly Asn Gln Ala Thr Pro Ala  
130 135 140

45

Asn Gln Ala Gly Gln Gly Asn Asn Gln Ala Thr Pro Asn Asn Asn Ala  
145 150 155 160

50

Thr Pro Ala Asn Gln Thr Gln Pro Ala Asn Ala Pro Ala Ala Ala Gln  
165 170 175

Pro Ala Ala Pro Val Ala Ala Asn Ala Gln Thr Gln Asp Pro Asn Ala  
180 185 190

55

Ser Asn Thr Gly Glu Gly Ser Ile Asn Thr Thr Leu Thr Phe Asp Asp  
195 200 205

	210	215	220
	Thr Asp Lys Val Asn Gly Tyr Ser Leu Ile Asn Asn Gly Lys Ile Gly		
	225	230	235 240
5	Phe Val Asn Ser Glu Leu Arg Arg Ser Asp Met Phe Asp Lys Asn Asn		
		245	250 255
	Pro Gln Asn Tyr Gln Ala Lys Gly Asn Val Ala Ala Leu Gly Arg Val		
10		260	265 270
	Asn Ala Asn Asp Ser Thr Asp His Gly Asn Phe Asn Gly Ile Ser Lys		
		275	280 285
15	Thr Val Asn Val Lys Pro Asp Ser Glu Leu Ile Ile Asn Phe Thr Thr		
		290	295 300
	Met Gln Thr Asn Ser Lys Gln Gly Ala Thr Asn Leu Val Ile Lys Asp		
		305	310 315 320
20	Ala Lys Lys Asn Thr Glu Leu Ala Thr Val Asn Val Ala Lys Thr Gly		
		325	330 335
	Thr Ala His Leu Phe Lys Val Pro Thr Asp Ala Asp Arg Leu Asp Leu		
		340	345 350
25	Gln Phe Ile Pro Asp Asn Thr Ala Val Ala Asp Ala Ser Arg Ile Thr		
		355	360 365
	Thr Asn Lys Asp Gly Tyr Lys Tyr Tyr Ser Phe Ile Asp Asn Val Gly		
30		370	375 380
	Leu Phe Ser Gly Ser His Leu Tyr Val Lys Asn Arg Asp Leu Ala Pro		
		385	390 395 400
35	Lys Ala Thr Asn Asn Lys Glu Tyr Thr Ile Asn Thr Glu Ile Gly Asn		
		405	410 415
	Asn Gly Asn Phe Gly Ala Ser Leu Lys Ala Asp Gln Phe Lys Tyr Glu		
		420	425 430
40	Val Thr Leu Pro Gln Gly Val Thr Tyr Val Asn Asn Ser Leu Thr Thr		
		435	440 445
	Thr Phe Pro Asn Gly Asn Glu Asp Ser Thr Val Leu Lys Asn Met Thr		
		450	455 460
45	Val Asn Tyr Asp Gln Asn Ala Asn Lys Val Thr Phe Thr Ser Gln Gly		
		465	470 475 480
	Val Thr Thr Ala Arg Gly Thr His Thr Lys Glu Val Leu Phe Pro Asp		
50		485	490 495
	Lys Ser Leu Lys Leu Ser Tyr Lys Val Asn Val Ala Asn Ile Asp Thr		
		500	505 510
55	Pro Lys Asn Ile Asp Phe Asn Glu Lys Leu Thr Tyr Arg Thr Ala Ser		
		515	520 525

530

535

540

## (2) INFORMATION FOR SEQ ID NO:5226:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5226:

```

Tyr Lys Glu Leu Ser His Gly Arg Leu Ile Gly Gly Thr Lys Met His
1           5           10           15
Lys Lys Tyr Phe Ile Gly Thr Ser Ile Leu Ile Ala Val Phe Val Val
20           20           25           30
Ile Phe Asp Gln Val Thr Lys Tyr Ile Ile Ala Thr Thr Met Lys Ile
35           40           45
Gly Asp Ser Phe Glu Val Ile Pro His Phe Leu Asn Ile Thr Ser His
50           55           60
Arg Asn Asn Gly Ala Ala Trp Gly Ile Leu Ser Gly Lys Met Thr Phe
65           70           75           80
Phe Phe Ile Ile Thr Ile Ile Ile Leu Ile Ala Leu Val Tyr Phe Phe
85           90           95
Ile Lys Asp Ala Gln Tyr Asn Leu Phe Met Gln Val Ala Ile Ser Leu
100          105          110
Leu Phe Ala Gly Ala Leu Gly Asn Phe Ile Asp Arg Ile Leu Thr Gly
115          120          125
Glu Val Val Asp Phe Ile Asp Thr Asn Ile Phe Gly Tyr Asp Phe Pro
130          135          140
Ile Phe Asn Ile Ala Asp Ser Ser Leu Thr Ile Gly Val Ile Leu Ile
145          150          155          160
Ile Ile Ala Leu Leu Lys Asp Thr Ser Asn Lys Lys Glu Lys Glu Val
165          170          175
Lys

```

## (2) INFORMATION FOR SEQ ID NO:5227:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5227:

Ala Gly Lys Ser Ser Leu Ile Lys Ser Leu Ile Gly Glu Phe Asn Ala  
 1 5 10 15  
 Thr Gly Thr Lys Leu Leu Tyr Asn Lys Pro Ile Gln Gln Gln Leu Gln  
 20 25 30  
 His Ile Thr Tyr Ile Pro Gln Lys Ala His Ile Asp Leu Asp Phe Pro  
 35 40 45  
 Ile Ser Val Glu Gln Val Ile Leu Ser Gly Cys Tyr Lys Glu Ile Gly  
 50 55 60  
 Trp Phe Arg Arg Pro Asn Lys Ser Ala Arg Asp Lys Leu Lys Gln Leu  
 65 70 75 80  
 Leu Ser Asp Leu Glu Leu Glu Ser Leu Arg His Arg Gln Ile Ser Glu  
 85 90 95  
 Leu Ser Gly Gly Gln Leu Gln Arg Val Leu Val Ala Arg Ala Leu Met  
 100 105 110  
 Ser Xaa Ser Glu Val Tyr Phe Leu Asp Glu Pro Phe Val Gly Ile Asp  
 115 120 125  
 Phe Ser Ser Glu Lys Leu Ile Met Thr Lys Ile Glu Asn Leu Lys Gln  
 130 135 140  
 Gln Gly Lys Leu Ile Leu Ile Ile His His Asp Leu Ser Lys Ala Lys  
 145 150 155 160  
 Gln Tyr Phe Asp Arg Ile Ile Leu Leu Asn Gln Thr Leu Arg Tyr Phe  
 165 170 175  
 Gly Asp Ser Glu Glu Ala Met Ser Val Thr Arg Leu Asn Glu Thr Phe  
 180 185 190  
 Met Ser Ser Thr Asp Cys Ser Asp Pro Ser Gln Arg Ser Asn Ile Thr  
 195 200 205  
 Cys

(2) INFORMATION FOR SEQ ID NO:5228:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 256 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5228:

5 Thr Phe Arg Ile Ile Phe Leu Leu Ser Ile Arg Lys Arg Ser Asn Arg  
 1 5 10 15  
 Thr His Val Ser Ile His Trp Ser Thr Val Asn Lys Glu Glu Ile Cys  
 20 25 30  
 10 Leu Arg Val Lys Asp Asn Leu Gln Gln Ile Ser Thr Gln Ile Asn Asp  
 35 40 45  
 Lys Ser Glu Lys Asn Asn Phe Ser Thr Lys Pro Asn Val Ile Ala Val  
 50 55 60  
 15 Thr Lys Tyr Val Thr Ile Glu Arg Ala Lys Glu Ala Tyr Glu Ala Gly  
 65 70 75 80  
 Ile Arg His Phe Gly Glu Asn Arg Leu Glu Gly Phe Phe Gln Lys Lys  
 85 90 95  
 20 Glu Ala Leu Pro Ser Asp Ala Val Ile His Phe Ile Gly Ser Leu Gln  
 100 105 110  
 Ser Arg Lys Val Lys Asp Val Ile Asn Asp Val Asp Tyr Phe His Ala  
 115 120 125  
 25 Leu Asp Arg Leu Ser Leu Ala Lys Glu Ile Asn Lys Arg Ala Glu His  
 130 135 140  
 30 Lys Ile Lys Cys Phe Leu Gln Val Asn Val Ser Gly Glu Ala Ser Lys  
 145 150 155 160  
 His Gly Ile Ala Leu Glu Asp Val Asp Gln Phe Ile Asp Asp Leu Lys  
 165 170 175  
 35 Lys Tyr Asp Lys Ile Glu Ile Val Gly Leu Met Thr Met Ala Pro Leu  
 180 185 190  
 Thr Asp Asp Glu Ala Tyr Ile Arg Ser Leu Phe Lys Gln Leu Arg Leu  
 195 200 205  
 40 Lys Lys Glu Glu Ile Gln Arg Leu Asn Leu Glu Tyr Ala Pro Cys Asp  
 210 215 220  
 Glu Leu Ser Met Gly Met Ser Asn Asp Tyr Leu Ile Ala Val Glu Glu  
 225 230 235 240  
 45 Gly Ala Thr Phe Val Arg Ile Gly Thr Lys Leu Val Gly Glu Glu Glu  
 245 250 255  
 50

## (2) INFORMATION FOR SEQ ID NO:5229:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 amino acids  
 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5229:

10

Lys His Lys Leu Thr Ile Ile Thr Gly Gly Phe Phe Thr Met Lys Lys  
 1 5 10 15

Thr Ile Met Ala Ser Ser Leu Ala Val Ala Leu Gly Val Thr Gly Tyr  
 20 25 30

15

Ala Ala Gly Thr Gly His Gln Ala His Ala Ala Glu Val Asn Val Asp  
 35 40 45

Gln Ala His Leu Val Asp Leu Ala His Asn His Gln Asp Gln Leu Asn  
 50 55 60

20

Ala Ala Pro Ile Lys Asp Gly Ala Tyr Asp Ile His Phe Val Lys Asp  
 65 70 75 80

Gly Phe Gln Tyr Asn Phe Thr Ser Asn Gly Thr Thr Trp Ser Trp Ser  
 85 90 95

25

Tyr Glu Ala Ala Asn Gly Gln Thr Ala Gly Phe Ser Asn Val Ala Gly  
 100 105 110

Ala Asp Tyr Thr Thr Ser Tyr Asn Gln Gly Ser Asn Val Gln Ser Val  
 115 120 125

30

Ser Tyr Asn Ala Gln Ser Ser Asn Ser Asn Val Glu Ala Val Ser Ala  
 130 135 140

Pro Thr Tyr His Asn Tyr Ser Thr Ser Thr Thr Ser Ser Ser Val Arg  
 145 150 155 160

Leu Ser Asn Gly Asn Thr Ala Gly Ala Thr Gly Ser Ser Ala Ala Gln  
 165 170 175

40

Ile Met Ala Gln Arg Thr Gly Val Ser Ala Ser Thr Trp Ala Ala Ile  
 180 185 190

Ile Ala Arg Glu Ser Asn Gly Gln Val Asn Ala Tyr Asn Pro Ser Gly  
 195 200 205

45

Ala Ser Gly Leu Phe Gln Thr Met Pro Gly Trp Gly Pro Thr Asn Thr  
 210 215 220

Val Asp Gln Gln Ile Asn Ala Ala Val Lys Ala Tyr Lys Ala Gln Gly  
 225 230 235 240

50

Leu Gly Ala Trp Gly Phe  
 245

55

(2) INFORMATION FOR SEQ ID NO:5230:

(A) LENGTH: 519 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5230:

Lys	Glu	Pro	His	Lys	Met	Lys	Lys	Ile	Tyr	Lys	Ser	Leu	Thr	Val	Ser	1	5	10	15
Ala	Ile	Val	Ala	Thr	Val	Ser	Leu	Ser	Ala	Leu	Pro	Gln	Ser	Leu	Ala	20	25	30	
Ile	Thr	His	Glu	Ser	Gln	Pro	Thr	Lys	Gln	Gln	Arg	Thr	Val	Leu	Phe	35	40	45	
Asp	Arg	Ser	His	Gly	Gln	Thr	Ala	Gly	Ala	Ala	Asp	Trp	Val	Ser	Asp	50	55	60	
Gly	Ala	Phe	Ser	Asp	Tyr	Ala	Asp	Ser	Ile	Gln	Lys	Gln	Gly	Tyr	Asp	65	70	75	80
Val	Lys	Ala	Ile	Asp	Gly	His	Ser	Asn	Ile	Thr	Glu	Ala	Ser	Leu	Lys	85	90	95	
Ser	Ser	Lys	Ile	Phe	Val	Ile	Pro	Glu	Ala	Asn	Ile	Pro	Phe	Lys	Glu	100	105	110	
Ser	Glu	Gln	Ala	Ala	Ile	Val	Lys	Tyr	Val	Lys	Gln	Gly	Gly	Asn	Val	115	120	125	
Val	Phe	Ile	Ser	Asp	His	Tyr	Asn	Ala	Asp	Arg	Asn	Leu	Asn	Arg	Ile	130	135	140	
Asp	Ser	Ser	Glu	Ala	Met	Asn	Gly	Tyr	Arg	Arg	Gly	Ala	Tyr	Glu	Asp	145	150	155	160
Met	Ser	Lys	Gly	Met	Asn	Ala	Glu	Glu	Lys	Ser	Ser	Thr	Ala	Met	Gln	165	170	175	
Gly	Val	Lys	Ser	Ser	Asp	Trp	Leu	Ser	Thr	Asn	Phe	Gly	Val	Arg	Phe	180	185	190	
Arg	Tyr	Asn	Ala	Leu	Gly	Asp	Leu	Asn	Thr	Ser	Asn	Ile	Val	Ser	Ser	195	200	205	
Lys	Glu	Ser	Phe	Gly	Ile	Thr	Glu	Gly	Val	Lys	Ser	Val	Ser	Met	His	210	215	220	
Ala	Gly	Ser	Thr	Leu	Ala	Ile	Thr	Asn	Pro	Glu	Lys	Ala	Lys	Gly	Ile	225	230	235	240
Val	Tyr	Thr	Pro	Glu	Gln	Leu	Pro	Ala	Lys	Ser	Lys	Trp	Ser	His	Ala	245	250	255	

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Val Asp Gln Gly Ile Tyr Asn Gly Gly Gly Lys Ala Glu Gly Pro Tyr  
260 265 270

Val Ala Ile Ser Lys Val Gly Lys Gly Lys Ala Ala Phe Ile Gly Asp  
275 280 285

Ser Ser Leu Val Glu Asp Ser Ser Pro Lys Tyr Val Arg Glu Asp Asn  
290 295 300

Gly Glu Lys Lys Lys Thr Tyr Asp Gly Phe Lys Glu Gln Asp Asn Gly  
305 310 315 320

Lys Leu Leu Asn Asn Ile Thr Ala Trp Met Ser Lys Asp Asn Asp Gly  
325 330 335

Lys Ser Leu Lys Ala Ser Ser Leu Thr Leu Asp Thr Lys Thr Lys Leu  
340 345 350

Leu Asp Phe Glu Arg Pro Glu Arg Ser Thr Glu Pro Glu Lys Glu Pro  
355 360 365

Trp Ser Gln Pro Pro Ser Gly Tyr Lys Trp Tyr Asp Pro Thr Thr Phe  
370 375 380

Lys Ala Gly Ser Tyr Gly Ser Glu Lys Gly Ala Asp Pro Gln Pro Asn  
385 390 395 400

Thr Pro Asp Asp His Thr Pro Pro Asn Gln Asn Glu Lys Val Thr Phe  
405 410 415

Asp Ile Pro Gln Asn Val Ser Val Asn Glu Pro Phe Glu Met Thr Ile  
420 425 430

His Leu Lys Gly Phe Glu Ala Asn Gln Thr Leu Glu Asn Leu Arg Val  
435 440 445

Gly Ile Tyr Lys Glu Gly Gly Arg Gln Ile Gly Gln Phe Ser Ser Lys  
450 455 460

Asp Asn Asp Tyr Asn Pro Pro Gly Tyr Ser Thr Leu Pro Thr Val Lys  
465 470 475 480

Ala Asp Glu Asn Gly Asn Val Thr Ile Lys Val Asn Ala Lys Val Leu  
485 490 495

Glu Ser Met Glu Gly Ser Lys Ile Arg Leu Lys Leu Gly Asp Lys Thr  
500 505 510

Leu Ile Thr Thr Asp Phe Lys  
515

(2) INFORMATION FOR SEQ ID NO:5231:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5231:

5	Arg	Asp	Glu	Arg	Ile	Lys	Thr	Met	Thr	Asn	Ser	Ser	Lys	Ser	Phe	Thr	1	5	10	15
	Lys	Phe	Met	Ala	Ala	Ser	Ala	Val	Phe	Thr	Met	Gly	Phe	Leu	Ser	Val	20	25	30	
10	Pro	Thr	Ala	Gly	Ala	Glu	Gln	Thr	Asn	Gln	Ile	Ala	Asn	Lys	Pro	Gln	35	40	45	
	Ala	Ile	Gln	Trp	His	Thr	Asn	Leu	Thr	Asn	Glu	Arg	Phe	Thr	Thr	Ile	50	55	60	
15	Ala	His	Arg	Gly	Ala	Ser	Gly	Tyr	Ala	Pro	Glu	His	Thr	Phe	Gln	Ala	65	70	75	80
	Tyr	Asp	Lys	Ser	His	Asn	Glu	Leu	Lys	Ala	Ser	Tyr	Ile	Glu	Ile	Asp	85	90	95	
20	Leu	Gln	Arg	Thr	Lys	Asp	Gly	His	Leu	Val	Ala	Met	His	Asp	Glu	Thr	100	105	110	
	Val	Asn	Arg	Thr	Thr	Asn	Gly	His	Gly	Lys	Val	Glu	Asp	Tyr	Thr	Leu	115	120	125	
25	Asp	Glu	Leu	Lys	Gln	Leu	Asp	Ala	Gly	Ser	Trp	Phe	Asn	Lys	Lys	Tyr	130	135	140	
30	Pro	Lys	Tyr	Ala	Arg	Ala	Ser	Tyr	Lys	Asn	Ala	Lys	Val	Pro	Thr	Leu	145	150	155	160
	Asp	Glu	Ile	Leu	Glu	Arg	Tyr	Gly	Pro	Asn	Ala	Asn	Tyr	Tyr	Ile	Glu	165	170	175	
35	Thr	Lys	Ser	Pro	Asp	Val	Tyr	Pro	Gly	Met	Glu	Glu	Gln	Leu	Leu	Ala	180	185	190	
40	Ser	Leu	Lys	Lys	His	His	Leu	Leu	Asn	Asn	Asn	Lys	Leu	Lys	Asn	Gly	195	200	205	
	His	Val	Met	Ile	Gln	Ser	Phe	Ser	Asp	Glu	Ser	Leu	Lys	Lys	Ile	His	210	215	220	
45	Arg	Gln	Asn	Lys	His	Val	Pro	Leu	Val	Lys	Leu	Val	Asp	Lys	Gly	Glu	225	230	235	240
	Leu	Gln	Gln	Phe	Asn	Asp	Gln	Arg	Leu	Lys	Glu	Ile	Arg	Ser	Tyr	Ala	245	250	255	
50	Ile	Gly	Leu	Gly	Pro	Asp	Tyr	Thr	Asp	Leu	Thr	Glu	Gln	Asn	Thr	His	260	265	270	
55	His	Leu	Lys	Asp	Leu	Gly	Phe	Ile	Val	His	Pro	Tyr	Thr	Val	Asn	Glu	275	280	285	

Lys Ala Asp Met Leu Arg Leu Asn Lys Tyr Gly Val Asp Gly Val Phe  
 290 295 300

Thr Asn Phe Ala Asp Lys Tyr Lys Glu Val Ile Lys  
 305 310 315

## (2) INFORMATION FOR SEQ ID NO:5232:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 433 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5232:

Arg Phe Met Lys Asn Leu Ile Ser Ile Ile Ile Ile Leu Cys Leu Thr  
 1 5 10 15

Leu Ser Ile Met Thr Pro Tyr Ala Gln Ala Thr Asn Ser Asp Val Thr  
 20 25 30

Pro Val Gln Ala Ala Asn Gln Tyr Gly Tyr Ala Gly Leu Ser Ala Ala  
 35 40 45

Tyr Glu Pro Thr Ser Ala Val Asn Val Ser Gln Thr Gly Gln Leu Leu  
 50 55 60

Tyr Gln Tyr Asn Ile Asp Thr Lys Trp Asn Pro Ala Ser Met Thr Lys  
 65 70 75 80

Leu Met Thr Met Tyr Leu Thr Leu Glu Ala Val Asn Lys Gly Gln Leu  
 85 90 95

Ser Leu Asp Asp Thr Val Thr Met Thr Asn Lys Glu Tyr Ile Met Ser  
 100 105 110

Thr Leu Pro Glu Leu Ser Asn Thr Lys Leu Tyr Pro Gly Gln Val Trp  
 115 120 125

Thr Ile Ala Asp Leu Leu Gln Ile Thr Val Ser Asn Ser Ser Asn Ala  
 130 135 140

Ala Ala Leu Ile Leu Ala Lys Lys Val Ser Lys Asn Thr Ser Asp Phe  
 145 150 155 160

Val Asp Leu Met Asn Asn Lys Ala Lys Ala Ile Gly Met Lys Asn Thr  
 165 170 175

His Phe Val Asn Pro Thr Gly Ala Glu Asn Ser Arg Leu Arg Thr Phe  
 180 185 190

Ala Pro Thr Lys Tyr Lys Asp Gln Glu Arg Thr Val Thr Thr Ala Arg  
 195 200 205

Asp Tyr Ala Ile Leu Asp Leu His Val Ile Lys Glu Thr Pro Lys Ile  
 210 215 220  
 5 Leu Asp Phe Thr Lys Gln Leu Ala Pro Thr Thr His Ala Val Thr Tyr  
 225 230 235 240  
 Tyr Thr Phe Asn Phe Ser Leu Glu Gly Ala Lys Met Ser Leu Pro Gly  
 245 250 255  
 10 Thr Asp Gly Leu Lys Thr Gly Ser Ser Asp Thr Ala Asn Tyr Asn His  
 260 265 270  
 Thr Ile Thr Thr Lys Arg Gly Lys Phe Arg Ile Asn Gln Val Ile Met  
 275 280 285  
 15 Gly Ala Gly Asp Tyr Lys Asn Leu Gly Gly Glu Lys Gln Arg Asn Met  
 290 295 300  
 Met Gly Asn Ala Leu Met Glu Arg Ser Phe Asp Gln Tyr Lys Tyr Val  
 305 310 315 320  
 20 Lys Ile Leu Ser Lys Gly Glu Gln Arg Ile Asn Gly Lys Lys Tyr Tyr  
 325 330 335  
 Val Glu Asn Asp Leu Tyr Asp Val Leu Pro Ser Asp Phe Ser Lys Lys  
 340 345 350  
 25 Asp Tyr Lys Leu Val Val Glu Asp Gly Lys Val His Ala Asp Tyr Pro  
 355 360 365  
 Arg Glu Phe Ile Asn Lys Asp Tyr Gly Pro Pro Thr Val Glu Val His  
 370 375 380  
 30 Gln Pro Ile Ile Gln Lys Ala Asn Thr Val Ala Lys Ser Met Trp Glu  
 385 390 395 400  
 35 Glu His Pro Leu Phe Thr Ile Ile Gly Gly Thr Cys Leu Val Ala Gly  
 405 410 415  
 Leu Ala Leu Ile Val His Met Ile Ile Asn Arg Leu Phe Arg Lys Arg  
 420 425 430  
 40 Lys

## (2) INFORMATION FOR SEQ ID NO:5233:

45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 151 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: protein

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5233:

Leu Thr Lys Glu Arg Glu Tyr Met Lys Leu Lys Ser Phe Ile Thr Val  
 1 5 10 15  
 Thr Leu Ala Leu Gly Met Ile Ala Thr Thr Gly Ala Thr Val Ala Gly  
 5 20 25 30  
 Asn Glu Val Ser Ala Ala Glu Lys Asp Lys Leu Pro Ala Thr Gln Lys  
 35 40 45  
 Ala Lys Glu Met Gln Asn Val Pro Tyr Thr Ile Ala Val Asp Gly Ile  
 10 50 55 60  
 Met Ala Phe Asn Gln Ser Tyr Leu Asn Leu Pro Lys Asp Ser Gln Leu  
 65 70 75 80  
 Ser Tyr Leu Asp Leu Gly Asn Lys Val Lys Ala Leu Leu Tyr Asp Glu  
 15 85 90 95  
 Arg Gly Val Thr Pro Glu Lys Ile Arg Asn Ala Lys Ser Ala Val Tyr  
 20 100 105 110  
 Thr Ile Thr Trp Lys Asp Gly Ser Lys Lys Glu Val Asp Leu Lys Lys  
 115 120 125  
 Asp Ser Tyr Thr Ala Asn Leu Phe Asp Ser Asn Ser Ile Lys Gln Ile  
 25 130 135 140  
 Asp Ile Asn Val Lys Thr Lys  
 145 150

## (2) INFORMATION FOR SEQ ID NO:5234:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 497 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5234:

Asn His Cys Asn Arg Ile Glu Arg Lys Met Ala Met Ser Asn Asn Phe  
 1 5 10 15  
 Lys Asp Asp Phe Glu Lys Asn Arg Gln Ser Ile Asp Thr Asn Ser His  
 20 25 30  
 Gln Asp His Thr Glu Asp Val Glu Lys Asp Gln Ser Glu Leu Glu His  
 35 40 45  
 Gln Asp Thr Ile Glu Asn Thr Glu Gln Gln Phe Pro Pro Arg Asn Ala  
 50 55 60  
 Gln Arg Arg Lys Arg Arg Arg Asp Leu Ala Thr Asn His Asn Lys Gln  
 55 65 70 75 80



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	Val	His	Asn	Glu	Ser	Gln	Thr	Ser	Glu	Asp	Asn	Val	Gln	Asn	Glu	Ala	
					85					90					95		
5	Gly	Thr	Ile	Asp	Asp	Arg	Gln	Val	Glu	Ser	Ser	His	Ser	Thr	Glu	Ser	
				100					105					110			
	Gln	Glu	Pro	Ser	His	Gln	Asp	Ser	Thr	Pro	Gln	His	Glu	Glu	Glu	Tyr	
			115					120					125				
10	Tyr	Asn	Lys	Asn	Ala	Phe	Ala	Met	Asp	Lys	Ser	His	Pro	Glu	Pro	Ile	
		130					135					140					
	Glu	Asp	Asn	Asp	Lys	His	Asp	Thr	Ile	Lys	Asn	Ala	Glu	Asn	Asn	Thr	
	145					150					155					160	
15	Glu	His	Ser	Thr	Val	Ser	Asp	Lys	Ser	Glu	Ala	Glu	Gln	Ser	Gln	Gln	
					165					170					175		
	Pro	Lys	Pro	Tyr	Phe	Thr	Thr	Gly	Ala	Asn	Gln	Ser	Glu	Thr	Ser	Lys	
				180					185						190		
20	Asn	Glu	His	Asp	Asn	Asp	Ser	Val	Lys	Gln	Asp	Gln	Asp	Glu	Pro	Lys	
			195					200					205				
	Glu	His	His	Asn	Gly	Lys	Lys	Ala	Ala	Ala	Ile	Gly	Ala	Gly	Thr	Ala	
25		210					215					220					
	Gly	Val	Ala	Gly	Ala	Ala	Gly	Ala	Met	Ala	Ala	Ser	Lys	Ala	Lys	Lys	
	225					230					235					240	
	His	Ser	Asn	Asp	Ala	Gln	Asn	Lys	Ser	Asn	Ser	Gly	Lys	Ala	Asn	Asn	
30					245					250					255		
	Ser	Thr	Glu	Asp	Lys	Ala	Ser	Gln	Asp	Lys	Ser	Lys	Asp	His	His	Asn	
				260					265					270			
35	Gly	Lys	Lys	Gly	Ala	Ala	Ile	Gly	Ala	Gly	Thr	Ala	Gly	Leu	Ala	Gly	
		275					280						285				
	Gly	Ala	Ala	Ser	Lys	Ser	Ala	Ser	Ala	Ala	Ser	Lys	Pro	His	Ala	Ser	
		290					295					300					
40	Asn	Asn	Ala	Ser	Gln	Asn	His	Asp	Glu	His	Asp	Asn	His	Asp	Arg	Asp	
	305					310					315					320	
	Lys	Glu	Arg	Lys	Lys	Gly	Gly	Met	Ala	Lys	Val	Leu	Leu	Pro	Leu	Ile	
					325					330				335			
45	Ala	Ala	Val	Leu	Ile	Ile	Gly	Ala	Leu	Ala	Ile	Phe	Gly	Gly	Met	Ala	
				340					345					350			
	Leu	Asn	Asn	His	Asn	Asn	Gly	Thr	Lys	Glu	Asn	Lys	Ile	Ala	Asn	Thr	
50			355					360					365				
	Asn	Lys	Asn	Asn	Ala	Asp	Glu	Ser	Lys	Asp	Lys	Asp	Thr	Ser	Lys	Asp	
		370					375					380					
55	Ala	Ser	Lys	Asp	Lys	Ser	Lys	Ser	Thr	Asp	Ser	Asp	Lys	Ser	Lys	Glu	
	385					390					395					400	

Asp Gln Asp Lys Ala Thr Lys Asp Glu Ser Asp Asn Asp Gln Asn Asn  
405 410 415

Ala Asn Gln Ala Asn Asn Gln Ala Gln Asn Asn Gln Asn Gln Gln  
420 425 430

Ala Asn Gln Asn Gln Gln Gln Gln Gln Arg Gln Gly Gly Gly Gln  
435 440 445

Arg His Thr Val Asn Gly Gln Glu Asn Leu Tyr Arg Ile Ala Ile Gln  
450 455 460

Tyr Tyr Gly Ser Gly Ser Pro Glu Asn Val Glu Lys Ile Arg Arg Ala  
465 470 475 480

Asn Gly Leu Ser Gly Asn Asn Ile Arg Asn Gly Gln Gln Ile Val Ile  
485 490 495

Pro

(2) INFORMATION FOR SEQ ID NO:5235:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 886 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5235:

Leu Leu Ser Ile Lys Tyr Asn Leu Ile Gly Val Val Asn Asn Met Asn  
1 5 10 15

Lys His His Pro Lys Leu Arg Ser Phe Tyr Ser Ile Arg Lys Ser Thr  
20 25 30

Leu Gly Val Ala Ser Val Ile Val Ser Thr Leu Phe Leu Ile Thr Ser  
35 40 45

Gln His Gln Ala Gln Ala Ala Glu Asn Thr Asn Thr Ser Asp Lys Ile  
50 55 60

Ser Glu Asn Gln Asn Asn Asn Ala Thr Thr Thr Gln Pro Pro Lys Asp  
65 70 75 80

Thr Asn Gln Thr Gln Pro Ala Thr Gln Pro Ala Asn Thr Ala Lys Asn  
85 90 95

Tyr Pro Ala Ala Asp Glu Ser Leu Lys Asp Ala Ile Lys Asp Pro Ala  
100 105 110

Leu Glu Asn Lys Glu His Asp Ile Gly Pro Arg Glu Gln Val Asn Phe  
115 120 125

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	Gln	Leu	Leu	Asp	Lys	Asn	Asn	Glu	Thr	Gln	Tyr	Tyr	His	Phe	Phe	Ser
	130						135					140				
5	Ile	Lys	Asp	Pro	Ala	Asp	Val	Tyr	Tyr	Thr	Lys	Lys	Lys	Ala	Glu	Val
	145					150					155					160
	Glu	Leu	Asp	Ile	Asn	Thr	Ala	Ser	Thr	Trp	Lys	Lys	Phe	Glu	Val	Tyr
					165					170					175	
10	Glu	Asn	Asn	Gln	Lys	Leu	Pro	Val	Arg	Leu	Val	Ser	Tyr	Ser	Pro	Val
				180					185					190		
	Pro	Glu	Asp	His	Ala	Tyr	Ile	Arg	Phe	Pro	Val	Ser	Asp	Gly	Thr	Gln
			195					200					205			
15	Glu	Leu	Lys	Ile	Val	Ser	Ser	Thr	Gln	Ile	Asp	Asp	Gly	Glu	Glu	Thr
	210						215					220				
	Asn	Tyr	Asp	Tyr	Thr	Lys	Leu	Val	Phe	Ala	Lys	Pro	Ile	Tyr	Asn	Asp
	225					230					235					240
20	Pro	Ser	Leu	Val	Lys	Ser	Asp	Thr	Asn	Asp	Ala	Val	Val	Thr	Asn	Asp
					245					250						255
	Gln	Ser	Ser	Ser	Val	Ala	Ser	Asn	Gln	Thr	Asn	Thr	Asn	Thr	Ser	Asn
25					260				265					270		
	Gln	Asn	Ile	Ser	Thr	Ile	Asn	Asn	Ala	Asn	Asn	Gln	Pro	Gln	Ala	Thr
					275			280					285			
30	Thr	Asn	Met	Ser	Gln	Pro	Ala	Gln	Pro	Lys	Ser	Ser	Thr	Asn	Ala	Asp
	290						295					300				
	Gln	Ala	Ser	Ser	Gln	Pro	Ala	His	Glu	Thr	Asn	Ser	Asn	Gly	Asn	Thr
	305					310					315					320
35	Asn	Asp	Lys	Thr	Asn	Glu	Ser	Ser	Asn	Gln	Ser	Asp	Val	Asn	Gln	Gln
					325					330					335	
	Tyr	Pro	Pro	Ala	Asp	Glu	Ser	Leu	Gln	Asp	Ala	Ile	Lys	Asn	Pro	Ala
				340					345					350		
40	Ile	Ile	Asp	Lys	Glu	His	Thr	Ala	Asp	Asn	Trp	Arg	Pro	Ile	Asp	Phe
			355					360					365			
	Gln	Met	Lys	Asn	Asp	Lys	Gly	Glu	Arg	Gln	Phe	Tyr	His	Tyr	Ala	Ser
	370						375					380				
45	Thr	Val	Glu	Pro	Ala	Thr	Val	Ile	Phe	Thr	Lys	Thr	Gly	Pro	Ile	Ile
	385					390					395					400
	Glu	Leu	Gly	Leu	Lys	Thr	Ala	Ser	Thr	Trp	Lys	Lys	Phe	Glu	Val	Tyr
50					405					410					415	
	Glu	Gly	Asp	Lys	Lys	Leu	Pro	Val	Glu	Leu	Val	Ser	Tyr	Asp	Ser	Asp
				420					425					430		
55	Lys	Asp	Tyr	Ala	Tyr	Ile	Arg	Phe	Pro	Val	Ser	Asn	Gly	Thr	Arg	Glu
				435				440					445			

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	Val	Lys	Ile	Val	Ser	Ser	Ile	Glu	Tyr	Gly	Glu	Asn	Ile	His	Glu	Asp	
	450						455					460					
5	Tyr	Asp	Tyr	Thr	Leu	Met	Val	Phe	Ala	Gln	Pro	Ile	Thr	Asn	Asn	Pro	
	465					470					475					480	
	Asp	Asp	Tyr	Val	Asp	Glu	Glu	Thr	Tyr	Asn	Leu	Gln	Lys	Leu	Leu	Ala	
					485					490						495	
10	Pro	Tyr	His	Lys	Ala	Lys	Thr	Leu	Glu	Arg	Gln	Val	Tyr	Glu	Leu	Glu	
				500					505					510			
	Lys	Leu	Gln	Glu	Lys	Leu	Pro	Glu	Lys	Tyr	Lys	Ala	Glu	Tyr	Lys	Lys	
			515					520					525				
15	Lys	Leu	Asp	Gln	Thr	Arg	Val	Glu	Leu	Ala	Asp	Gln	Val	Lys	Ser	Ala	
			530					535					540				
	Val	Thr	Glu	Phe	Glu	Asn	Val	Thr	Pro	Thr	Asn	Asp	Gln	Leu	Thr	Asp	
	545					550					555					560	
20	Leu	Gln	Glu	Ala	His	Phe	Val	Val	Phe	Glu	Ser	Glu	Glu	Asn	Ser	Glu	
					565					570						575	
	Ser	Val	Met	Asp	Gly	Phe	Val	Glu	His	Pro	Phe	Tyr	Thr	Ala	Thr	Leu	
25				580					585							590	
	Asn	Gly	Gln	Lys	Tyr	Val	Val	Met	Lys	Thr	Lys	Asp	Asp	Ser	Tyr	Trp	
			595					600					605				
30	Lys	Asp	Leu	Ile	Val	Glu	Gly	Lys	Arg	Val	Thr	Thr	Val	Ser	Lys	Asp	
	610						615					620					
	Pro	Lys	Asn	Asn	Ser	Arg	Thr	Leu	Ile	Phe	Pro	Tyr	Ile	Pro	Asp	Lys	
	625					630					635					640	
35	Ala	Val	Tyr	Asn	Ala	Ile	Val	Lys	Val	Val	Val	Ala	Asn	Ile	Gly	Tyr	
					645					650						655	
	Glu	Gly	Gln	Tyr	His	Val	Arg	Ile	Ile	Asn	Gln	Asp	Ile	Asn	Thr	Lys	
				660					665					670			
40	Asp	Asp	Asp	Thr	Ser	Gln	Asn	Asn	Thr	Ser	Glu	Pro	Leu	Asn	Val	Gln	
			675					680					685				
	Thr	Gly	Gln	Glu	Gly	Lys	Val	Ala	Asp	Thr	Asp	Val	Ala	Glu	Asn	Ser	
45		690					695					700					
	Ser	Thr	Ala	Thr	Asn	Pro	Lys	Asp	Ala	Ser	Asp	Lys	Ala	Asp	Val	Ile	
	705					710					715					720	
	Glu	Pro	Glu	Ser	Asp	Val	Val	Lys	Asp	Ala	Asp	Asn	Asn	Ile	Asp	Lys	
50					725					730						735	
	Asp	Val	Gln	His	Asp	Val	Asp	His	Leu	Ser	Asp	Met	Ser	Asp	Asn	Asn	
				740					745					750			
55	His	Phe	Asp	Lys	Tyr	Asp	Leu	Lys	Glu	Met	Asp	Thr	Gln	Ile	Ala	Lys	
			755					760						765			

Asp Thr Asp Arg Asn Val Asp Lys Asp Ala Asp Asn Ser Val Gly Met  
 770 775 780  
 Ser Ser Asn Val Asp Thr Asp Lys Asp Ser Asn Lys Asn Lys Asp Lys  
 5 785 790 795 800  
 Val Ile Gln Leu Asn His Ile Ala Asp Lys Asn Asn His Thr Gly Lys  
 805 810 815  
 Ala Ala Lys Leu Asp Val Val Lys Gln Asn Tyr Asn Asn Thr Asp Lys  
 10 820 825 830  
 Val Thr Asp Lys Lys Thr Thr Glu His Leu Pro Ser Asp Ile His Lys  
 835 840 845  
 Thr Val Asp Lys Thr Val Lys Thr Lys Glu Lys Ala Gly Thr Pro Ser  
 15 850 855 860  
 Lys Glu Asn Lys Leu Ser Gln Ser Lys Met Leu Thr Lys Asn Trp Arg  
 865 870 875 880  
 20 Asn Asn Xaa Gln Ala Asn  
 885

## (2) INFORMATION FOR SEQ ID NO:5236:

25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 236 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 30 (ii) MOLECULE TYPE: protein  
 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5236:  
 Asn Met Asn Lys Asn Val Met Val Lys Gly Leu Thr Ala Leu Thr Ile  
 1 5 10 15  
 40 Leu Thr Ser Leu Gly Phe Ala Glu Asn Ile Ser Asn Gln Xaa His Ser  
 20 25 30  
 Ile Ala Lys Ala Glu Lys Asn Val Lys Glu Ile Thr Asp Ala Thr Lys  
 35 40 45  
 Glu Pro Tyr Asn Ser Val Val Ala Phe Val Gly Gly Thr Gly Val Val  
 50 55 60  
 Val Gly Lys Asn Thr Ile Val Thr Asn Lys His Ile Ala Lys Ser Asn  
 50 65 70 75 80  
 Asp Ile Phe Lys Asn Arg Val Ser Ala His His Ser Ser Lys Gly Lys  
 85 90 95  
 55 Gly Gly Gly Asn Tyr Asp Val Lys Asp Ile Val Glu Tyr Pro Gly Lys  
 100 105 110

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Glu Asp Leu Ala Ile Val His Val His Glu Thr Ser Thr Glu Gly Leu  
 115 120 125  
 Asn Phe Asn Lys Asn Val Ser Tyr Thr Lys Phe Ala Asp Gly Ala Lys  
 130 135 140  
 Val Lys Asp Arg Ile Ser Val Ile Gly Tyr Pro Lys Gly Ala Gln Thr  
 145 150 155 160  
 Lys Tyr Lys Met Phe Glu Ser Thr Gly Thr Ile Asn His Ile Ser Gly  
 165 170 175  
 Thr Phe Met Glu Phe Asp Ala Tyr Ala Gln Pro Gly Asn Ser Gly Ser  
 180 185 190  
 Pro Val Leu Asn Ser Lys His Xaa Leu Ile Gly Ile Leu Tyr Ala Gly  
 195 200 205  
 Ser Gly Lys Asp Glu Ser Glu Lys Asn Phe Gly Val Tyr Phe Thr Pro  
 210 215 220  
 Gln Leu Xaa Xaa Phe Ile Pro Asn Asn Ile Glu Lys  
 225 230 235

(2) INFORMATION FOR SEQ ID NO:5237:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5237:

Tyr Arg Leu Glu His Thr Ile Met Lys Met Arg Thr Ile Ala Lys Thr  
 1 5 10 15  
 Ser Leu Ala Leu Gly Leu Leu Thr Thr Gly Ala Ile Thr Val Thr Thr  
 20 25 30  
 Gln Ser Val Lys Ala Glu Lys Ile Gln Ser Thr Lys Val Asp Lys Val  
 35 40 45  
 Pro Thr Leu Lys Ala Glu Arg Leu Ala Met Ile Asn Ile Thr Ala Gly  
 50 55 60  
 Ala Asn Ser Ala Thr Thr Gln Ala Ala Asn Thr Arg Gln Glu Arg Thr  
 65 70 75 80  
 Pro Lys Leu Glu Lys Ala Pro Asn Thr Asn Glu Glu Lys Thr Ser Ala  
 85 90 95  
 Ser Lys Ile Glu Lys Ile Ser Gln Pro Lys Gln Glu Glu Gln Lys Thr  
 100 105 110

Leu Asn Ile Ser Ala Thr Pro Ala Pro Lys Gln Glu Gln Ser Gln Thr  
 115 120 125  
 5 Thr Thr Glu Ser Thr Thr Pro Lys Thr Lys Val Thr Thr Pro Pro Ser  
 130 135 140  
 Thr Asn Thr Pro Gln Pro Met Gln Ser Thr Lys Ser Asp Thr Pro Gln  
 145 150 155 160  
 10 Ser Pro Thr Ile Lys Gln Ala Gln Thr Asp Met Thr Pro Lys Tyr Glu  
 165 170 175  
 Asp Leu Arg Ala Tyr Tyr Thr Lys Pro Ser Phe Glu Phe Glu Lys Gln  
 180 185 190  
 15 Phe Gly Phe Met Leu Lys Pro Trp Thr Thr Val Arg Phe Met Asn Val  
 195 200 205  
 Ile Pro Asn Arg Phe Ile Tyr Lys Ile Ala Leu Val Gly Lys Asp Glu  
 210 215 220  
 20 Lys Lys Tyr Lys Asp Gly Pro Tyr Asp Asn Ile Asp Val Phe Ile Val  
 225 230 235 240  
 Leu Glu Asp Asn Lys Tyr Gln Leu Lys Lys Tyr Ser Val Gly Gly Ile  
 245 250 255  
 25 Thr Lys Thr Asn Ser Lys Lys Val Asn His Lys Val Glu Leu Ser Ile  
 260 265 270  
 30 Thr Lys Lys Asp Asn Gln Gly Met Ile Ser Arg Asp Val Ser Glu Tyr  
 275 280 285  
 Met Ile Thr Lys Glu Glu Ile Ser Leu Lys Glu Leu Asp Phe Lys Leu  
 290 295 300  
 35 Arg Lys Gln Leu Ile Glu Lys His Asn Leu Tyr Gly Asn Met Gly Ser  
 305 310 315 320  
 Gly Thr Ile Val Ile Lys Met Lys Asn Gly Gly Lys Tyr Thr Phe Glu  
 325 330 335  
 40 Leu His Lys Lys Leu Gln Glu His Arg Met Ala Asp Val Ile Asp Gly  
 340 345 350  
 45 Thr Asn Ile Asp Asn Ile Glu Val Asn Ile Lys  
 355 360

## (2) INFORMATION FOR SEQ ID NO:5238:

- 50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 150 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

- 55 (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5238:

5 Phe Met Lys Phe Lys Ser Leu Ile Thr Thr Thr Leu Ala Leu Gly Val  
 1 5 10 15  
 Leu Ala Ser Thr Gly Ala Asn Phe Asn Asn Asn Glu Ala Ser Ala Ala  
 20 25 30  
 10 Ala Lys Pro Leu Asp Lys Ser Ser Ser Ser Leu His His Gly Tyr Ser  
 35 40 45  
 Lys Val His Val Pro Tyr Ala Ile Thr Val Asn Gly Thr Ser Gln Asn  
 50 55 60  
 15 Ile Leu Ser Ser Leu Thr Phe Asn Lys Asn Gln Asn Ile Ser Tyr Lys  
 65 70 75 80  
 Asp Leu Glu Asp Arg Val Lys Ser Val Leu Lys Ser Asp Arg Gly Ile  
 85 90 95  
 20 Ser Asp Ile Asp Leu Arg Leu Ser Lys Gln Ala Lys Tyr Thr Val Tyr  
 100 105 110  
 Phe Lys Asn Gly Thr Lys Lys Val Ile Asp Leu Lys Ala Gly Ile Tyr  
 115 120 125  
 25 Thr Ala Asp Leu Ile Asn Thr Ser Glu Ile Lys Ala Ile Asn Ile Asn  
 130 135 140  
 Val Asp Thr Lys Lys Gln  
 145 150  
 30

## (2) INFORMATION FOR SEQ ID NO:5239:

## (i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 239 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5239:

45 Glu Lys Arg Phe Met Gln Met Ala Arg Lys Val Val Val Val Asp Asp  
 1 5 10 15  
 Glu Lys Pro Ile Ala Asp Ile Leu Glu Phe Asn Leu Lys Lys Glu Gly  
 20 25 30  
 50 Tyr Asp Val Tyr Cys Ala Tyr Asp Gly Asn Asp Ala Val Asp Leu Ile  
 35 40 45  
 Tyr Glu Glu Glu Pro Asp Ile Val Leu Leu Asp Ile Met Leu Pro Gly  
 50 55 60  
 55



Arg Asp Gly Met Glu Val Cys Arg Glu Val Arg Lys Lys Tyr Glu Met  
 65 70 75 80  
 Pro Ile Ile Met Leu Thr Ala Lys Asp Ser Glu Ile Asp Lys Val Leu  
 5 85 90 95  
 Gly Leu Glu Leu Gly Ala Asp Asp Tyr Val Thr Lys Pro Phe Ser Thr  
 100 105 110  
 Arg Glu Leu Ile Ala Arg Val Lys Ala Asn Leu Arg Arg His Tyr Ser  
 10 115 120 125  
 Gln Pro Ala Gln Asp Thr Gly Asn Val Thr Asn Glu Ile Thr Ile Lys  
 130 135 140  
 Asp Ile Val Ile Tyr Pro Asp Ala Tyr Ser Ile Lys Lys Arg Gly Glu  
 15 145 150 155 160  
 Asp Ile Glu Leu Thr His Arg Glu Phe Glu Leu Phe His Tyr Leu Ser  
 165 170 175  
 Lys His Met Gly Gln Val Met Thr Arg Glu His Leu Leu Gln Thr Val  
 180 185 190  
 Trp Gly Tyr Asp Tyr Phe Gly Asp Val Arg Thr Val Asp Val Thr Ile  
 25 195 200 205  
 Arg Arg Leu Arg Glu Lys Ile Glu Asp Asp Pro Ser His Pro Glu Tyr  
 210 215 220  
 Ile Val Thr Arg Arg Gly Val Gly Tyr Phe Leu Gln Gln His Glu  
 30 225 230 235

## (2) INFORMATION FOR SEQ ID NO:5240:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5240:

Xaa Leu Ser Thr Val Ile Gly Ala Xaa Leu Phe Phe Lys Ser Ser Val  
 1 5 10 15  
 Ser Leu Val Phe Lys Met Val Lys Lys Phe Arg Xaa Gly Val Ile Ser  
 20 25 30  
 Val Asn Asp Val Met Phe Ser Ser Ser Ile Met Tyr Arg Ile Lys Lys  
 35 40 45  
 Asn Ala Phe Ser Leu Thr Val Met Ala Ile Ile Ser Ala Ile Thr Val  
 50 55 60

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Ser Val Leu Cys Phe Ala Ala Ile Ser Arg Ala Ser Leu Ser Ser Glu  
65 70 75 80  
Ile Lys Tyr Thr Ala Pro His Asp Val Thr Ile Lys Asp Gln Gln Lys  
85 90 95  
Ala Asn Gln Leu Ala Ser Glu Leu Asn Asn Gln Lys Ile Pro His Phe  
100 105 110  
Tyr Asn Tyr Lys Glu Val Ile His Thr Lys Leu Tyr Lys Asp Asn Leu  
115 120 125  
Phe Asp Val Lys Ala  
130

(2) INFORMATION FOR SEQ ID NO:5241:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 508 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5241:

Glu Ile Tyr Ile Ile Ala Asn Lys Gln Arg Arg Asp Asn Met Ala Val  
1 5 10 15  
Asn Val Arg Asp Tyr Ile Ala Glu Asn Tyr Gly Leu Phe Ile Asn Gly  
20 25 30  
Glu Phe Val Lys Gly Ser Ser Asp Glu Thr Ile Glu Val Thr Asn Pro  
35 40 45  
Ala Thr Gly Glu Thr Leu Ser His Ile Thr Arg Ala Lys Asp Lys Asp  
50 55 60  
Val Asp His Ala Val Lys Val Ala Gln Glu Ala Phe Glu Ser Trp Ser  
65 70 75 80  
Leu Thr Ser Lys Ser Glu Arg Ala Gln Met Leu Arg Asp Ile Gly Asp  
85 90 95  
Lys Leu Met Ala Gln Lys Asp Lys Ile Ala Met Ile Glu Thr Leu Asn  
100 105 110  
Asn Gly Lys Pro Ile Arg Glu Thr Thr Ala Ile Asp Ile Pro Phe Ala  
115 120 125  
Ala Arg His Phe His Tyr Phe Ala Ser Val Ile Glu Thr Glu Glu Gly  
130 135 140  
Thr Val Asn Asp Ile Asp Lys Asp Thr Met Ser Ile Val Arg His Glu  
145 150 155 160

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	Pro	Ile	Gly	Val	Val	Gly	Ala	Val	Val	Ala	Trp	Asn	Phe	Pro	Met	Leu
					165					170					175	
5	Leu	Ala	Ala	Trp	Lys	Ile	Ala	Pro	Ala	Ile	Ala	Ala	Gly	Asn	Thr	Ile
				180				185						190		
	Val	Ile	Gln	Pro	Ser	Ser	Ser	Thr	Pro	Leu	Ser	Leu	Leu	Glu	Val	Ala
			195					200					205			
10	Lys	Ile	Phe	Gln	Glu	Val	Leu	Pro	Lys	Gly	Val	Val	Asn	Ile	Leu	Thr
		210					215					220				
	Gly	Lys	Gly	Ser	Glu	Ser	Gly	Asn	Ala	Ile	Phe	Asn	His	Asp	Gly	Val
	225					230					235				240	
15	Asp	Lys	Leu	Ser	Phe	Thr	Gly	Ser	Thr	Asp	Val	Gly	Tyr	Gln	Val	Ala
					245					250					255	
	Glu	Ala	Ala	Ala	Lys	His	Leu	Val	Pro	Ala	Thr	Leu	Glu	Leu	Gly	Gly
					260				265					270		
20	Lys	Ser	Ala	Asn	Ile	Ile	Leu	Asp	Asp	Ala	Asn	Leu	Asp	Leu	Ala	Val
			275					280					285			
	Glu	Gly	Ile	Gln	Leu	Gly	Ile	Leu	Phe	Asn	Gln	Gly	Glu	Val	Cys	Ser
25		290					295					300				
	Ala	Gly	Ser	Arg	Leu	Leu	Val	His	Glu	Lys	Ile	Tyr	Asp	Gln	Leu	Val
	305					310					315				320	
	Pro	Arg	Leu	Gln	Glu	Ala	Phe	Ser	Asn	Ile	Lys	Val	Gly	Asn	Pro	Gln
30					325					330				335		
	Asp	Glu	Ala	Thr	Gln	Met	Gly	Ser	Gln	Thr	Gly	Lys	Asp	Gln	Leu	Asp
					340				345					350		
35	Lys	Ile	Gln	Ser	Tyr	Ile	Asp	Ala	Ala	Lys	Glu	Ser	Asp	Ala	Gln	Ile
			355				360						365			
	Leu	Ala	Gly	Gly	His	Arg	Leu	Thr	Glu	Asn	Gly	Leu	Asp	Lys	Gly	Phe
		370					375					380				
40	Phe	Phe	Glu	Pro	Thr	Leu	Ile	Ala	Val	Pro	Asp	Asn	His	His	Lys	Leu
	385					390					395				400	
	Ala	Gln	Glu	Glu	Ile	Phe	Gly	Pro	Val	Leu	Thr	Val	Ile	Lys	Val	Lys
					405					410					415	
45	Asp	Asp	Gln	Glu	Ala	Ile	Asp	Ile	Ala	Asn	Asp	Ser	Glu	Tyr	Gly	Leu
				420					425					430		
	Ala	Gly	Gly	Val	Phe	Ser	Gln	Asn	Ile	Thr	Arg	Ala	Leu	Asn	Ile	Ala
		435						440					445			
50	Lys	Ala	Val	Arg	Thr	Gly	Arg	Ile	Trp	Ile	Asn	Thr	Tyr	Asn	Gln	Val
		450					455					460				
	Pro	Glu	Gly	Ala	Pro	Phe	Gly	Gly	Tyr	Lys	Lys	Ser	Gly	Ile	Gly	Arg
55		465				470					475				480	

Glu Thr Tyr Lys Gly Ala Leu Ser Asn Tyr Gln Gln Val Lys Asn Ile  
 485 490 495

Tyr Ile Asp Thr Ser Asn Ala Leu Lys Gly Leu Tyr  
 500 505

## (2) INFORMATION FOR SEQ ID NO:5242:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 540 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5242:

Asn His Leu Thr Ala Arg Ile Ile Asn Gln Glu Asp Asp Leu Met Asn  
 1 5 10 15  
 Leu Phe Arg Gln Gln Lys Phe Ser Ile Arg Lys Phe Asn Val Gly Ile  
 20 25 30  
 Phe Ser Ala Leu Ile Ala Thr Val Thr Phe Ile Ser Thr Asn Pro Thr  
 35 40 45  
 Thr Ala Ser Ala Ala Glu Gln Asn Gln Pro Ala Gln Asn Gln Pro Ala  
 50 55 60  
 Gln Pro Ala Asp Ala Asn Thr Gln Pro Asn Ala Asn Ala Gly Ala Gln  
 65 70 75 80  
 Ala Asn Pro Thr Ala Gln Pro Ala Ala Pro Ala Asn Gln Gly Gln Pro  
 85 90 95  
 Ala Val Gln Pro Ala Asn Gln Gly Gly Gln Ala Asn Pro Ala Gly Gly  
 100 105 110  
 Ala Ala Gln Pro Asn Thr Gln Pro Ala Gly Gln Gly Asp Gln Ala Asp  
 115 120 125  
 Pro Asn Asn Ala Ala Gln Ala Gln Pro Gly Asn Gln Ala Thr Pro Ala  
 130 135 140  
 Asn Gln Ala Gly Gln Gly Asn Asn Gln Ala Thr Pro Asn Asn Asn Ala  
 145 150 155 160  
 Thr Pro Ala Asn Gln Thr Gln Pro Ala Asn Ala Pro Ala Ala Ala Gln  
 165 170 175  
 Pro Ala Ala Pro Val Ala Ala Asn Ala Gln Thr Gln Asp Pro Asn Ala  
 180 185 190  
 Ser Asn Thr Gly Glu Gly Ser Ile Asn Thr Thr Leu Thr Phe Asp Asp  
 195 200 205

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	Pro	Ala	Ile	Ser	Thr	Asp	Glu	Asn	Arg	Gln	Asp	Pro	Thr	Val	Thr	Val	
	210						215					220					
5	Thr	Asp	Lys	Val	Asn	Gly	Tyr	Ser	Leu	Ile	Asn	Asn	Gly	Lys	Ile	Gly	
	225					230					235					240	
	Phe	Val	Asn	Ser	Glu	Leu	Arg	Arg	Ser	Asp	Met	Phe	Asp	Lys	Asn	Asn	
					245					250					255		
10	Pro	Gln	Asn	Tyr	Gln	Ala	Lys	Gly	Asn	Val	Ala	Ala	Leu	Gly	Arg	Val	
					260				265					270			
	Asn	Ala	Asn	Asp	Ser	Thr	Asp	His	Gly	Asn	Phe	Asn	Gly	Ile	Ser	Lys	
			275					280					285				
15	Thr	Val	Asn	Val	Lys	Pro	Asp	Ser	Glu	Leu	Ile	Ile	Asn	Phe	Thr	Thr	
	290						295					300					
	Met	Gln	Thr	Asn	Ser	Lys	Gln	Gly	Ala	Thr	Asn	Leu	Val	Ile	Lys	Asp	
	305					310					315					320	
20	Ala	Lys	Lys	Asn	Thr	Glu	Leu	Ala	Thr	Val	Asn	Val	Ala	Lys	Thr	Gly	
					325					330					335		
	Thr	Ala	His	Leu	Phe	Lys	Val	Pro	Thr	Asp	Ala	Asp	Arg	Leu	Asp	Leu	
25				340					345					350			
	Gln	Phe	Ile	Pro	Asp	Asn	Thr	Ala	Val	Ala	Asp	Ala	Ser	Arg	Ile	Thr	
			355				360						365				
	Thr	Asn	Lys	Asp	Gly	Tyr	Lys	Tyr	Tyr	Ser	Phe	Ile	Asp	Asn	Val	Gly	
30		370					375					380					
	Leu	Phe	Ser	Gly	Ser	His	Leu	Tyr	Val	Lys	Asn	Arg	Asp	Leu	Ala	Pro	
	385					390					395					400	
	Lys	Ala	Thr	Asn	Asn	Lys	Glu	Tyr	Thr	Ile	Asn	Thr	Glu	Ile	Gly	Asn	
35					405					410					415		
	Asn	Gly	Asn	Phe	Gly	Ala	Ser	Leu	Lys	Ala	Asp	Gln	Phe	Lys	Tyr	Glu	
			420						425					430			
40	Val	Thr	Leu	Pro	Gln	Gly	Val	Thr	Tyr	Val	Asn	Asn	Ser	Leu	Thr	Thr	
		435						440					445				
	Thr	Phe	Pro	Asn	Gly	Asn	Glu	Asp	Ser	Thr	Val	Leu	Lys	Asn	Met	Thr	
		450					455					460					
45	Val	Asn	Tyr	Asp	Gln	Asn	Ala	Asn	Lys	Val	Thr	Phe	Thr	Ser	Gln	Gly	
	465					470					475					480	
	Val	Thr	Thr	Ala	Arg	Gly	Thr	His	Thr	Lys	Glu	Val	Leu	Phe	Pro	Asp	
				485						490					495		
50	Lys	Ser	Leu	Lys	Leu	Ser	Tyr	Lys	Val	Asn	Val	Ala	Asn	Ile	Asp	Thr	
				500					505					510			
	Pro	Lys	Asn	Ile	Asp	Phe	Asn	Glu	Lys	Leu	Thr	Tyr	Arg	Thr	Ala	Ser	
55			515					520					525				

Asp Val Val Ile Asn Asn Ala Gln Pro Glu Val His  
 530 535 540

(2) INFORMATION FOR SEQ ID NO:5243:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5243:

Ile Thr Leu Lys Thr Val Ser Gln Leu Ile Asp Met Lys Gln Lys Gln  
 1 5 10 15  
 Thr Lys Ile Ser Met Val Thr Ala Tyr Asp Phe Pro Ser Ala Lys Gln  
 20 25 30  
 Val Glu Ala Ala Gly Ile Asp Met Ile Leu Val Gly Asp Ser Leu Gly  
 25 35 40 45  
 Met Thr Val Leu Gly Tyr Glu Ser Thr Val Gln Val Thr Leu Ala Asp  
 50 55 60  
 Met Ile His His Gly Arg Ala Val Arg Arg Gly Ala Pro Asn Thr Phe  
 30 65 70 75 80  
 Val Val Val Asp Met Pro Ile Gly Ala Val Gly Ile Ser Met Thr Gln  
 85 90 95  
 Asp Leu Asn His Ala Leu Lys Leu Tyr Gln Glu Thr Asn Ala Asn Ala  
 35 100 105 110  
 Ile Lys Ala Glu Gly Ala His Ile Thr Pro Phe Ile Glu Lys Ala Thr  
 115 120 125  
 Ala Ile Gly Ile Pro Val Val Ala His Leu Gly Leu Thr Pro Gln Ser  
 40 130 135 140  
 Val Gly Val Met Gly Tyr Lys Leu Gln Gly Ala Thr Lys Glu Ala Ala  
 145 150 155 160  
 Glu Gln Leu Ile Leu Asp Ala Lys Asn Val Glu Gln Ala Gly Ala Val  
 45 165 170 175  
 Ala Leu Val Leu Glu Ala Ile Pro Asn Asp Leu Ala Glu Glu Ile Ser  
 180 185 190  
 Lys His Leu Thr Ile Pro Val Ile Gly Ile Gly Ala Gly Lys Gly Thr  
 50 195 200 205  
 Asp Gly Gln Val Leu Val Tyr His Asp Met Leu Asn Tyr Gly Val Glu  
 55 210 215 220

His Lys Ala Lys Phe Val Lys Gln Phe Ala Asp Phe Ser Val Gly Val  
225 230 235 240

Asp Gly Leu Lys Gln Tyr Asp Gln Glu Val Lys Ser Gly Ala Phe Pro  
245 250 255

Ser Glu Glu Tyr Thr Tyr Lys Lys Lys Ile Met Asn Glu Val Asn Asn  
260 265 270

Asn Asp

(2) INFORMATION FOR SEQ ID NO:5244:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 430 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5244:

Ser Asp Asp Trp Pro Lys Ser Ile Thr Ser Leu Ser Ile Arg Gly Val  
1 5 10 15

Arg Met Lys His Gln Glu Thr Thr Ser Gln Gln Tyr Asn Phe Ser Ile  
20 25 30

Ile Lys His Gly Asp Ile Ser Thr Pro Gln Gly Phe Thr Ala Gly Gly  
35 40 45

Met His Ile Gly Leu Arg Ala Asn Lys Lys Asp Phe Gly Trp Ile Tyr  
50 55 60

Ser Ser Ser Leu Ala Ser Ala Ala Ala Val Tyr Thr Leu Asn Gln Phe  
65 70 75 80

Lys Ala Ala Pro Leu Ile Val Thr Glu Asp Thr Leu Gln Lys Ser Lys  
85 90 95

Gly Lys Leu Gln Ala Leu Val Val Asn Ser Ala Asn Ala Asn Ser Cys  
100 105 110

Thr Gly Gln Gln Gly Ile Asp Asp Ala Arg Gln Thr Gln Thr Trp Val  
115 120 125

Ala Gln Gln Leu Gln Ile Pro Ser Glu His Val Ala Val Ala Ser Thr  
130 135 140

Gly Val Ile Gly Glu Tyr Leu Pro Met Asp Lys Ile Lys Thr Gly Thr  
145 150 155 160

Glu His Ile Lys Asp Ala Asn Phe Ala Thr Pro Gly Ala Phe Asn Glu  
165 170 175

Ala Ile Leu Thr Thr Asp Thr Cys Thr Lys His Ile Ala Val Ser Leu  
180 185 190

5 Lys Ile Asp Gly Lys Thr Val Thr Ile Gly Gly Ser Thr Lys Gly Ser  
195 200 205

Gly Met Ile His Pro Asn Met Ala Thr Met Leu Ala Phe Ile Thr Thr  
210 215 220

10 Asp Ala Ser Ile Glu Ser Asn Thr Leu His Gln Leu Leu Lys Ser Ser  
225 230 235 240

Thr Asp His Thr Phe Asn Met Ile Thr Val Asp Gly Asp Thr Ser Thr  
245 250 255

15 Asn Asp Met Val Leu Val Met Ala Asn His Gln Val Glu His Gln Ile  
260 265 270

Leu Ser Gln Asp His Pro Gln Trp Glu Thr Phe Val Asp Ala Phe Asn  
275 280 285

20 Phe Val Cys Thr Phe Leu Ala Lys Ala Ile Ala Arg Asp Gly Glu Gly  
290 295 300

Ala Thr Lys Leu Ile Ser Val Asn Val Ser Gly Ala Lys Ser Ile Ser  
305 310 315 320

Asp Ala Arg Lys Ile Gly Lys Thr Ile Val Ser Ser Asn Leu Val Lys  
325 330 335

30 Ser Ala Ile Phe Gly Glu Asp Ala Asn Phe Gly Arg Ile Ile Thr Ala  
340 345 350

Ile Gly Tyr Ser Gly Cys Glu Ile Asp Pro Asn Cys Thr Tyr Val Gln  
355 360 365

35 Leu Asn Gln Ile Pro Val Val Asp Lys Gly Met Ala Val Leu Phe Asp  
370 375 380

Glu Gln Ala Met Ser Asn Thr Leu Thr His Glu Asn Val Thr Ile Asp  
385 390 395 400

Val Gln Leu Gly Leu Gly Asn Ala Ala Ala Thr Ala Tyr Gly Cys Asp  
405 410 415

45 Leu Ser Tyr Asp Tyr Val Arg Ile Asn Ala Ser Tyr Arg Thr  
420 425 430

## (2) INFORMATION FOR SEQ ID NO:5245:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5245:

5	Asn	Pro	Ala	Leu	Thr	Val	Phe	Ala	Phe	Ile	Met	Ile	Ile	Ser	Ile	Leu	1	5	10	15
	Leu	Ala	Tyr	Val	Phe	Lys	Trp	Leu	Gly	Leu	Val	Asp	Asp	Val	Leu	Leu	20	25	30	
10	Met	Val	Ile	Ile	Ile	Ser	Thr	Ile	Ser	Leu	Gly	Val	Val	Val	Pro	Thr	35	40	45	
	Leu	Lys	Glu	Met	Asn	Ile	Met	Arg	Thr	Thr	Ile	Gly	Gln	Phe	Ile	Leu	50	55	60	
15	Leu	Val	Ala	Val	Leu	Ala	Asp	Leu	Val	Thr	Met	Ile	Leu	Leu	Thr	Val	65	70	75	80
	Tyr	Gly	Ala	Ile	Asn	Gly	Gln	Gly	Gly	Ser	Thr	Ile	Trp	Leu	Ile	Gly	85	90	95	
20	Ile	Leu	Val	Val	Phe	Thr	Ala	Ile	Ser	Tyr	Ile	Leu	Gly	Val	Gln	Phe	100	105	110	
	Lys	Arg	Met	Ser	Phe	Leu	Gln	Lys	Leu	Met	Asp	Gly	Thr	Thr	Gln	Ile	115	120	125	
25	Gly	Ile	Arg	Ala	Val	Phe	Ala	Leu	Ile	Ile	Leu	Leu	Val	Ala	Leu	Ala	130	135	140	
30	Glu	Gly	Val	Gly	Ala	Glu	Asn	Ile	Leu	Gly	Ala	Phe	Leu	Ala	Gly	Val	145	150	155	160
	Val	Val	Ser	Leu	Leu	Asn	Pro	Asp	Glu	Glu	Met	Val	Glu	Lys	Leu	Asp	165	170	175	
35	Ser	Phe	Gly	Tyr	Gly	Phe	Phe	Ile	Pro	Ile	Phe	Phe	Ile	Met	Xaa	Gly	180	185	190	
	Val	Asp	Leu	Asn	Ile	Pro	Ser	Leu	Ile	Lys	Glu	Pro	Lys	Leu	Leu	Ile	195	200	205	
40	Ile	Ile	Pro	Ile	Leu	Ile	Val	Ala	Phe	Ile	Ile	Ser	Lys	Leu	Ile	Pro	210	215	220	
	Val	Met	Phe	Ile	Arg	Arg	Trp	Phe	Asp	Met	Lys	Thr	Thr	Ile	Ala	Ser	225	230	235	240
45	Ala	Phe	Leu	Leu	Thr	Ser	Thr	Leu	Ser	Leu	Val	Ile	Ala	Ala	Ala	Lys	245	250	255	
50	Ile	Ser	Glu	Arg	Leu	Asn	Ala	Ile	Ser	Ala	Glu	Thr	Ser	Gly	Ile	Leu	260	265	270	
	Ile	Leu	Ser	Ala	Val	Ile	Thr	Cys	Val	Phe	Val	Pro	Ile	Ile	Phe	Lys	275	280	285	
55	Lys	Leu	Phe	Pro	Val	Pro	Asp	Glu	Phe	Asn	Arg	Lys	Ile	Glu	Val	Ser	290	295	300	

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Leu Ile Gly Lys Asn Gln Leu Thr Ile Pro Ile Ala Gln Asn Leu Thr  
305 310 315 320

5 Ser Gln Leu Tyr Asp Val Thr Leu Tyr Tyr Arg Lys Asp Leu Ser Asp  
325 330 335

Arg Arg Gln Leu Ser Asp Asp Ile Thr Met Ile Glu Ile Ala Asp Tyr  
340 345 350

10 Glu Gln Asp Val Leu Glu Arg Leu Gly Leu Phe Asp Arg Asp Ile Val  
355 360 365

Val Cys Ala Thr Asn Asp Asp Asp Ile Asn Arg Lys Val Ala Lys Leu  
370 375 380

15 Ala Lys Ala His Gln Val Glu Arg Val Ile Cys Arg Leu Glu Ser Thr  
385 390 395 400

Thr Asp Asp Thr Glu Leu Val Asp Ser Gly Ile Glu Ile Phe Ser Ser  
405 410 415

20 Tyr Leu Ser Asn Lys Ile Leu Leu Lys Gly Leu Ile Glu Thr Pro Asn  
420 425 430

Met Leu Asn Leu Leu Ser Asn Val Glu Thr Ser Leu Tyr Glu Ile Gln  
25 435 440 445

Met Leu Asn Tyr Lys Tyr Glu Asn Ile Gln Leu Arg Asn Phe Pro Phe  
450 455 460

30 Gly Gly Asp Ile Ile  
465

(2) INFORMATION FOR SEQ ID NO:5246:

- 35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 414 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear
- 40 (ii) MOLECULE TYPE: protein

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5246:

Ala Ile Ile Val Ile Leu Leu Phe Leu Arg Asn Ile Arg Thr Thr Ala  
1 5 10 15

Ile Ser Ile Ile Ser Ile Pro Leu Ser Leu Leu Met Ala Leu Ile Ala  
50 20 25 30

Leu Lys Leu Ser Asp Val Ser Leu Asn Ile Leu Thr Leu Gly Ala Leu  
35 40 45

55 Thr Val Ala Ile Gly Arg Val Ile Asp Asp Ser Ile Val Val Val Glu  
50 55 60

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	Asn	Ile	Tyr	Arg	Arg	Leu	Thr	Asp	Ser	Glu	Glu	Gln	Leu	Lys	Gly	Glu	65	70	75	80
5	Asn	Leu	Ile	Ile	Ser	Ala	Thr	Thr	Glu	Val	Phe	Lys	Pro	Ile	Met	Ser	85	90	95	
	Ser	Thr	Leu	Val	Thr	Ile	Ile	Val	Phe	Leu	Pro	Leu	Val	Phe	Val	Ser	100	105	110	
10	Gly	Ser	Val	Gly	Glu	Met	Phe	Arg	Pro	Phe	Ala	Leu	Ala	Ile	Ala	Phe	115	120	125	
	Ser	Leu	Leu	Ala	Ser	Leu	Leu	Val	Ser	Ile	Thr	Leu	Val	Pro	Ala	Leu	130	135	140	
15	Ala	Ala	Thr	Leu	Phe	Lys	Lys	Gly	Val	Lys	Arg	Arg	Asn	Lys	Gln	His	145	150	155	160
	Gln	Glu	Gly	Leu	Gly	Val	Val	Ser	Thr	Thr	Tyr	Lys	Lys	Val	Leu	His	165	170	175	
20	Trp	Ser	Leu	Asn	His	Lys	Trp	Ile	Val	Ile	Ile	Leu	Ser	Thr	Leu	Ile	180	185	190	
	Leu	Val	Ala	Thr	Ile	Val	Phe	Gly	Gly	Pro	Arg	Leu	Gly	Thr	Ser	Phe	195	200	205	
25	Ile	Ser	Ala	Gly	Asp	Asp	Lys	Phe	Leu	Ala	Ile	Thr	Tyr	Thr	Pro	Lys	210	215	220	
	Pro	Gly	Glu	Thr	Glu	Gln	Ala	Val	Leu	Asn	His	Ala	Lys	Asp	Val	Glu	225	230	235	240
30	Lys	Tyr	Leu	Lys	Gln	Lys	Lys	His	Val	Lys	Thr	Ile	Gln	Tyr	Ser	Val	245	250	255	
35	Gly	Gly	Ser	Ser	Pro	Val	Asp	Pro	Thr	Gly	Ser	Thr	Asn	Ser	Met	Ala	260	265	270	
	Ile	Met	Val	Glu	Tyr	Asp	Asn	Asp	Thr	Pro	Asn	Phe	Asp	Val	Glu	Ala	275	280	285	
40	Asp	Lys	Val	Ile	Lys	His	Ala	Asp	Gly	Phe	Lys	His	Pro	Gly	Glu	Trp	290	295	300	
	Lys	Asn	Gln	Asp	Leu	Gly	Thr	Gly	Ala	Gly	Asn	Lys	Ser	Val	Glu	Val	305	310	315	320
45	Thr	Val	Lys	Gly	Pro	Ser	Met	Asp	Ala	Ile	Lys	Ser	Thr	Val	Lys	Asp	325	330	335	
	Ile	Glu	Gln	Lys	Met	Lys	Gln	Val	Lys	Gly	Leu	Ala	Asn	Val	Lys	Ser	340	345	350	
50	Asp	Leu	Ser	Gln	Thr	Tyr	Asp	Gln	Tyr	Glu	Ile	Lys	Val	Asp	Gln	Asn	355	360	365	
55	Lys	Ala	Ala	Glu	Asn	Gly	Ile	Ser	Ala	Ser	Gln	Leu	Ala	Met	His	Leu	370	375	380	

Asn Glu Asn Leu Pro Glu Lys Thr Val Thr Thr Val Lys Glu Asn Gly  
 385 390 395 400

Lys Thr Val Asp Val Lys Val Lys Gln Asn Lys Gln Thr Ala  
 405 410

## (2) INFORMATION FOR SEQ ID NO:5247:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 555 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5247:

Gly Lys Pro Phe Ile Ile Gly Leu Gly Asp Ile Ile Val Lys Lys Leu  
 1 5 10 15  
 Thr Thr Ile Leu Phe Gln Tyr Lys Ile Phe Pro Val Leu Met Phe Leu  
 20 25 30  
 Val Ser Thr Gly Leu Gly Ile Ile Val Ile Thr Gln Asn Ile Leu Ile  
 35 40 45  
 Ala Asp Phe Leu Ala Lys Ile Ile Arg His Gln Phe Gln Gly Leu Trp  
 50 55 60  
 Ile Val Leu Phe Ile Leu Leu Gly Val Leu Leu Leu Arg Ala Thr Val  
 65 70 75 80  
 Gln Phe Leu Asn Gln Trp Leu Gly Asp Thr Leu Ala Phe Lys Val Lys  
 85 90 95  
 His Met Leu Arg Gln Arg Val Ile Tyr Lys Asn Asn Gly His Pro Ile  
 100 105 110  
 Gly Glu Gln Met Thr Ile Leu Thr Glu Asn Ile Asp Gly Leu Ala Pro  
 115 120 125  
 Phe Tyr Lys Ser Tyr Leu Pro Gln Val Phe Lys Ser Met Met Val Pro  
 130 135 140  
 Leu Ile Ile Ile Ile Ala Met Phe Phe Ile His Phe Asn Thr Ala Leu  
 145 150 155 160  
 Ile Met Leu Ile Thr Ala Pro Phe Ile Pro Leu Phe Tyr Ile Ile Phe  
 165 170 175  
 Gly Leu Lys Thr Arg Asp Glu Ser Lys Asp Gln Met Thr Tyr Leu Asn  
 180 185 190  
 Gln Phe Ser Gln Arg Phe Leu Asn Ile Ala Lys Gly Leu Val Thr Leu  
 195 200 205

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Lys Leu Phe Asn Arg Thr Glu Gln Thr Glu Lys His Ile Tyr Asp Asp  
 210 215 220  
 5 Ser Thr Gln Phe Arg Thr Leu Thr Met Arg Ile Leu Arg Ser Ala Phe  
 225 230 235 240  
 Leu Ser Gly Leu Met Leu Glu Phe Ile Ser Met Leu Gly Ile Gly Leu  
 245 250 255  
 10 Val Ala Leu Glu Ala Thr Leu Ser Leu Val Val Phe His Asn Ile Asp  
 260 265 270  
 Phe Lys Thr Ala Ala Ile Ala Ile Ile Leu Ala Pro Glu Phe Tyr Asn  
 275 280 285  
 15 Ala Ile Lys Asp Leu Gly Gln Ala Phe His Thr Gly Lys Gln Ser Glu  
 290 295 300  
 Gly Ala Ser Asp Val Val Phe Glu Phe Leu Glu Gln Pro Asn Tyr Asn  
 305 310 315 320  
 20 Asn Glu Phe Leu Leu Lys Tyr Glu Glu Asn Gln Lys Pro Phe Ile Gln  
 325 330 335  
 Leu Thr Asp Ile Ser Phe Arg Tyr Asp Asp Ser Asp Arg Leu Val Leu  
 340 345 350  
 25 Asn Asp Leu Asn Leu Glu Ile Phe Lys Gly Asp Gln Ile Ala Leu Val  
 355 360 365  
 Gly Pro Ser Gly Ala Gly Lys Ser Thr Leu Thr His Leu Ile Ala Gly  
 370 375 380  
 30 Val Tyr Gln Pro Thr Ile Gly Thr Ile Ser Thr Asn Gln Arg Asp Leu  
 385 390 395 400  
 Asn Ile Gly Ile Leu Ser Gln Gln Pro Tyr Ile Phe Ser Ala Ser Ile  
 405 410 415  
 35 Lys Glu Asn Ile Thr Met Phe Lys Asp Ile Glu Asn Asn Thr Ile Glu  
 420 425 430  
 Glu Val Leu Asp Glu Val Gly Leu Leu Asp Lys Val Gln Ser Phe Thr  
 435 440 445  
 40 Lys Gly Ile Asn Thr Ile Ile Gly Glu Gly Gly Glu Met Leu Ser Gly  
 450 455 460  
 45 Gly Gln Met Arg Arg Ile Glu Leu Cys Arg Leu Leu Val Met Lys Pro  
 465 470 475 480  
 Asp Leu Val Ile Phe Asp Glu Pro Ala Thr Gly Leu Asp Ile Gln Thr  
 485 490 495  
 50 Glu His Met Ile Gln Asn Val Leu Phe Gln His Phe Lys Asp Thr Thr  
 500 505 510  
 Met Ile Val Ile Ala His Arg Asp Asn Thr Ile Arg His Leu Gln Arg  
 515 520 525  
 55

Arg Leu Tyr Ile Glu Asn Gly Arg Leu Ile Ala Asp Asp Arg Asn Ile  
 530 535 540

Ser Val Asn Ile Thr Glu Asn Gly Asp Asp Leu  
 545 550 555

## (2) INFORMATION FOR SEQ ID NO:5248:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5248:

Val Trp Lys Leu Lys Met Arg Trp Ile Lys Arg Lys Lys Lys Asn Phe  
 1 5 10 15  
 Leu Asn Ser Lys Phe Asn Phe Asn Asn Gly Lys Ile Ala Thr Tyr Leu  
 20 25 30  
 Tyr Lys Glu Arg Thr Ala Met Trp Asn Lys Asn Arg Leu Thr Gln Met  
 35 40 45  
 Leu Ser Ile Glu Tyr Pro Ile Ile Gln Ala Gly Met Ala Gly Ser Thr  
 50 55 60  
 Thr Pro Lys Leu Val Ala Ser Val Ser Asn Ser Gly Gly Leu Gly Thr  
 65 70 75 80  
 Ile Gly Ala Gly Tyr Phe Asn Thr Gln Gln Leu Glu Asp Glu Ile Asp  
 85 90 95  
 Tyr Val Arg Gln Leu Thr Ser Asn Ser Phe Gly Val Asn Val Phe Val  
 100 105 110  
 Pro Ser Gln Gln Ser Tyr Thr Ser Ser Gln Ile Glu Asn Met Asn Ala  
 115 120 125  
 Trp Leu Lys Pro Tyr Arg Arg Ala Leu His Leu Glu Glu Pro Val Val  
 130 135 140  
 Lys Ile Thr Glu Glu Gln Gln Phe Lys Cys His Ile Asp Thr Ile Ile  
 145 150 155 160  
 Lys Lys Gln Val Pro Val Cys Cys Phe Thr Phe Gly Ile Pro Ser Glu  
 165 170 175  
 Gln Ile Ile Ser Arg Leu Lys Ala Ala Asn Val Lys Leu Ile Gly Thr  
 180 185 190  
 Ala Thr Ser Val Asp Glu Ala Ile Ala Asn Glu Lys Ala Gly Met Asp  
 195 200 205

Ala Ile Val Ala Gln Gly Ser Glu Ala Gly Gly His Arg Gly Ser Phe  
210 215 220

5 Leu Lys Pro Lys Asn Gln Leu Pro Met Val Gly Thr Ile Ser Leu Val  
225 230 235 240

Pro Gln Ile Val Asp Val Val Ser Ile Pro Val Ile Ala Ala Gly Gly  
245 250 255

10 Ile Met Asp Gly Arg Gly Val Leu Ala Ser Ile Val Leu Gly Ala Glu  
260 265 270

Gly Val Gln Met Gly Thr Ala Phe Leu Thr Ser Gln Asp Ser Asn Ala  
275 280 285

15 Ser Glu Leu Leu Arg Asp Ala Ile Ile Asn Ser Lys Glu Thr Asp Thr  
290 295 300

Val Ile Thr Lys Ala Phe Ser Gly Lys Leu Ala Arg Gly Ile Asn Asn  
305 310 315 320

20 Arg Phe Ile Glu Glu Met Ser Gln Tyr Glu Gly Asp Ile Pro Asp Tyr  
325 330 335

Pro Ile Gln Asn Glu Leu Thr Ser Ser Ile Arg Lys Ala Ala Ala Asn  
340 345 350

25 Ile Gly Asp Lys Glu Leu Ile His Met Trp Ser Gly Gln Ser Pro Arg  
355 360 365

Leu Ala Thr Thr His Pro Ala Asn Thr Ile Met Ser Asn Ile Ile Asn  
370 375 380

30 Gln Ile Asn Gln Ile Met Gln Tyr Lys  
385 390

## (2) INFORMATION FOR SEQ ID NO:5249:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 936 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5249:

Asn Asp Phe Leu Lys Arg Gly Asn Lys Met Asn Met Lys Lys Lys Glu  
1 5 10 15

Lys His Ala Ile Arg Lys Lys Ser Ile Gly Val Ala Ser Val Leu Val  
20 25 30

Gly Thr Leu Ile Gly Phe Gly Leu Leu Ser Ser Lys Glu Ala Asp Ala  
35 40 45

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	Ser	Glu	Asn	Ser	Val	Thr	Gln	Ser	Asp	Ser	Ala	Ser	Asn	Glu	Ser	Lys	
	50						55					60					
5	Ser	Asn	Asp	Ser	Ser	Ser	Val	Ser	Ala	Ala	Pro	Lys	Thr	Asp	Asp	Thr	
	65					70				75						80	
	Asn	Val	Ser	Asp	Thr	Lys	Thr	Ser	Ser	Asn	Thr	Asn	Asn	Gly	Glu	Thr	
					85					90					95		
10	Ser	Val	Ala	Gln	Asn	Pro	Ala	Gln	Gln	Glu	Thr	Thr	Gln	Ser	Ser	Ser	
				100					105					110			
	Thr	Asn	Ala	Thr	Thr	Glu	Glu	Thr	Pro	Val	Thr	Gly	Glu	Ala	Thr	Thr	
			115					120					125				
15	Thr	Thr	Thr	Asn	Gln	Ala	Asn	Thr	Pro	Ala	Thr	Thr	Gln	Ser	Ser	Asn	
		130					135						140				
	Thr	Asn	Ala	Glu	Glu	Leu	Val	Asn	Gln	Thr	Ser	Asn	Glu	Thr	Thr	Ser	
	145					150					155					160	
20	Asn	Asp	Thr	Asn	Thr	Val	Ser	Ser	Val	Asn	Ser	Pro	Gln	Asn	Ser	Thr	
					165					170					175		
	Asn	Ala	Glu	Asn	Val	Ser	Thr	Thr	Gln	Asp	Thr	Ser	Thr	Glu	Ala	Thr	
25				180					185					190			
	Pro	Ser	Asn	Asn	Glu	Ser	Ala	Pro	Gln	Ser	Thr	Asp	Ala	Ser	Asn	Lys	
			195					200					205				
30	Asp	Val	Val	Asn	Gln	Ala	Val	Asn	Thr	Ser	Ala	Pro	Arg	Met	Arg	Ala	
		210					215						220				
	Phe	Ser	Leu	Ala	Ala	Val	Ala	Ala	Asp	Ala	Pro	Val	Ala	Gly	Thr	Asp	
	225					230					235					240	
35	Ile	Thr	Asn	Gln	Leu	Thr	Asn	Val	Thr	Val	Gly	Ile	Asp	Ser	Gly	Thr	
					245						250				255		
	Thr	Val	Tyr	Pro	His	Gln	Ala	Gly	Tyr	Val	Lys	Leu	Asn	Tyr	Gly	Phe	
				260					265					270			
40	Ser	Val	Pro	Asn	Ser	Ala	Val	Lys	Gly	Asp	Thr	Phe	Lys	Ile	Thr	Val	
			275					280					285				
	Pro	Lys	Glu	Leu	Asn	Leu	Asn	Gly	Val	Thr	Ser	Thr	Ala	Lys	Val	Pro	
		290					295					300					
45	Pro	Ile	Met	Ala	Gly	Asp	Gln	Val	Leu	Ala	Asn	Gly	Val	Ile	Asp	Ser	
	305					310					315					320	
	Asp	Gly	Asn	Val	Ile	Tyr	Thr	Phe	Thr	Asp	Tyr	Val	Asn	Thr	Lys	Asp	
					325					330					335		
50	Asp	Val	Lys	Ala	Thr	Leu	Thr	Met	Pro	Ala	Tyr	Ile	Asp	Pro	Glu	Asn	
				340					345					350			
	Val	Lys	Lys	Thr	Gly	Asn	Val	Thr	Leu	Ala	Thr	Gly	Ile	Gly	Ser	Thr	
55			355					360					365				



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	Thr	Ala	Asn	Lys	Thr	Val	Leu	Val	Asp	Tyr	Glu	Lys	Tyr	Gly	Lys	Phe	
	370						375					380					
5	Tyr	Asn	Leu	Ser	Ile	Lys	Gly	Thr	Ile	Asp	Gln	Ile	Asp	Lys	Thr	Asn	
	385					390					395					400	
	Asn	Thr	Tyr	Arg	Gln	Thr	Ile	Tyr	Val	Asn	Pro	Ser	Gly	Asp	Asn	Val	
					405					410					415		
10	Ile	Ala	Pro	Val	Leu	Thr	Gly	Asn	Leu	Lys	Pro	Asn	Thr	Asp	Ser	Asn	
					420					425					430		
	Ala	Leu	Ile	Asp	Gln	Gln	Asn	Thr	Ser	Ile	Lys	Val	Tyr	Lys	Val	Asp	
					435					440				445			
15	Asn	Ala	Ala	Asp	Leu	Ser	Glu	Ser	Tyr	Phe	Val	Asn	Pro	Glu	Asn	Phe	
					450					455				460			
	Glu	Asp	Val	Thr	Asn	Ser	Val	Asn	Ile	Thr	Phe	Pro	Asn	Pro	Asn	Gln	
	465					470					475					480	
20	Tyr	Lys	Val	Glu	Phe	Asn	Thr	Pro	Asp	Asp	Gln	Ile	Thr	Thr	Pro	Tyr	
					485					490						495	
	Ile	Val	Val	Val	Asn	Gly	His	Ile	Asp	Pro	Asn	Ser	Lys	Gly	Asp	Leu	
25					500					505					510		
	Ala	Leu	Arg	Ser	Thr	Leu	Tyr	Gly	Tyr	Asn	Ser	Asn	Ile	Ile	Trp	Arg	
					515					520					525		
	Ser	Met	Ser	Trp	Asp	Asn	Glu	Val	Ala	Phe	Asn	Asn	Gly	Ser	Gly	Ser	
30					530					535				540			
	Gly	Asp	Gly	Ile	Asp	Lys	Pro	Val	Val	Pro	Glu	Gln	Pro	Asp	Glu	Pro	
	545					550					555					560	
35	Gly	Glu	Ile	Glu	Pro	Ile	Pro	Glu	Asp	Ser	Asp	Ser	Asp	Pro	Gly	Ser	
					565					570					575		
	Asp	Ser	Gly	Ser	Asp	Ser	Asn	Ser	Asp	Ser	Gly	Ser	Asp	Ser	Gly	Ser	
					580					585					590		
40	Asp	Ser	Thr	Ser	Asp	Ser	Gly	Ser	Asp	Ser	Ala	Ser	Asp	Ser	Asp	Ser	
					595					600				605			
	Ala	Ser	Asp	Ser	Asp	Ser	Ala	Ser	Asp	Ser	Asp	Ser	Ala	Ser	Asp	Ser	
					610					615				620			
45	Asp	Ser	Ala	Ser	Asp	Ser	Asp	Ser	Asp	Asn	Asp	Ser	Asp	Ser	Asp	Ser	
	625					630					635					640	
	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	
					645					650					655		
50	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	
					660					665				670			
	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	
55					675					680				685			

Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser  
 690 695 700  
 5 Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser  
 705 710 715 720  
 Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser  
 725 730 735  
 10 Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser  
 740 745 750  
 Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser  
 755 760 765  
 15 Asp Ser Asp Ser Asp Ser Asp Ser Ala Ser Asp Ser Asp Ser Asp Ser Asp Ser  
 770 775 780  
 Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser  
 20 785 790 795 800  
 Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser  
 805 810 815  
 25 Glu Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser  
 820 825 830  
 Asp Ser Asp Ser Asp Ser Asp Ser Ala Ser Asp Ser Asp Ser Asp Ser Gly Ser  
 835 840 845  
 30 Asp Ser Asp Ser Ser Ser Asp Ser Asp Ser Glu Ser Asp Ser Asn Ser  
 850 855 860  
 Asp Ser Glu Ser Val Ser Asn Asn Asn Val Val Pro Pro Asn Ser Pro  
 35 865 870 875 880  
 Lys Asn Gly Thr Asn Ala Ser Asn Lys Asn Glu Ala Lys Asp Ser Lys  
 885 890 895  
 40 Glu Pro Leu Pro Asp Thr Gly Ser Glu Asp Glu Ala Asn Thr Ser Leu  
 900 905 910  
 Ile Trp Gly Leu Leu Ala Ser Ile Gly Ser Leu Leu Leu Phe Arg Arg  
 915 920 925  
 45 Lys Lys Glu Asn Lys Asp Lys Lys  
 930 935

## (2) INFORMATION FOR SEQ ID NO:5250:

- 50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 194 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 55 (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5250:

5 Val Ser Lys Leu Lys Lys Glu Ile Leu Glu Trp Ile Ile Ser Ile Ala  
 1 5 10 15  
 Val Ala Phe Val Ile Leu Phe Ile Val Gly Lys Phe Ile Val Thr Pro  
 20 25 30  
 10 Tyr Thr Ile Lys Gly Glu Ser Met Asp Pro Thr Leu Lys Asp Gly Glu  
 35 40 45  
 Arg Val Ala Val Asn Ile Val Gly Tyr Lys Thr Gly Gly Leu Glu Lys  
 50 55 60  
 15 Gly Asn Val Val Val Phe His Ala Asn Lys Asn Asp Asp Tyr Val Lys  
 65 70 75 80  
 Arg Val Ile Gly Val Pro Gly Asp Lys Val Glu Tyr Lys Asn Asp Thr  
 85 90 95  
 20 Leu Tyr Val Asn Gly Lys Lys Gln Asp Glu Pro Tyr Leu Asn Tyr Asn  
 100 105 110  
 Leu Lys His Lys Gln Gly Asp Tyr Ile Thr Gly Thr Phe Gln Val Lys  
 115 120 125  
 25 Asp Leu Pro Asn Ala Asn Pro Lys Ser Asn Val Ile Pro Lys Gly Lys  
 130 135 140  
 Tyr Leu Val Leu Gly Asp Asn Arg Glu Val Ser Lys Asp Ser Arg Ala  
 145 150 155 160  
 Phe Gly Leu Ile Asp Glu Asp Gln Ile Val Gly Lys Val Ser Phe Gln  
 165 170 175  
 35 Val Leu Ala His Phe Ser Glu Phe Gln Thr Ser Ile Ser Xaa Leu Lys  
 180 185 190  
 Ile Leu

40

## (2) INFORMATION FOR SEQ ID NO:5251:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 559 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

45

## (ii) MOLECULE TYPE: protein

50

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5251:

55

Leu Lys Ala Xaa Tyr Ala Lys Leu Asp Asp Val Ser Lys Phe Glu Asp  
 1 5 10 15

Val Thr Asp Asn Met Ser Leu Asp Phe Asp Thr Asn Gly Gly Tyr Ser  
 20 25 30  
 5 Leu Asn Phe Asn Asn Leu Asp Gln Ser Lys Asn Tyr Val Ile Lys Tyr  
 35 40 45  
 Glu Gly Tyr Tyr Asp Ser Asn Ala Ser Asn Leu Glu Phe Gln Thr His  
 50 55 60  
 10 Leu Phe Gly Tyr Tyr Asn Tyr Tyr Tyr Thr Ser Asn Leu Thr Trp Lys  
 65 70 75 80  
 Asn Gly Val Ala Phe Tyr Ser Asn Asn Ala Gln Gly Asp Gly Lys Asp  
 85 90 95  
 15 Lys Leu Lys Glu Pro Ile Ile Glu His Ser Thr Pro Ile Glu Leu Glu  
 100 105 110  
 Phe Lys Ser Glu Pro Pro Val Glu Lys His Glu Leu Thr Gly Thr Ile  
 115 120 125  
 20 Glu Glu Ser Asn Asp Ser Lys Pro Ile Asp Phe Glu Tyr His Thr Ala  
 130 135 140  
 25 Val Glu Gly Ala Glu Gly His Ala Glu Gly Thr Ile Glu Thr Glu Glu  
 145 150 155 160  
 Asp Ser Ile His Val Asp Phe Glu Glu Ser Thr His Glu Asn Ser Lys  
 165 170 175  
 30 His His Ala Asp Val Val Glu Tyr Glu Glu Asp Thr Asn Pro Gly Gly  
 180 185 190  
 Gly Gln Val Thr Thr Glu Ser Asn Leu Val Glu Phe Asp Glu Asp Ser  
 195 200 205  
 35 Thr Lys Gly Ile Val Thr Gly Ala Val Ser Asp His Thr Thr Ile Glu  
 210 215 220  
 Asp Thr Lys Glu Tyr Thr Thr Glu Ser Asn Leu Ile Glu Leu Val Asp  
 225 230 235 240  
 40 Glu Leu Pro Glu Glu His Gly Gln Ala Gln Gly Pro Ile Glu Glu Ile  
 245 250 255  
 Thr Glu Asn Asn His His Ile Ser His Ser Gly Leu Gly Thr Glu Asn  
 260 265 270  
 45 Gly His Gly Asn Tyr Gly Val Ile Glu Glu Ile Glu Glu Asn Ser His  
 275 280 285  
 50 Val Asp Ile Lys Ser Glu Leu Gly Tyr Glu Gly Gly Gln Asn Ser Gly  
 290 295 300  
 Asn Gln Ser Phe Glu Glu Asp Thr Glu Glu Asp Lys Pro Lys Tyr Glu  
 305 310 315 320  
 55 Gln Gly Gly Asn Ile Val Asp Ile Asp Phe Asp Ser Val Pro Gln Ile  
 325 330 335

His Gly Gln Asn Asn Gly Asn Gln Ser Phe Glu Glu Asp Thr Glu Lys  
 340 345 350  
 Asp Lys Pro Lys Tyr Glu Gln Gly Gly Asn Ile Ile Asp Ile Asp Phe  
 355 360 365  
 Asp Ser Val Pro His Ile His Gly Phe Asn Lys His Thr Glu Ile Ile  
 370 375 380  
 Glu Glu Asp Thr Asn Lys Asp Lys Pro Asn Tyr Gln Phe Gly Gly His  
 385 390 395 400  
 Asn Ser Val Asp Phe Glu Glu Asp Thr Leu Pro Gln Val Ser Gly His  
 405 410 415  
 Asn Glu Gly Gln Gln Thr Ile Glu Glu Asp Thr Thr Pro Pro Ile Val  
 420 425 430  
 Pro Pro Thr Pro Pro Thr Pro Glu Val Pro Ser Glu Pro Glu Thr Pro  
 435 440 445  
 Thr Pro Pro Thr Pro Glu Val Pro Ser Glu Pro Glu Thr Pro Thr Pro  
 450 455 460  
 Pro Thr Pro Glu Val Pro Thr Glu Pro Gly Lys Pro Ile Pro Pro Ala  
 465 470 475 480  
 Lys Glu Glu Pro Lys Lys Pro Ser Lys Pro Val Glu Gln Gly Lys Val  
 485 490 495  
 Val Thr Pro Val Ile Glu Ile Asn Glu Lys Val Lys Ala Val Val Pro  
 500 505 510  
 Thr Lys Lys Ala Gln Ser Lys Lys Ser Glu Leu Pro Glu Thr Gly Gly  
 515 520 525  
 Glu Glu Ser Thr Asn Asn Gly Met Leu Phe Gly Gly Leu Phe Ser Ile  
 530 535 540  
 Leu Gly Leu Ala Leu Leu Arg Arg Asn Lys Lys Asn His Lys Ala  
 545 550 555

## (2) INFORMATION FOR SEQ ID NO:5252:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5252:

Thr Lys Asn Glu Lys Ile Asn Asp Val Thr Ala Val Ala Glu Lys Glu  
 1 5 10 15

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Val Val Glu Glu Thr Lys Ala Thr Gly Thr Asp Val Thr Asn Lys Val  
20 25 30

5 Glu Val Glu Glu Gly Ser Glu Ile Val Gly His Lys Gln Asp Thr Asn  
35 40 45

Val Val Asn Pro His Asn Ala Glu Arg Val Thr Leu Lys Tyr Lys Trp  
50 55 60

10 Lys Phe Gly Glu Gly Ile Lys Ala Gly Asp Tyr Phe Asp Phe Thr Leu  
65 70 75 80

Ser Asp Asn Val Glu Thr His Gly Ile Ser Thr Leu Arg Lys Val Pro  
85 90 95

15 Glu Ile Lys Ser Thr Asp Gly Gln Val Met Ala Thr Gly Glu Ile Ile  
100 105 110

Gly Glu Arg Lys Val Arg Tyr Thr Phe Lys Glu Tyr Val Gln Glu Lys  
115 120 125

20 Lys Asp Leu Thr Ala Glu Leu Ser Leu Asn Leu Phe Ile Asp Pro Thr  
130 135 140

Thr Val Thr Gln Lys Gly Asn Gln Asn Val Glu Val Lys Leu Gly Glu  
145 150 155 160

25 Thr Thr Val Ser Lys Ile Phe Asn Ile Gln Tyr Leu Gly Gly Val Arg  
165 170 175

30 Asp Asn Trp Gly Val Thr Ala Asn Gly Arg Ile Asp Thr Leu Asn Lys  
180 185 190

Val Asp Gly Lys Phe Ser His Phe Ala Tyr Met Lys Pro Asn Asn Gln  
195 200 205

35 Ser Leu Ser Ser Val Thr Val Thr Gly Gln Val Thr Lys Gly Asn Lys  
210 215 220

Pro Gly Val Asn Asn Pro Thr Val Lys Val Tyr Lys His Ile Gly Ser  
225 230 235 240

40 Asp Asp Leu Ala Glu Ser Xaa Xaa Cys Lys Ala  
245 250

(2) INFORMATION FOR SEQ ID NO:5253:

45 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 163 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: protein

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5253:

1 Ile Leu His Leu Arg Glu Asn Ile Ile Val Lys Ser Asn Leu Arg Tyr  
 5 Gly Ile Arg Lys His Lys Leu Gly Ala Ala Ser Val Phe Leu Gly Thr  
 Met Ile Val Val Gly Met Gly Gln Glu Lys Glu Ala Ala Ala Ser Glu  
 10 Gln Asn Asn Thr Thr Val Glu Glu Ser Gly Ser Ser Ala Thr Glu Ser  
 Lys Ala Ser Glu Thr Gln Thr Thr Thr Asn Asn Val Asn Thr Ile Asp  
 15 Glu Thr Gln Ser Tyr Ser Ala Thr Ser Thr Glu Gln Pro Ser Gln Ser  
 Thr Gln Val Thr Thr Glu Glu Ala Pro Lys Thr Val Gln Ala Pro Lys  
 20 Val Glu Thr Ser Arg Val Asp Leu Pro Ser Glu Lys Val Ala Asp Lys  
 Glu Thr Thr Gly Thr Gln Val Asp Ile Ala Gln Pro Ser Asn Val Ser  
 25 Glu Ile Lys Pro Arg Met Lys Arg Ser Met Thr Leu Gln Gln Leu Gln  
 Arg Lys Lys

## (2) INFORMATION FOR SEQ ID NO:5254:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1027 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5254:

1 Ile Leu His Leu Lys Gly Asp Ile Ile Val Lys Asn Asn Leu Arg Tyr  
 5 Gly Ile Arg Lys His Lys Leu Gly Ala Ala Ser Val Phe Leu Gly Thr  
 20 Met Ile Val Val Gly Met Gly Gln Asp Lys Glu Ala Ala Ala Ser Glu  
 35 Gln Lys Thr Thr Thr Val Glu Asn Gly Asn Ser Ala Thr Asp Asn  
 50 55 60

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Lys Thr Ser Glu Thr Gln Thr Thr Ala Thr Asn Val Asn His Ile Glu  
 65 70 75 80  
 5 Glu Thr Gln Ser Tyr Asn Ala Thr Val Thr Glu Gln Pro Ser Asn Ala  
 85 90 95  
 Thr Gln Val Thr Thr Glu Glu Ala Pro Lys Ala Val Gln Ala Pro Gln  
 100 105 110  
 10 Thr Ala Gln Pro Ala Asn Ile Glu Thr Val Lys Glu Glu Val Val Lys  
 115 120 125  
 Glu Glu Ala Lys Pro Gln Val Lys Glu Thr Thr Gln Ser Gln Asp Asn  
 130 135 140  
 15 Ser Gly Asp Gln Arg Gln Val Asp Leu Thr Pro Lys Lys Ala Thr Gln  
 145 150 155 160  
 Asn Gln Val Ala Glu Thr Gln Val Glu Val Ala Gln Pro Arg Thr Ala  
 165 170 175  
 20 Ser Glu Ser Lys Pro Arg Val Thr Arg Ser Ala Asp Val Ala Glu Ala  
 180 185 190  
 Lys Glu Ala Ser Asn Ala Lys Val Glu Thr Gly Thr Asp Val Thr Ser  
 195 200 205  
 25 Lys Val Thr Val Glu Ile Gly Ser Ile Glu Gly His Asn Asn Thr Asn  
 210 215 220  
 Lys Val Glu Pro His Ala Gly Gln Arg Ala Val Leu Lys Tyr Lys Leu  
 225 230 235 240  
 Lys Phe Glu Asn Gly Leu His Gln Gly Asp Tyr Phe Asp Phe Thr Leu  
 245 250 255  
 35 Ser Asn Asn Val Asn Thr His Gly Val Ser Thr Ala Arg Lys Val Pro  
 260 265 270  
 Glu Ile Lys Asn Gly Ser Val Val Met Ala Thr Gly Glu Val Leu Glu  
 275 280 285  
 40 Gly Gly Lys Ile Arg Tyr Thr Phe Thr Asn Asp Ile Glu Asp Lys Val  
 290 295 300  
 Asp Val Thr Ala Glu Leu Glu Ile Asn Leu Phe Ile Asp Pro Lys Thr  
 305 310 315 320  
 45 Val Gln Thr Asn Gly Asn Gln Thr Ile Thr Ser Thr Leu Asn Glu Glu  
 325 330 335  
 Gln Thr Ser Lys Glu Leu Asp Val Lys Tyr Lys Asp Gly Ile Gly Asn  
 340 345 350  
 50 Tyr Tyr Ala Asn Leu Asn Gly Ser Ile Glu Thr Phe Asn Lys Ala Asn  
 355 360 365  
 55 Asn Arg Phe Ser His Val Ala Phe Ile Lys Pro Asn Asn Gly Lys Thr  
 370 375 380



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	Thr Ser Val Thr Val Thr Gly Thr Leu Met Lys Gly Ser Asn Gln Asn	385	390	395	400
5	Gly Asn Gln Pro Lys Val Arg Ile Phe Glu Tyr Leu Gly Asn Asn Glu	405	410	415	
	Asp Ile Ala Lys Ser Val Tyr Ala Asn Thr Thr Asp Thr Ser Lys Phe	420	425	430	
10	Lys Glu Val Thr Ser Asn Met Ser Gly Asn Leu Asn Leu Gln Asn Asn	435	440	445	
	Gly Ser Tyr Ser Leu Asn Ile Glu Asn Leu Asp Lys Thr Tyr Val Val	450	455	460	
15	His Tyr Asp Gly Glu Tyr Leu Asn Gly Thr Asp Glu Val Asp Phe Arg	465	470	475	480
	Thr Gln Met Val Gly His Pro Glu Gln Leu Tyr Lys Tyr Tyr Tyr Asp	485	490	495	
20	Arg Gly Tyr Thr Leu Thr Trp Asp Asn Gly Leu Val Leu Tyr Ser Asn	500	505	510	
	Lys Ala Asn Gly Asn Glu Lys Asn Gly Pro Ile Ile Gln Asn Asn Lys	515	520	525	
25	Phe Glu Tyr Lys Glu Asp Thr Ile Lys Glu Thr Leu Thr Gly Gln Tyr	530	535	540	
	Asp Lys Asn Leu Val Thr Thr Val Glu Glu Glu Tyr Asp Ser Ser Thr	545	550	555	560
30	Leu Asp Ile Asp Tyr His Thr Ala Ile Asp Gly Gly Gly Tyr Val	565	570	575	
	Asp Gly Tyr Ile Glu Thr Ile Glu Glu Thr Asp Ser Ser Ala Ile Asp	580	585	590	
35	Ile Asp Tyr His Thr Ala Val Asp Ser Glu Ala Gly His Val Gly Gly	595	600	605	
	Tyr Thr Glu Ser Ser Glu Glu Ser Asn Pro Ile Asp Phe Glu Glu Ser	610	615	620	
40	Thr His Glu Asn Ser Lys His His Ala Asp Val Val Glu Tyr Glu Glu	625	630	635	640
45	Asp Thr Asn Pro Gly Gly Gly Gln Val Thr Thr Glu Ser Asn Leu Val	645	650	655	
	Glu Phe Asp Glu Glu Ser Thr Lys Gly Ile Val Thr Gly Ala Val Ser	660	665	670	
50	Asp His Thr Thr Val Glu Asp Thr Lys Glu Tyr Thr Thr Glu Ser Asn	675	680	685	
	Leu Ile Glu Leu Val Asp Glu Leu Pro Glu Glu His Gly Gln Ala Gln	690	695	700	

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Gly Pro Val Glu Glu Ile Thr Lys Asn Asn His His Ile Ser His Ser  
 705 710 715 720  
 5 Gly Leu Gly Thr Glu Asn Gly His Gly Asn Tyr Asp Val Ile Glu Glu  
 725 730 735  
 Ile Glu Glu Asn Ser His Val Asp Ile Lys Ser Glu Leu Gly Tyr Glu  
 740 745 750  
 10 Gly Gly Gln Asn Ser Gly Asn Gln Ser Phe Glu Glu Asp Thr Glu Glu  
 755 760 765  
 Asp Lys Pro Lys Tyr Glu Gln Gly Gly Asn Ile Val Asp Ile Asp Phe  
 770 775 780  
 15 Asp Ser Val Pro Gln Ile His Gly Gln Asn Lys Gly Asn Gln Ser Phe  
 785 790 795 800  
 Glu Glu Asp Thr Glu Lys Asp Lys Pro Lys Tyr Glu His Gly Gly Asn  
 805 810 815  
 20 Ile Ile Asp Ile Asp Phe Asp Ser Val Pro His Ile His Gly Phe Asn  
 820 825 830  
 Lys His Thr Glu Ile Ile Glu Glu Asp Thr Asn Lys Asp Lys Pro Ser  
 835 840 845  
 25 Tyr Gln Phe Gly Gly His Asn Ser Val Asp Phe Glu Glu Asp Thr Leu  
 850 855 860  
 Pro Lys Val Ser Gly Gln Asn Glu Gly Gln Gln Thr Ile Glu Glu Asp  
 865 870 875 880  
 30 Thr Thr Pro Pro Ile Val Pro Pro Thr Pro Pro Thr Pro Glu Val Pro  
 885 890 895  
 35 Ser Glu Pro Glu Thr Pro Thr Pro Pro Thr Pro Glu Val Pro Ser Glu  
 900 905 910  
 Pro Glu Thr Pro Thr Pro Pro Thr Pro Glu Val Pro Ser Glu Pro Glu  
 915 920 925  
 40 Thr Pro Thr Pro Pro Thr Pro Glu Val Pro Ala Glu Pro Gly Lys Pro  
 930 935 940  
 Val Pro Pro Ala Lys Glu Glu Pro Lys Lys Pro Ser Lys Pro Val Glu  
 945 950 955 960  
 45 Gln Gly Lys Val Val Thr Pro Val Ile Glu Ile Asn Glu Lys Val Lys  
 965 970 975  
 Ala Val Ala Pro Thr Lys Lys Pro Gln Ser Lys Lys Ser Glu Leu Pro  
 980 985 990  
 50 Glu Thr Gly Gly Glu Glu Ser Thr Asn Lys Gly Met Leu Phe Gly Gly  
 995 1000 1005  
 55 Leu Phe Ser Ile Leu Gly Leu Ala Leu Leu Arg Arg Asn Lys Lys Asn  
 1010 1015 1020

His Lys Ala  
1025

5 (2) INFORMATION FOR SEQ ID NO:5255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids  
(B) TYPE: amino acid  
10 (C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5255:

20 Gly Glu Lys Cys Met Phe Leu Ala Trp Asn Glu Ile Arg Arg Asn Lys  
1 5 10 15  
Leu Lys Phe Gly Leu Ile Ile Gly Val Leu Thr Met Ile Ser Tyr Leu  
20 25 30  
25 Leu Phe Leu Leu Ser Gly Leu Ala Asn Gly Leu Ile Asn Met Asn Lys  
35 40 45  
Glu Gly Ile Asp Lys Trp Gln Ala Asp Ala Ile Val Leu Asn Lys Asp  
50 55 60  
30 Ala Asn Gln Thr Val Gln Gln Ser Val Phe Asn Lys Lys Asp Ile Glu  
65 70 75 80  
Asn Lys Tyr Lys Lys Gln Ala Thr Leu Lys Gln Thr Gly Glu Ile Val  
35 85 90 95  
Ser Asn Gly His Gln Lys Asp Asn Val Leu Val Phe Gly Val Glu Lys  
100 105 110  
40 Ser Ser Phe Leu Val Pro Ser Leu Ile Glu Gly His Lys Ala Thr Lys  
115 120 125  
Asp Asn Glu Val Leu Ala Asp Glu Thr Leu Lys Asn Lys Gly Leu Lys  
45 130 135 140  
Leu Gly Asp Thr Leu Ser Leu Ser Xaa Xaa Arg  
145 150 155

50 Claims

- 55 1. Computer readable medium having recorded thereon a nucleotide sequence of the Staphylococcus aureus genome as depicted in SEQ ID NOS:1-5,191, a representative fragment thereof or a nucleotide sequence at least 95 % identical to a nucleotide sequence depicted in SEQ ID NOS:1-5,191.
2. Computer readable medium having recorded thereon any one of the fragments of SEQ ID NOS:1-5,191 depicted in Tables 2 and 3 or a degenerate variant thereof.

3. The computer readable medium of claim 1, wherein said medium is selected from the group consisting of a floppy disc, a hard disc, random access memory (RAM), read only memory (ROM), and CD-ROM.
4. The computer readable medium of claim 3, wherein said medium is selected from the group consisting of a floppy disc, a hard disc, random access memory (RAM), read only memory (ROM), and CD-ROM.
5. A computer-based system for identifying fragments of the *Staphylococcus aureus* genome of commercial importance comprising the following elements:
  - (a) a data storage means comprising the nucleotide sequence of SEQ ID NOS:1-5,191, a representative fragment thereof, or a nucleotide sequence at least 95% identical to a nucleotide sequence of SEQ ID NOS:1-5,191;
  - (b) search means for comparing a target sequence to the nucleotide sequence of the data storage means of step (a) to identify homologous sequence(s), and
  - (c) retrieval means for obtaining said homologous sequence(s) of step (b).
6. A method for identifying commercially important nucleic acid fragments of the *Staphylococcus aureus* genome comprising the step of comparing a database comprising the nucleotide sequences depicted in SEQ ID NOS:1-5,191, a representative fragment thereof, or a nucleotide sequence at least 95% identical to a nucleotide sequence of SEQ ID NOS:1-5,191 with a target sequence to obtain a nucleic acid molecule comprised of a complementary nucleotide sequence to said target sequence, wherein said target sequence is not randomly selected.
7. A method for identifying an expression modulating fragment of *Staphylococcus aureus* genome comprising the step of comparing a database comprising the nucleotide sequences depicted in SEQ ID NOS:1-5,191, a representative fragment thereof, or a nucleotide sequence at least 95% identical to the nucleotide sequence of SEQ ID NOS:1-5,191 with a target sequence to obtain a nucleic acid molecule comprised of a complementary nucleotide sequence to said target sequence, wherein said target sequence comprises sequences known to regulate gene expression.
8. A protein-encoding nucleic acid fragment of the *Staphylococcus aureus* genome, wherein said fragment comprises the nucleotide sequence of any one of the fragments of SEQ ID NOS:1-5,191 depicted in Tables 2 and 3 or a nucleotide sequence at least 95% identical to such a nucleotide sequence, or a degenerate variant of any of the aforementioned sequences.
9. The nucleic acid fragment of claim 8 which is DNA.
10. The nucleic acid fragment of claim 8 which is RNA.
11. A vector comprising a fragment of claim 8.
12. A fragment of the *Staphylococcus aureus* genome, wherein said fragment modulates the expression of an operably linked open reading frame, wherein said fragment consists of the nucleotide sequence from about 10 to 200 bases in length which is 5' to any one of the open reading frames depicted in Tables 2 and 3 or a nucleotide sequence at least 95% identical to such a nucleotide sequence or a degenerate variant of any of the aforementioned sequences.
13. A vector comprising a fragment of claim 12.
14. An organism which has been altered to contain any one of the fragments of the *Staphylococcus aureus* genome of claim 8.
15. A method for producing a polypeptide in a host cell comprising the steps of:
  - (a) incubating an organism of claim 14 under conditions where said fragment is expressed to produce said protein, and
  - (b) isolating said protein.
16. An organism which has been altered to contain any one of the fragments of the *Staphylococcus aureus* genome

of claim 12.

17. A method for regulating the expression of a nucleic acid molecule comprising the step of covalently attaching to said nucleic acid molecule a nucleic acid molecule consisting of the nucleotide sequence from about 30 to 300 bases 5' to any one of the fragments of the *Staphylococcus aureus* genome depicted in Seq ID Nos:1-5,191 and Tables 2 and 3 or a nucleotide sequence at least 95% identical to such a nucleotide sequence or a degenerate variant of any of the aforementioned sequences.
18. A nucleic acid molecule being a homolog of any of the fragments of the *Staphylococcus aureus* genome of SEQ ID NOS:1-5,191 and Tables 2 and 3, wherein said nucleic acid molecule is produced by a process comprising the steps of:
  - (a) screening a genomic DNA library using as a probe a target sequence defined by any of SEQ ID NOS: 1-5,191 and Tables 2 and 3, including fragments thereof;
  - (b) identifying members of said library which contain sequences that hybridize to said target sequence;
  - (c) isolating the nucleic acid molecules from said members identified in step (b).
19. A DNA molecule being a homolog of any one of the fragments of the *Staphylococcus aureus* genome of SEQ ID NOS:1-5,191 and Tables 2 and 3, wherein said nucleic acid molecule is produced by a process comprising the steps of:
  - (a) isolating mRNA, DNA, or cDNA produced from an organism;
  - (b) amplifying nucleic acid molecules whose nucleotide sequence is homologous to amplification primers derived from said fragment of said *Staphylococcus aureus* genome to prime said amplification;
  - (c) isolating said amplified sequences produced in step (b).
20. A polypeptide encoded by a fragment of claim 8.
21. An antibody which selectively binds to any one of the polypeptides of claim 20.
22. A kit for analyzing samples for the presence of polynucleotides derived from *Staphylococcus aureus*, comprising at least one polynucleotide containing a nucleotide sequence of any one of the fragments SEQ ID NOS:1-5,191 depicted in Tables 2 and 3 or a nucleotide sequence at least 95% identical thereto or a degenerate variant of any of the aforementioned sequences, that will hybridize to a *staphylococcus aureus* polynucleotide under stringent hybridization conditions, and a suitable container.
23. A *Staphylococcus aureus* polypeptide comprising an amino acid sequence identical to an amino acid sequence selected from the group consisting of SEQ ID NOS:5,192 to 5,255 or comprising an amino acid sequence having at least 95% identity to such a sequence.
24. A *Staphylococcus aureus* polypeptide antigen comprising at least one epitope derived from a *Staphylococcus aureus* polypeptide selected from the group consisting of SEQ ID NOS:5,192 to 5,255.
25. A polypeptide comprising at least one epitope encoded by a *Staphylococcus aureus* amino acid sequence selected from the group consisting of the epitopic sequences listed in Table 4.
26. The polypeptide of claim 24 or 26, wherein said polypeptide is fixed to a solid phase.
27. A diagnostic kit for detecting *Staphylococcus aureus* infection comprising
  - (a) an isolated polypeptide antigen of claim 24, and
  - (b) means for detecting the binding of an antibody contained in a biological fluid to said antigen.
28. A vaccine composition comprising a polypeptide of claim 24 present in a pharmaceutically acceptable carrier.
29. A method of vaccinating an individual against *Staphylococcus aureus* infection comprising, administering to an individual the vaccine composition of claim 28.

Figure 1

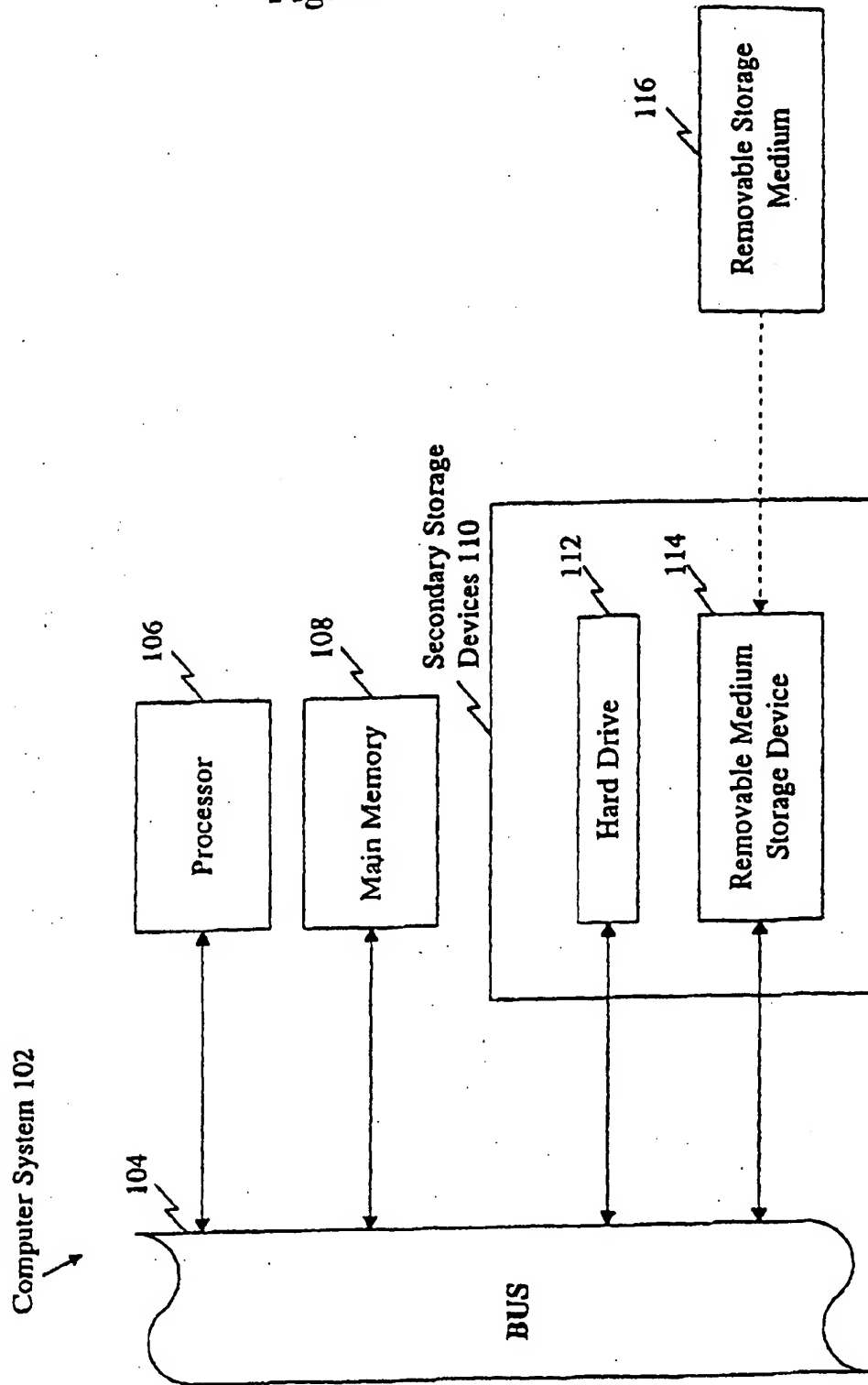


Figure 2

